Proteomics Clinical Applications

Supporting Information
for
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Comparison of two phenotypically distinct lattice corneal dystrophies caused by mutations in the transforming growth factor beta induced (*TGFBI*) gene

Control – technical replicate # 1

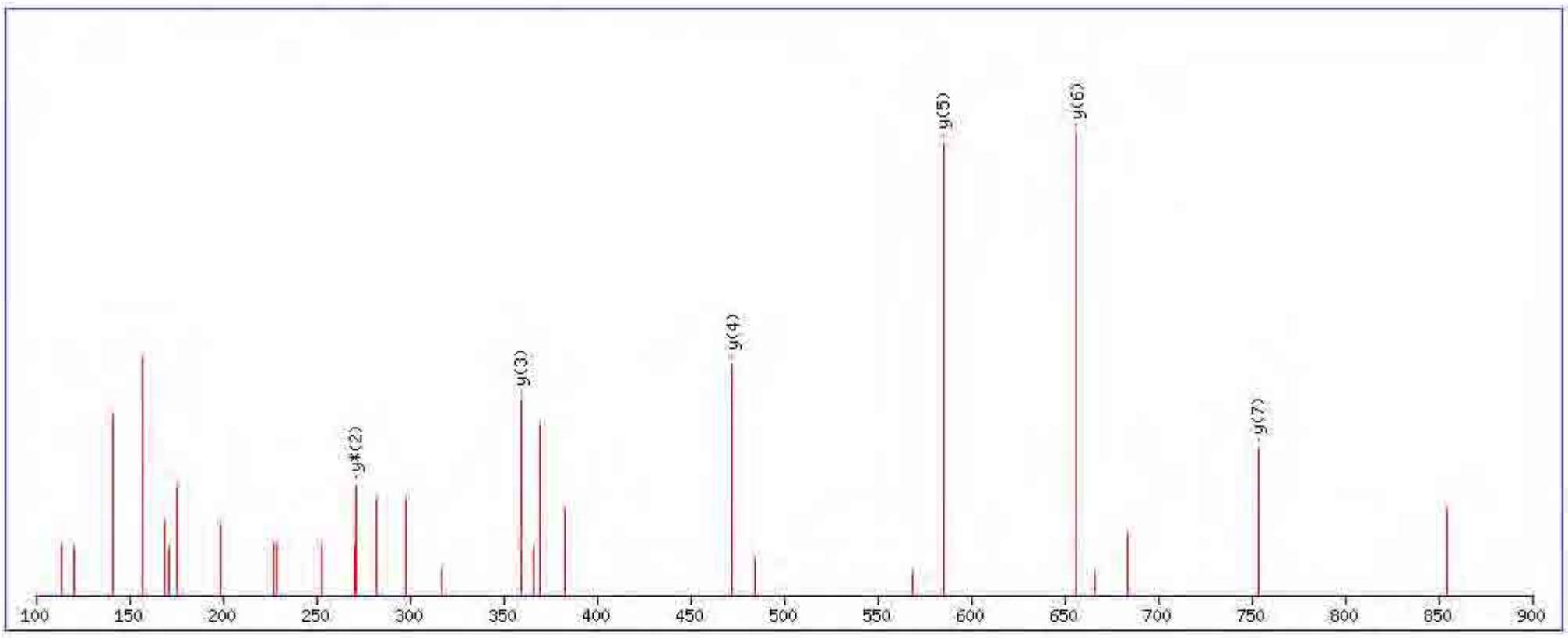
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPALIALR**
Found in **AK1C1_HUMAN**, Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1

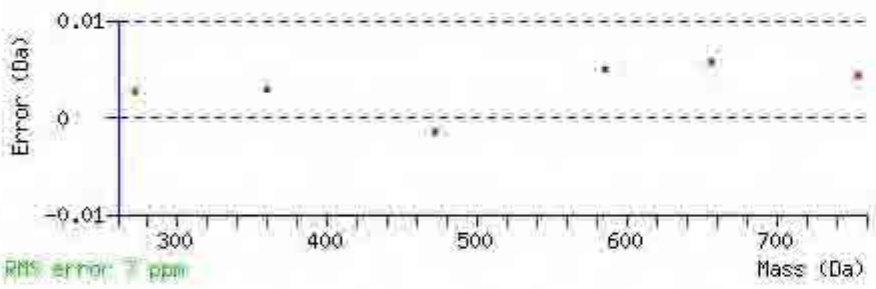
Match to Query 1405: 853.538528 from(427.776540,2+) rtinseconds(1662) index(12676)
Title: Locus:1.1.1.1754.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

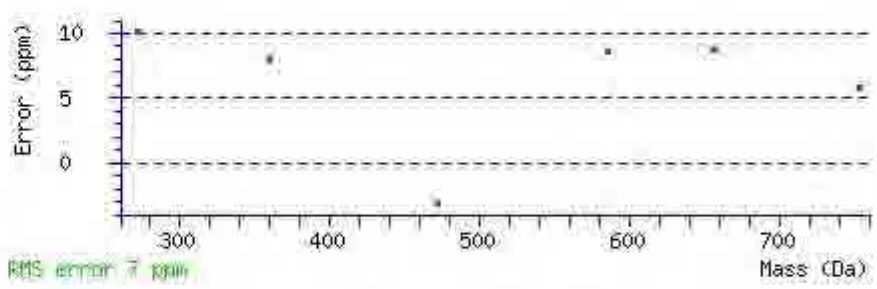
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 853.538513
Ions Score: 48 **Expect:** 0.00048
Matches : 6/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	102.054955	51.531116	84.044390	42.525833	T					8
2	199.107719	100.057497	181.097154	91.052215	P	*753.498136*	377.252706	736.471587	368.739432	7
3	270.144833	135.576055	252.134268	126.570772	A	*656.445372*	328.726324	639.418823	320.213050	6
4	383.228897	192.118087	365.218332	183.112804	L	*585.408258*	293.207767	568.381709	284.694493	5
5	496.312961	248.660119	478.302396	239.654836	I	*472.324194*	236.665735	455.297645	228.152461	4
6	567.350075	284.178676	549.339510	275.173393	A	*359.240130*	180.123703	342.213581	171.610429	3
7	680.434139	340.720708	662.423574	331.715425	L	288.203016	144.605146	271.176467	136.091872	2
8					R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of TPALIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	853.538513	0.000015	TPALIALR
16.6	853.538528	-0.000000	RLLLVGAP
16.6	853.538528	-0.000000	RLPILVQ
16.6	853.538528	-0.000000	RPLLLQV
16.6	853.538528	-0.000000	RPLLVPK
14.5	853.538513	0.000015	TALPLALR
14.1	853.538528	-0.000000	VVAIRPAI
14.0	853.538528	-0.000000	AVVLPLAR
13.0	853.538513	0.000015	LRILDPK
13.0	853.538528	-0.000000	LRLPPVK

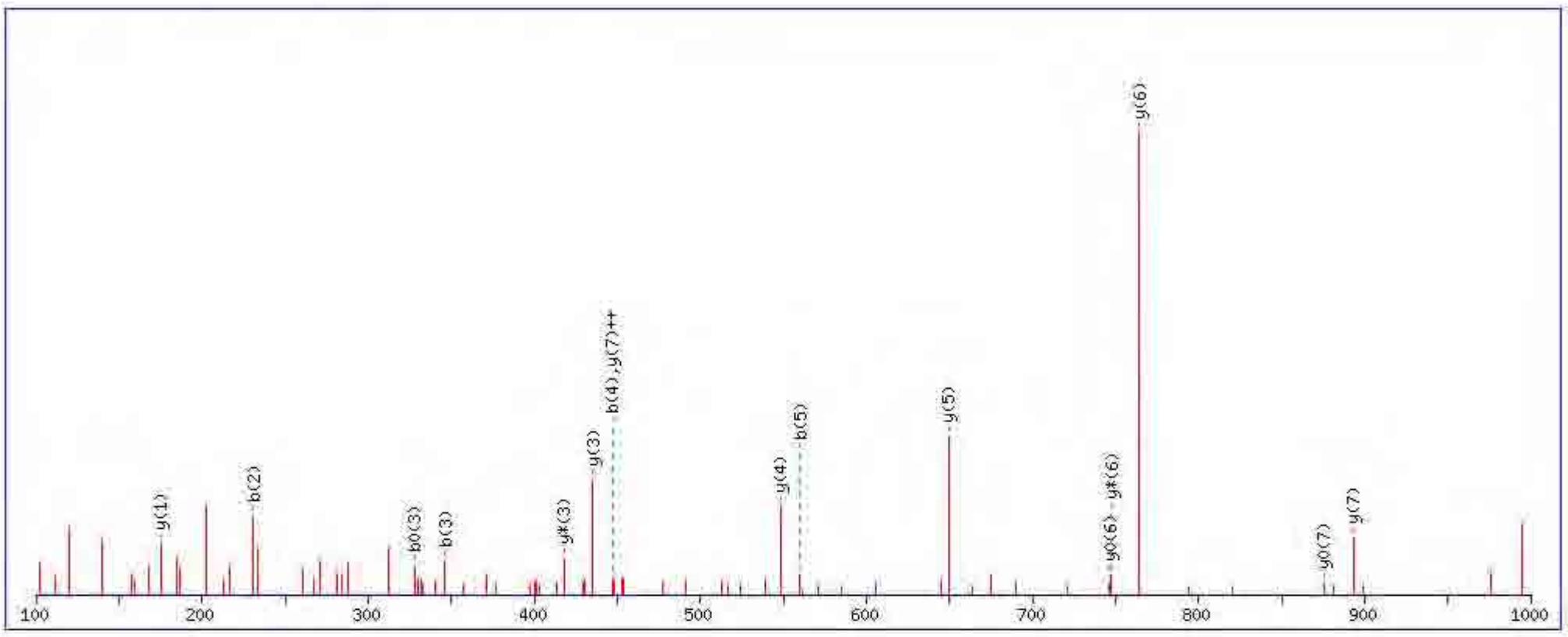
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEDTIFLR**
Found in **A1AG1_HUMAN**, Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

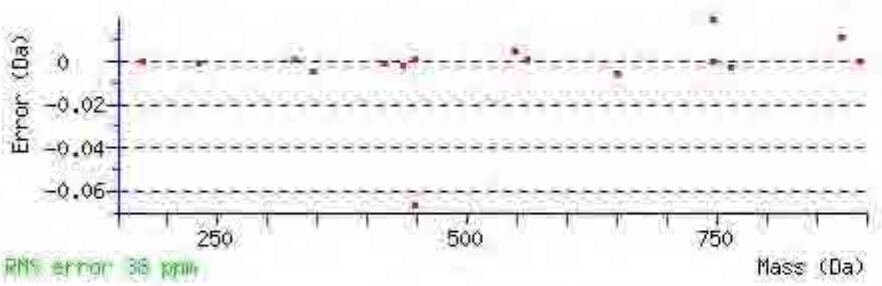
Match to Query 4127: 993.509748 from(497.762150,2+) rtinseconds(1640) index(12379)
Title: Locus:1.1.1.1742.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

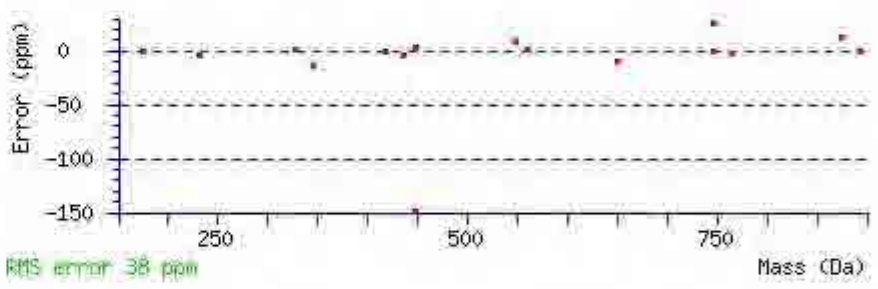
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 993.513107
Ions Score: 43 **Expect:** 0.0024
Matches : 16/62 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	231.097548	116.052412	213.086983	107.047130	E	*893.472709*	447.239993	876.446160	438.726718	875.462144	438.234710	7
3	346.124491	173.565884	328.113926	164.560601	D	*764.430116*	382.718696	747.403567	374.205422	746.419551	373.713414	6
4	447.172170	224.089723	429.161605	215.084441	T	*649.403173*	325.205225	632.376624	316.691950	631.392608	316.199942	5
5	560.256234	280.631755	542.245669	271.626473	I	*548.355494*	274.681385	531.328945	266.168111			4
6	707.324648	354.165962	689.314083	345.160680	F	*435.271430*	218.139353	418.244881	209.626079			3
7	820.408712	410.707994	802.398147	401.702712	L	288.203016	144.605146	271.176467	136.091872			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TEDTIFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	993.513107	-0.003359	TEDTIFLR
14.0	993.509933	-0.000185	GSCAKLMLR
13.5	993.506607	0.003141	TVCNFGVVR
11.1	993.501907	0.007841	FTPLTTTDV
10.5	993.501877	0.007871	LLYGDISPT
10.3	993.513092	-0.003344	LYLGSNNLT
8.8	993.501892	0.007856	TFAVTDELV
8.7	993.513077	-0.003329	TEELAYLR
8.7	993.513092	-0.003344	TEHSYPR
8.5	993.501892	0.007856	SFVLPVEST

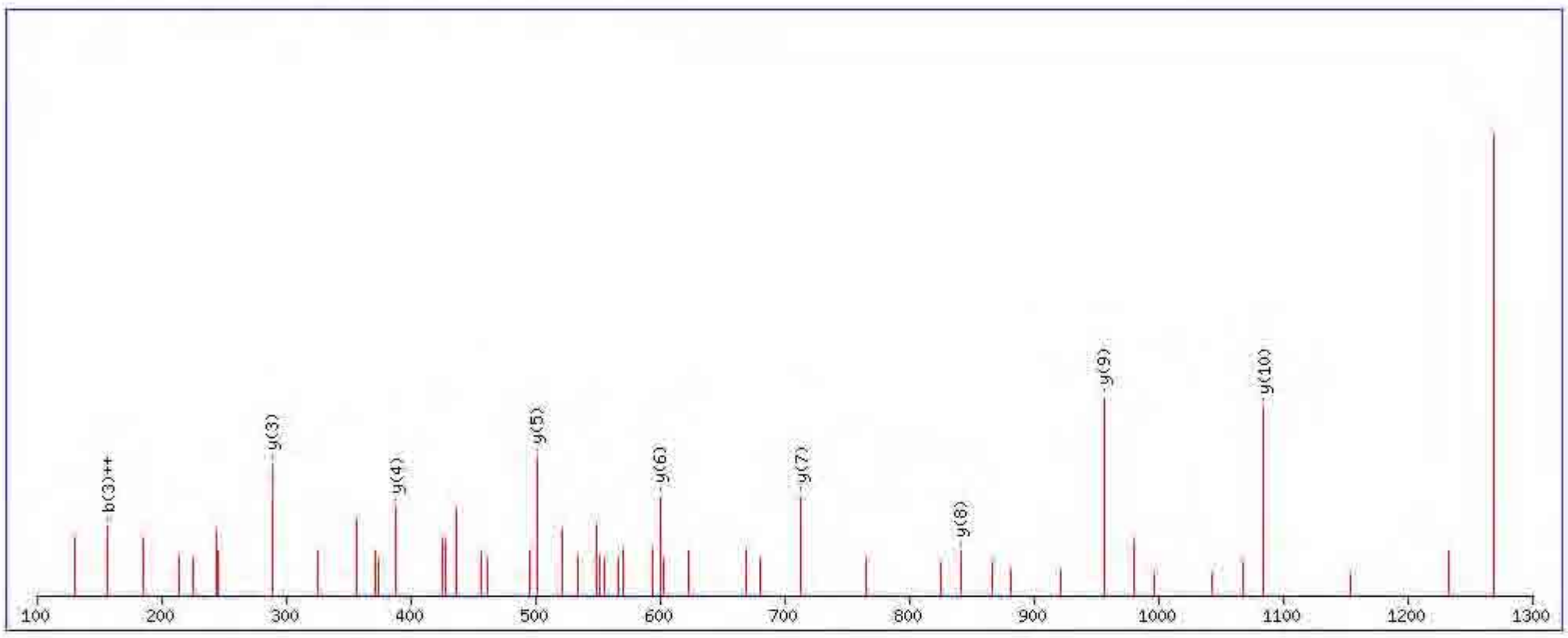
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALQDQLVLVAAK**
Found in **ANGT_HUMAN**, Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1

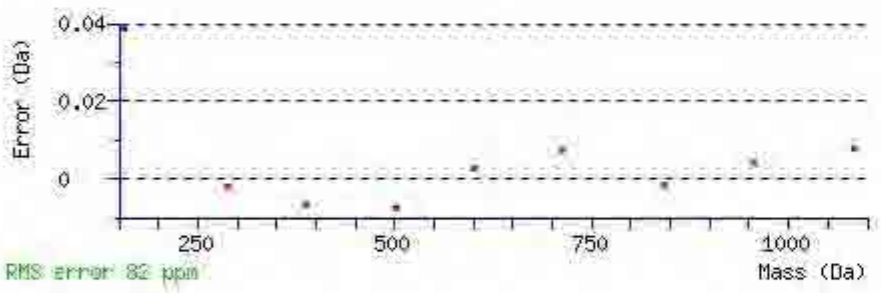
Match to Query 11275: 1267.737288 from(634.875920,2+) rtinseconds(1894) index(15136)
Title: Locus:1.1.1.1901.14
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

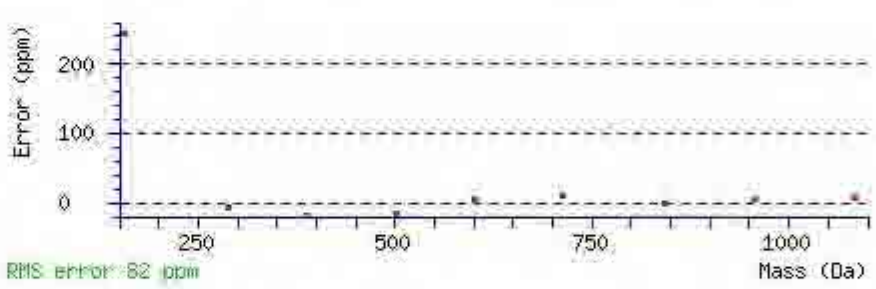
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1267.749969
Ions Score: 67 **Expect:** 2.9e-006
Matches : 9/106 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	185.128454	93.067865					L	1197.720151	599.363714	1180.693602	590.850439	1179.709586	590.358431	11
3	313.187032	157.097154	296.160483	148.583879			Q	*1084.636087*	542.821682	1067.609538	534.308407	1066.625522	533.816399	10
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	D	*956.577509*	478.792393	939.550960	470.279118	938.566944	469.787110	9
5	556.272553	278.639915	539.246004	270.126640	538.261988	269.634632	Q	*841.550566*	421.278921	824.524017	412.765646			8
6	669.356617	335.181947	652.330068	326.668672	651.346052	326.176664	L	*713.491988*	357.249632	696.465439	348.736358			7
7	768.425031	384.716154	751.398482	376.202879	750.414466	375.710871	V	*600.407924*	300.707600	583.381375	292.194325			6
8	881.509095	441.258186	864.482546	432.744911	863.498530	432.252903	L	*501.339510*	251.173393	484.312961	242.660118			5
9	980.577509	490.792393	963.550960	482.279118	962.566944	481.787110	V	*388.255446*	194.631361	371.228897	186.118086			4
10	1051.614623	526.310949	1034.588074	517.797675	1033.604058	517.305667	A	*289.187032*	145.097154	272.160483	136.583879			3
11	1122.651737	561.829506	1105.625188	553.316232	1104.641172	552.824224	A	218.149918	109.578597	201.123369	101.065322			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ALQDQLVLVAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.8	1267.749969	-0.012681	ALQDQLVLVAAK
7.3	1267.736053	0.001235	EARGAALGGVVLR
6.2	1267.724792	0.012496	SRLAKPKPNLE
6.1	1267.724823	0.012465	SVGQSPLRSPLK
5.0	1267.749969	-0.012681	ITLDLLSRIPQ
4.3	1267.743439	-0.006151	MKGAVLINGLPR
4.0	1267.749969	-0.012681	LQDQLLGIVAAK
3.2	1267.736053	0.001235	SGLQLTLQPRR
3.1	1267.749954	-0.012666	SLLALGNVINALA
2.4	1267.724808	0.012480	EVAGAPALRLQK

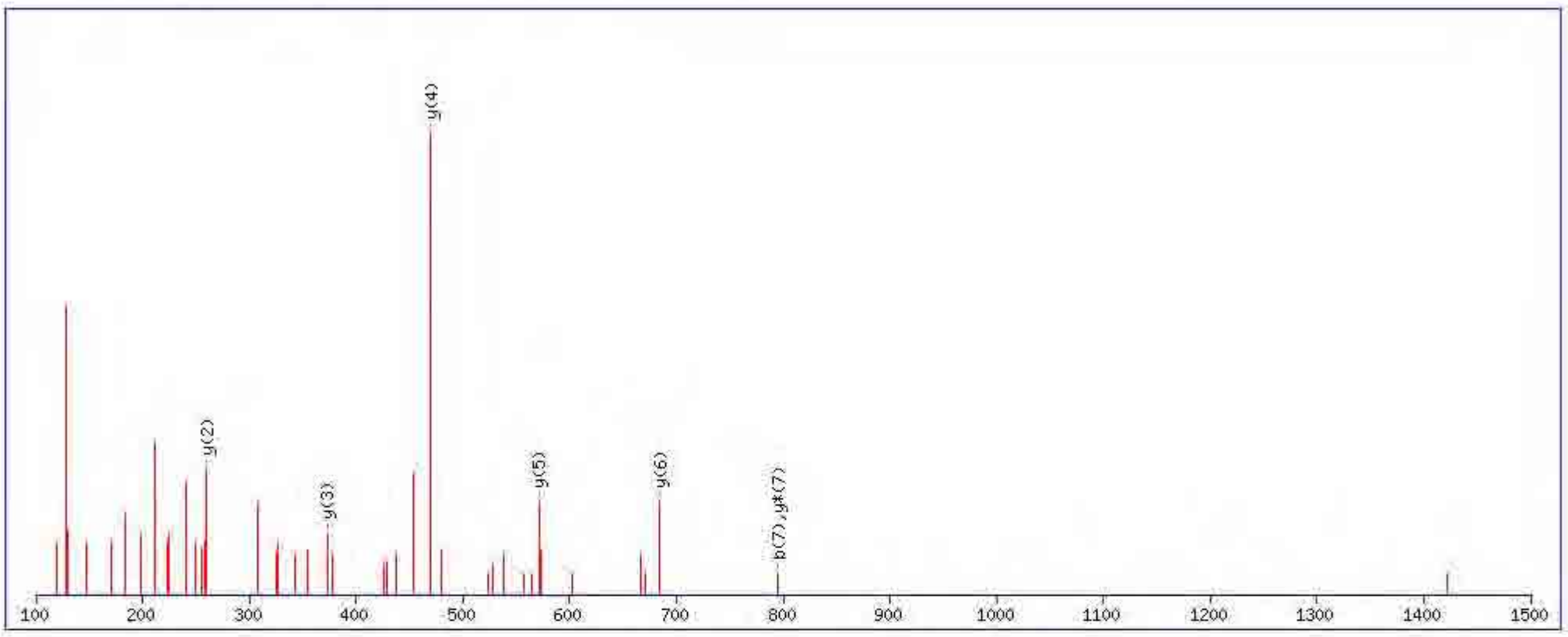
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLTPLIK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

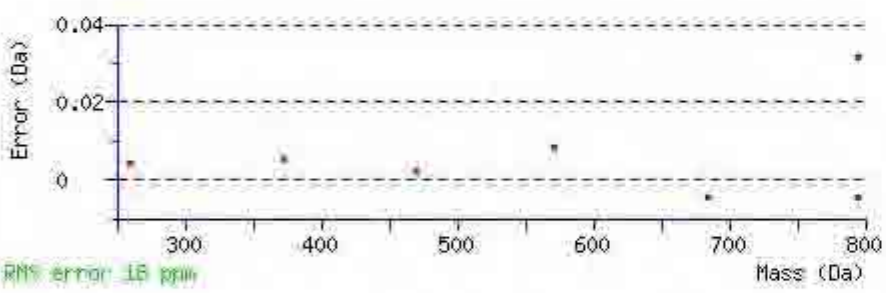
Match to Query 2950: 940.549908 from(471.282230,2+) rtinseconds(1523) index(10988)
Title: Locus:1.1.1.1678.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

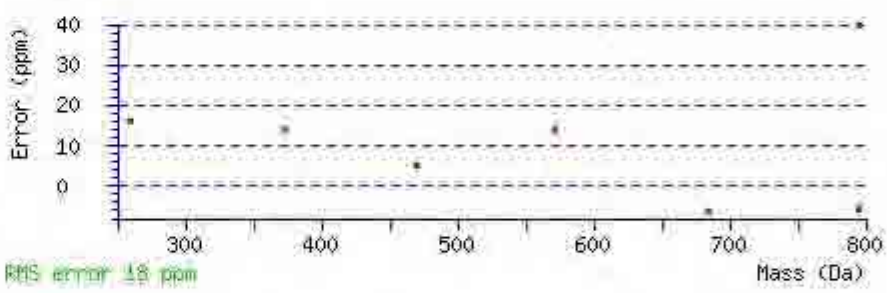
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 940.559311
Ions Score: 44 **Expect:** 0.0051
Matches : 7/74 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							8
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	812.524017	406.765647	795.497468	398.252372	794.513452	397.760364	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	L	*684.465439*	342.736358	667.438890	334.223083	666.454874	333.731075	6
4	472.240190	236.623733	455.213641	228.110459	454.229625	227.618451	T	*571.381375*	286.194326	554.354826	277.681051	553.370810	277.189043	5
5	569.292954	285.150115	552.266405	276.636841	551.282389	276.144833	P	*470.333696*	235.670486	453.307147	227.157212			4
6	682.377018	341.692147	665.350469	333.178873	664.366453	332.686865	L	*373.280932*	187.144104	356.254383	178.630830			3
7	795.461082	398.234179	778.434533	389.720905	777.450517	389.228897	I	*260.196868*	130.602072	243.170319	122.088798			2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EQLTPLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	940.559311	-0.009403	EQLTPLIK
24.6	940.541565	0.008343	QLMPLPVK
23.9	940.559311	-0.009403	QLETIPLK
23.7	940.559311	-0.009403	KPEDVLLK
23.7	940.541550	0.008358	MKLPEPVK
16.4	940.559311	-0.009403	KDPLDLLK
15.7	940.541565	0.008343	MKPVLPLQ
15.5	940.559311	-0.009403	KDLLDPIK
15.5	940.559311	-0.009403	KPEDIVLK
14.4	940.552795	-0.002887	MKVLVHSK

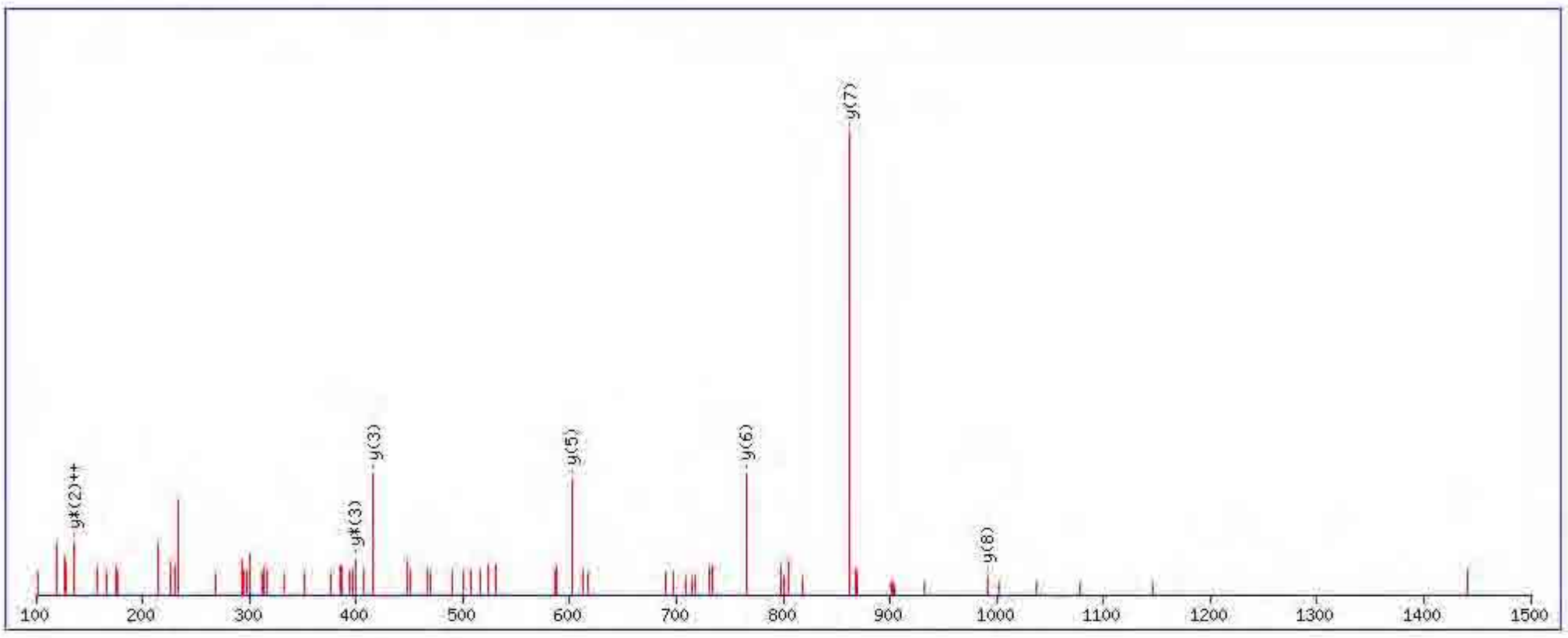
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPYADQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

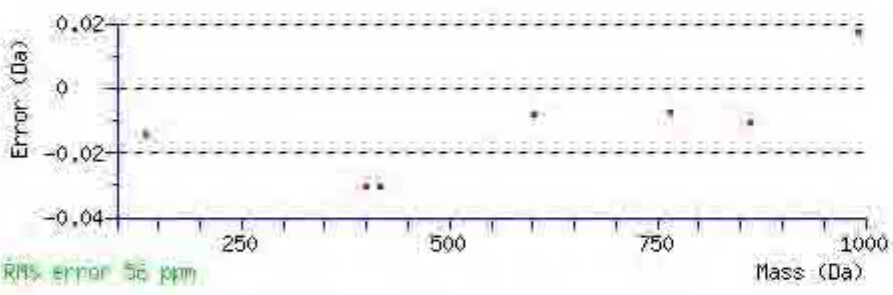
Match to Query 6680: 1103.563448 from(552.789000,2+) rtinseconds(1365) index(9021)
Title: Locus:1.1.1.1593.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

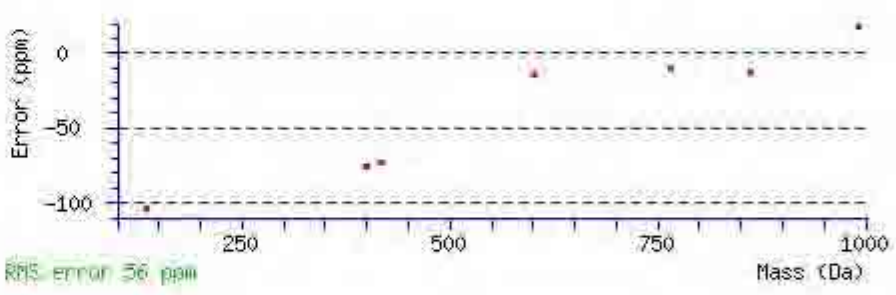
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1103.561096
Ions Score: 37 **Expect:** 0.0085
Matches : 7/76 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	243.133933	122.070605			225.123368	113.065322	E	*991.484337*	496.245807	974.457788	487.732532	973.473772	487.240524	8
3	340.186697	170.596987			322.176132	161.591704	P	*862.441744*	431.724510	845.415195	423.211236	844.431179	422.719228	7
4	503.250026	252.128651			485.239461	243.123369	Y	*765.388980*	383.198128	748.362431	374.684854	747.378415	374.192846	6
5	574.287140	287.647208			556.276575	278.641926	A	*602.325651*	301.666464	585.299102	293.153189	584.315086	292.661181	5
6	689.314083	345.160680			671.303518	336.155397	D	531.288537	266.147907	514.261988	257.634632	513.277972	257.142624	4
7	817.372661	409.189969	800.346112	400.676694	799.362096	400.184686	Q	*416.261594*	208.634435	399.235045	200.121161			3
8	930.456725	465.732001	913.430176	457.218726	912.446160	456.726718	L	288.203016	144.605146	271.176467	136.091872			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LEPYADQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.9	1103.561096	0.002352	LEPYADQLR
13.9	1103.564484	-0.001036	IQSCAAQAVLT
11.7	1103.564468	-0.001020	IEEMVAQLR
11.7	1103.564468	-0.001020	LEAEVMQLR
11.7	1103.561111	0.002337	PEEIGFQIR
9.9	1103.570999	-0.007551	LESLDISNTL
9.5	1103.561111	0.002337	LEGFQNPTAK
7.6	1103.553909	0.009539	FLPEPLFPF
7.5	1103.561096	0.002352	IEPNLPSYR
7.5	1103.561111	0.002337	IEPPSGIYGR

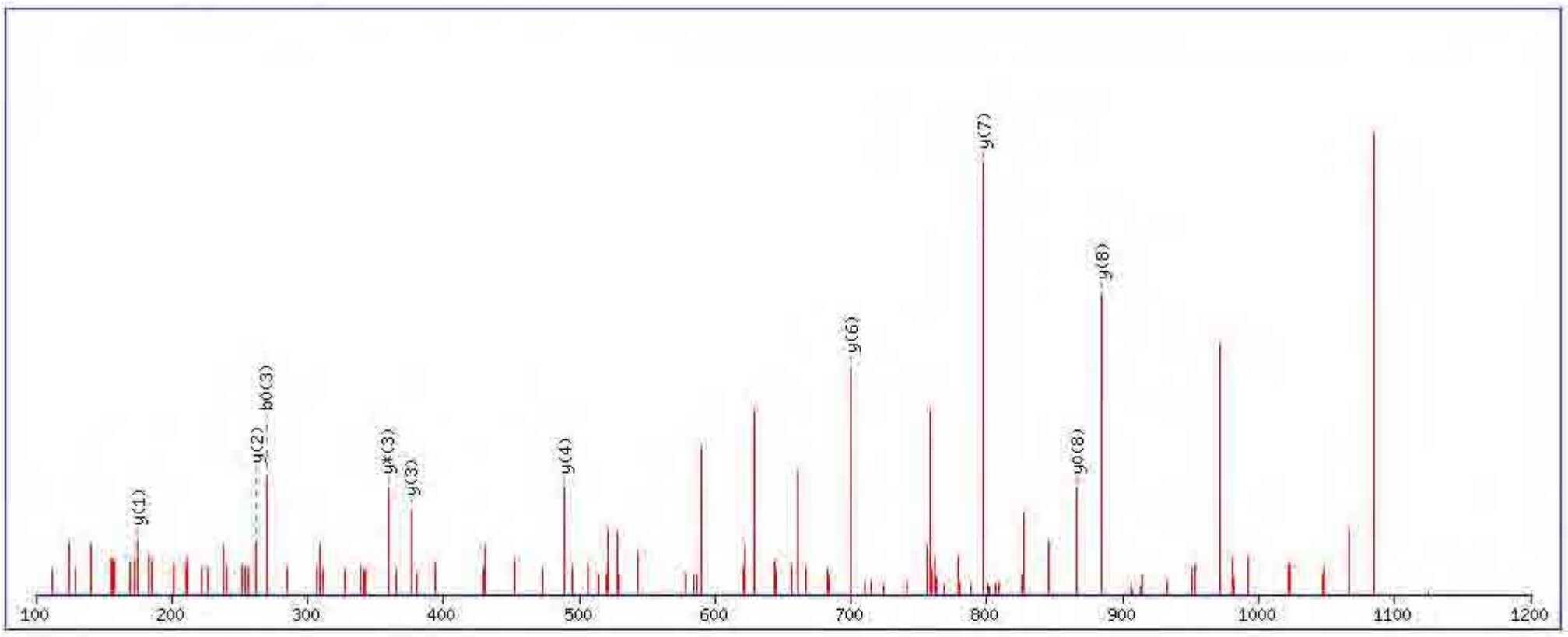
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLSPNPLNSR**
Found in **BIRC2_HUMAN**, Baculoviral IAP repeat-containing protein 2 OS=Homo sapiens GN=BIRC2 PE=1 SV=2

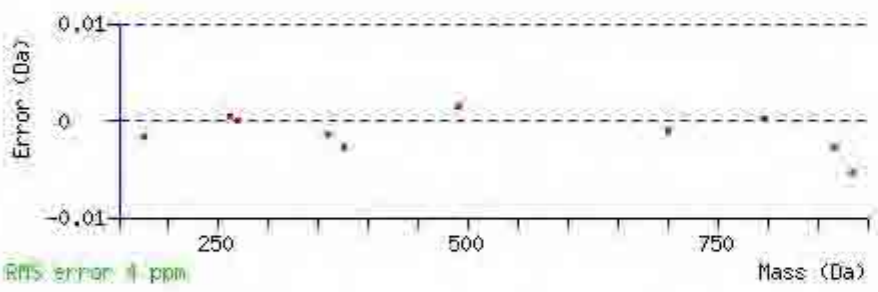
Match to Query 6168: 1083.560728 from(542.787640,2+) rtinseconds(1013) index(5146)
Title: Locus:1.1.1.1401.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

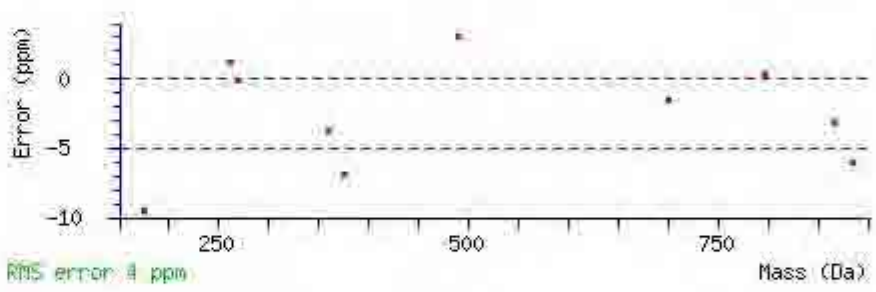
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1083.567245
Ions Score: 45 **Expect:** 0.0053
Matches : 10/98 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							10
2	201.123368	101.065322			183.112803	92.060039	L	997.542518	499.274897	980.515969	490.761623	979.531953	490.269615	9
3	288.155396	144.581336			270.144831	135.576053	S	*884.458454*	442.732865	867.431905	434.219591	866.447889	433.727583	8
4	385.208160	193.107718			367.197595	184.102435	P	*797.426426*	399.216851	780.399877	390.703577	779.415861	390.211569	7
5	499.251087	250.129181	482.224538	241.615907	481.240522	241.123899	N	*700.373662*	350.690469	683.347113	342.177195	682.363097	341.685187	6
6	596.303851	298.655564	579.277302	290.142289	578.293286	289.650281	P	586.330735	293.669006	569.304186	285.155731	568.320170	284.663723	5
7	709.387915	355.197596	692.361366	346.684321	691.377350	346.192313	L	*489.277971*	245.142623	472.251422	236.629349	471.267406	236.137341	4
8	823.430842	412.219059	806.404293	403.705784	805.420277	403.213776	N	*376.193907*	188.600591	359.167358	180.087317	358.183342	179.595309	3
9	910.462870	455.735073	893.436321	447.221798	892.452305	446.729790	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SLSPNPLNSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1083.567245	-0.006517	SLSPNPLNSR
25.6	1083.556046	0.004682	LSSSPPVPPR
20.2	1083.556046	0.004682	LSSSPPVPPR
19.5	1083.556030	0.004698	LAPSVPEAPR
19.4	1083.556046	0.004682	LSSSPPVPPR
19.4	1083.556046	0.004682	LSSSPPVPPR
19.4	1083.556046	0.004682	PSSGPLLPPR
17.5	1083.567261	-0.006533	PRDVEAIPR
17.4	1083.556046	0.004682	PGTPLDISPR
17.1	1083.567261	-0.006533	PSKAGTAPSPR

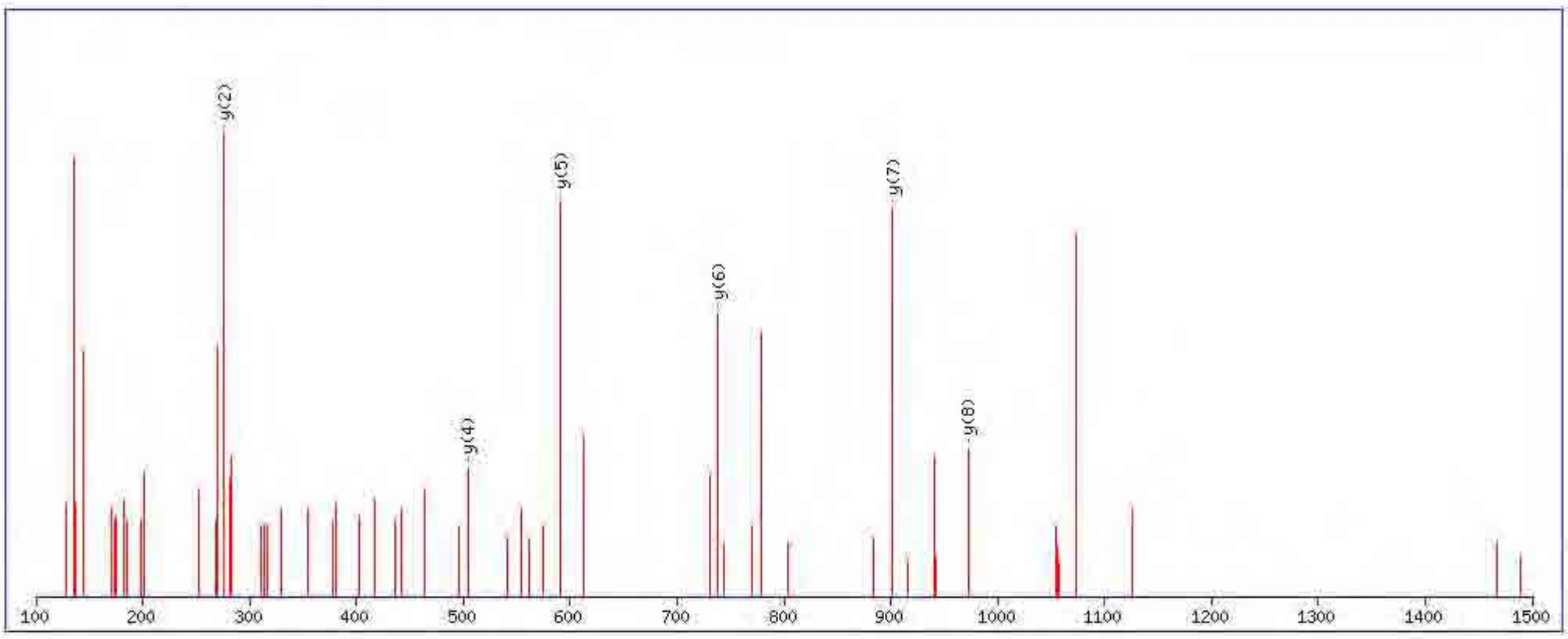
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAYFSLDTR**
Found in **CADH1_HUMAN**, Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3

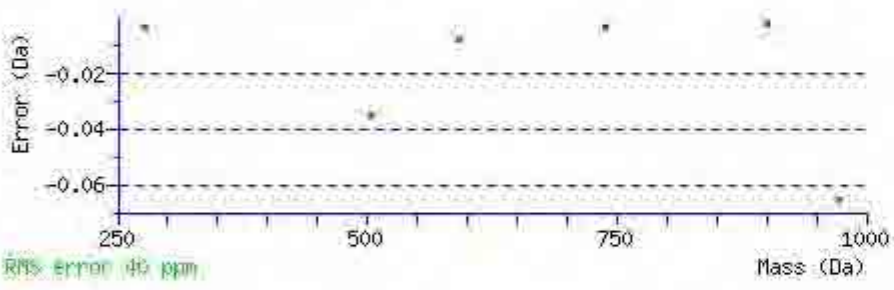
Match to Query 5882: 1072.517148 from(537.265850,2+) rtinseconds(1690) index(13054)
Title: Locus:1.1.1.1769.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

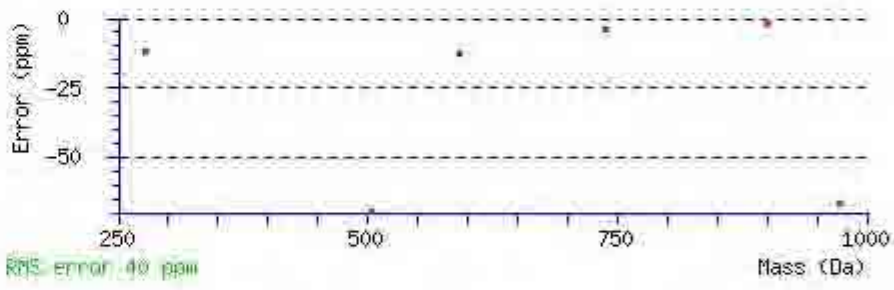
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1072.518921
Ions Score: 47 **Expect:** 0.0025
Matches : 6/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	173.092069	87.049672	155.081504	78.044390	A	*972.478523*	486.742900	955.451974	478.229625	954.467958	477.737617	8
3	336.155398	168.581337	318.144833	159.576055	Y	*901.441409*	451.224343	884.414860	442.711068	883.430844	442.219060	7
4	483.223812	242.115544	465.213247	233.110262	F	*738.378080*	369.692678	721.351531	361.179403	720.367515	360.687395	6
5	570.255840	285.631558	552.245275	276.626276	S	*591.309666*	296.158471	574.283117	287.645197	573.299101	287.153189	5
6	683.339904	342.173590	665.329339	333.168308	L	*504.277638*	252.642457	487.251089	244.129182	486.267073	243.637174	4
7	798.366847	399.687062	780.356282	390.681779	D	391.193574	196.100425	374.167025	187.587150	373.183009	187.095142	3
8	899.414526	450.210901	881.403961	441.205619	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TAYFSLDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	1072.518921	-0.001773	TAYFSLDTR
17.7	1072.508560	0.008588	FKMPSFGML
12.7	1072.514908	0.002240	TVPQQSPER
10.3	1072.522308	-0.005160	TANVPQTVPM
10.3	1072.522308	-0.005160	TANVPQTVPM
7.3	1072.507675	0.009473	ATYDSFLEK
6.7	1072.508362	0.008786	TAAHCISNTR
6.2	1072.518936	-0.001788	TPHDLFSSGL
6.1	1072.507690	0.009458	FSTSFLDEK
4.8	1072.508362	0.008786	MESSRGRPGP

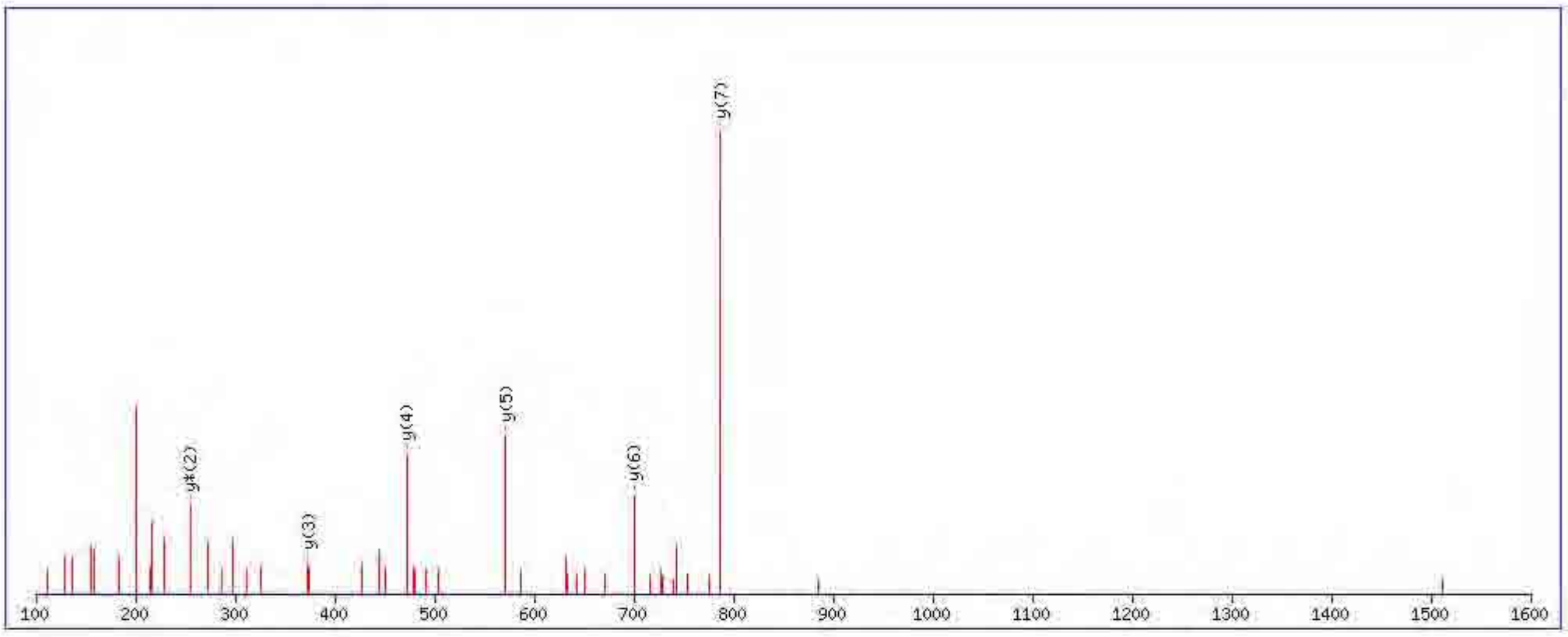
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DISEVVTPR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

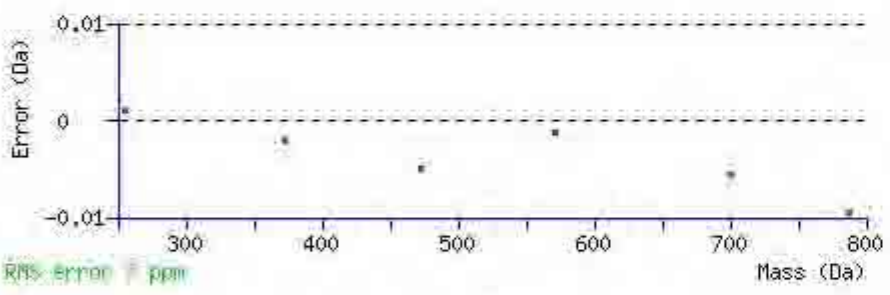
Match to Query 4561: 1014.530528 from(508.272540,2+) rtinseconds(1391) index(9360)
Title: Locus:1.1.1.1607.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

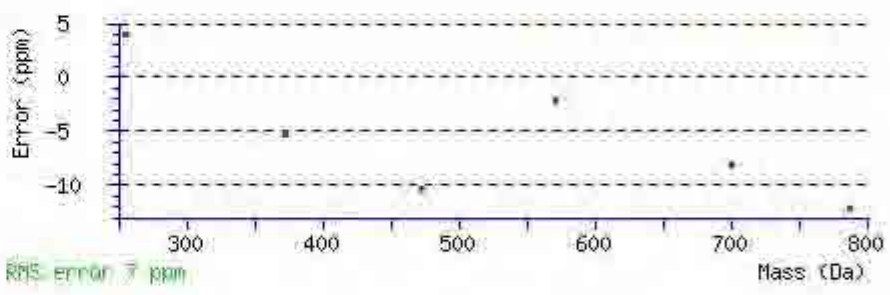
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1014.534576
Ions Score: 40 **Expect:** 0.0078
Matches : 6/76 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	229.118283	115.062779	211.107718	106.057497	I	900.514908	450.761092	883.488359	442.247818	882.504343	441.755810	8
3	316.150311	158.578793	298.139746	149.573511	S	*787.430844*	394.219060	770.404295	385.705786	769.420279	385.213778	7
4	445.192904	223.100090	427.182339	214.094808	E	*700.398816*	350.703046	683.372267	342.189772	682.388251	341.697764	6
5	544.261318	272.634297	526.250753	263.629015	V	*571.356223*	286.181750	554.329674	277.668475	553.345658	277.176467	5
6	643.329732	322.168504	625.319167	313.163222	V	*472.287809*	236.647543	455.261260	228.134268	454.277244	227.642260	4
7	744.377411	372.692344	726.366846	363.687061	T	*373.219395*	187.113336	356.192846	178.600061	355.208830	178.108053	3
8	841.430175	421.218726	823.419610	412.213443	P	272.171716	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DISEVVTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1014.534576	-0.004048	DISEVVTPR
14.1	1014.534561	-0.004033	LDSIDPALR
11.4	1014.538605	-0.008077	AGPFLTPSPL
11.3	1014.538620	-0.008092	TVVLTWSPP
11.3	1014.538620	-0.008092	TVVLTWSPP
11.1	1014.523331	0.007197	VESEIKVPD
11.1	1014.534561	-0.004033	VESEPIVAR
11.0	1014.523331	0.007197	DLSDLPLDK
10.6	1014.538605	-0.008077	VEPAFVPPK
10.3	1014.523346	0.007182	DPSTPIPLK

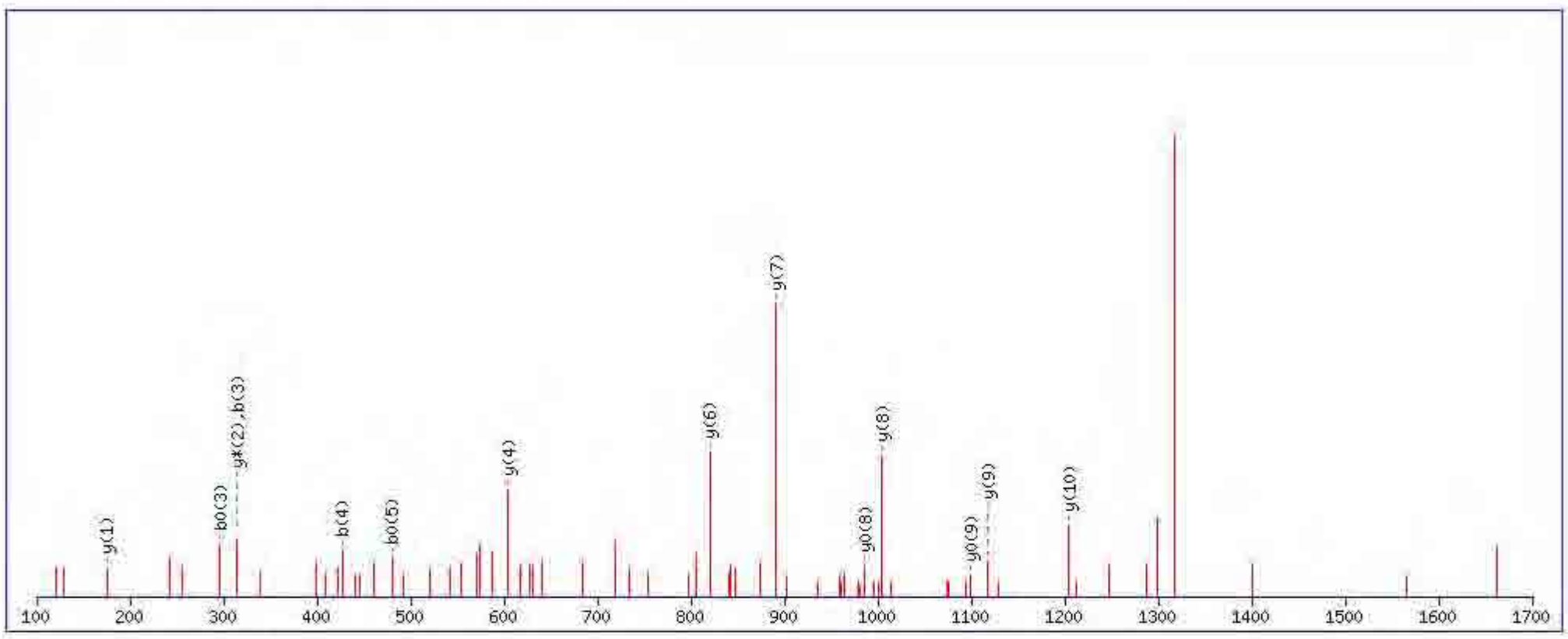
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSPPADTSWRR**
Found in **CRTC1_HUMAN**, CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=2

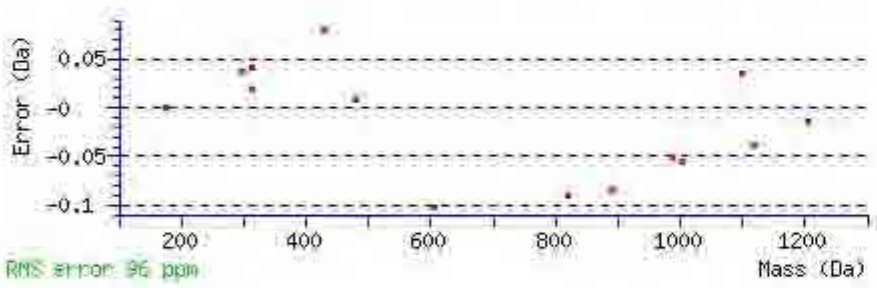
Match to Query 12439: 1316.640468 from(659.327510,2+) rtinseconds(1696) index(13140)
Title: Locus:1.1.1.1772.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

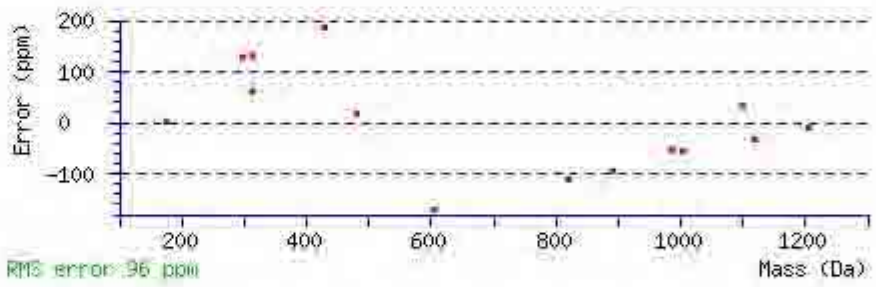
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1316.647308
Variable modifications:
P3 : Oxidation (P)
P4 : Oxidation (P)
Ions Score: 48 **Expect:** 0.0039
Matches : 14/94 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	201.123368	101.065322			183.112803	92.060039	S	*1204.570526*	602.788901	1187.543977	594.275627	1186.559961	593.783618	10
3	**314.171047**	157.589161			296.160482	148.583879	P	*1117.538498*	559.272887	1100.511949	550.759613	1099.527933	550.267604	9
4	**427.218726**	214.113001			409.208161	205.107719	P	*1004.490819*	502.749047	987.464270	494.235773	986.480254	493.743765	8
5	498.255840	249.631558			480.245275	240.626275	A	*891.443140*	446.225208	874.416591	437.711933	873.432575	437.219925	7
6	613.282783	307.145030			595.272218	298.139747	D	*820.406026*	410.706651	803.379477	402.193376	802.395461	401.701368	6
7	714.330462	357.668869			696.319897	348.663587	T	705.379083	353.193179	688.352534	344.679905	687.368518	344.187897	5
8	801.362490	401.184883			783.351925	392.179600	S	*604.331404*	302.669340	587.304855	294.156065	586.320839	293.664057	4
9	987.441803	494.224539			969.431238	485.219257	W	517.299376	259.153326	500.272827	250.640051			3
10	1143.542914	572.275095	1126.516365	563.761821	1125.532349	563.269812	R	331.220063	166.113669	**314.193514**	157.600395			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSPPADTSWRR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	1316.647308	-0.006840	LSPPADTSWRR
28.4	1316.628220	0.012248	PSPVVSPTEMNK
25.9	1316.647293	-0.006825	PPSPPASRAAYR
22.7	1316.639435	0.001033	LSPPRLMANSPS
22.7	1316.639435	0.001033	LSPPRLMANSPS
20.6	1316.636078	0.004390	PAEPAPPPGAPPR
20.6	1316.636078	0.004390	PAEPAPPPGAPPR
20.6	1316.636078	0.004390	PAEPAPPPGAPPR
20.1	1316.636063	0.004405	AELPAHAAAAPGPP
20.1	1316.636063	0.004405	AELPAHAAAAPGPP

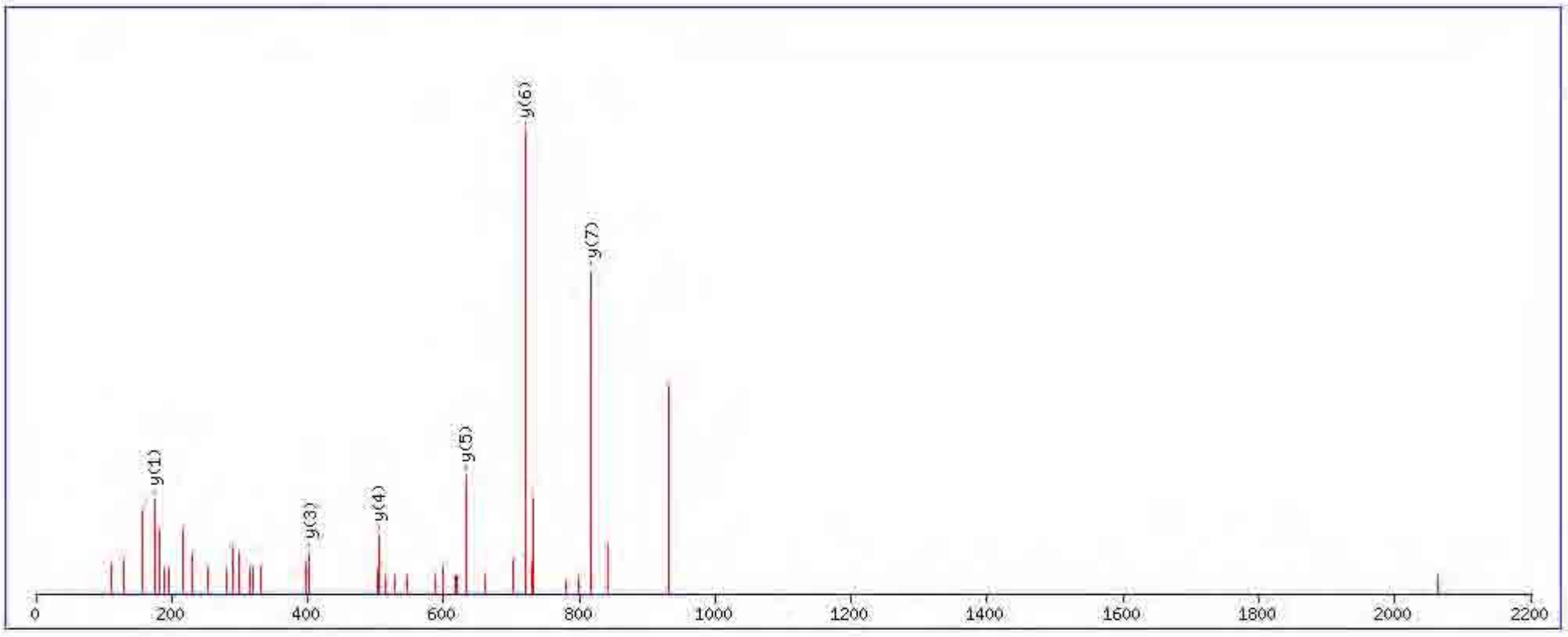
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPSETDLR**
Found in **CCNL1_HUMAN**, Cyclin-L1 OS=Homo sapiens GN=CCNL1 PE=1 SV=1

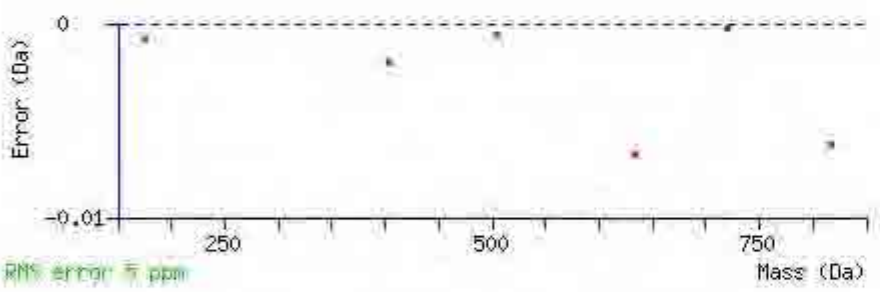
Match to Query 2748: 929.478748 from(465.746650,2+) rtinseconds(1008) index(5104)
Title: Locus:1.1.1.1398.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

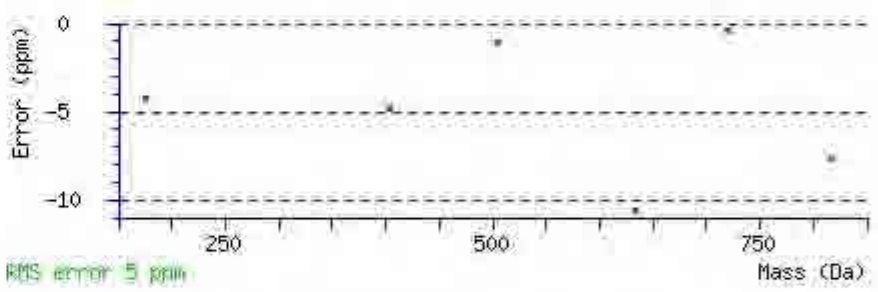
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 929.481796
Ions Score: 55 **Expect:** 0.00076
Matches : 6/62 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	211.144104	106.075690			P	*817.405023*	409.206150	800.378474	400.692875	799.394458	400.200867	7
3	298.176132	149.591704	280.165567	140.586422	S	*720.352259*	360.679768	703.325710	352.166493	702.341694	351.674485	6
4	427.218725	214.113001	409.208160	205.107718	E	*633.320231*	317.163754	616.293682	308.650479	615.309666	308.158471	5
5	528.266404	264.636840	510.255839	255.631558	T	*504.277638*	252.642457	487.251089	244.129183	486.267073	243.637175	4
6	643.293347	322.150312	625.282782	313.145029	D	*403.229959*	202.118618	386.203410	193.605343	385.219394	193.113335	3
7	756.377411	378.692344	738.366846	369.687061	L	288.203016	144.605146	271.176467	136.091872			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LPSETDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.8	929.481796	-0.003048	LPSETDLR
24.4	929.481796	-0.003048	AILETPDR
24.3	929.475266	0.003482	LPSCQLNR
24.3	929.471909	0.006839	LPSSFHSR
24.3	929.471909	0.006839	LPSSFSHR
23.4	929.481796	-0.003048	IIEATPDR
22.0	929.481766	-0.003018	LLAEEEAR
17.3	929.471909	0.006839	ISPSSHFR
17.3	929.475266	0.003482	IPNCSKPR
15.2	929.470596	0.008152	LPSVPTVDS

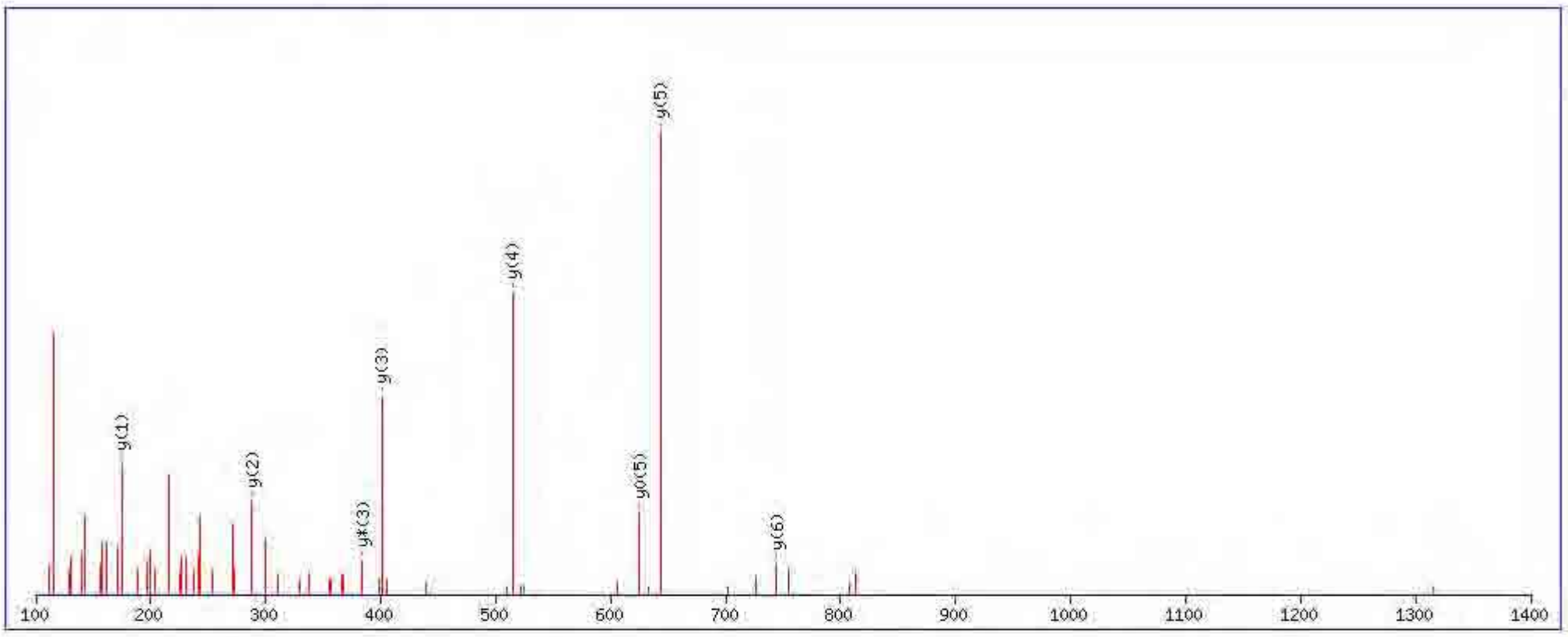
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELIPR**
Found in **DMRTD_HUMAN**, Doublesex- and mab-3-related transcription factor C2 OS=Homo sapiens GN=DMRTC2 PE=2 SV=2

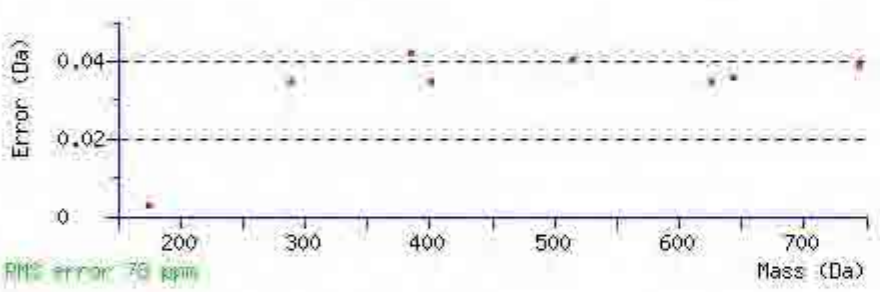
Match to Query 1016: 830.455268 from(416.234910,2+) rtinseconds(1359) index(8939)
Title: Locus:1.1.1.1590.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

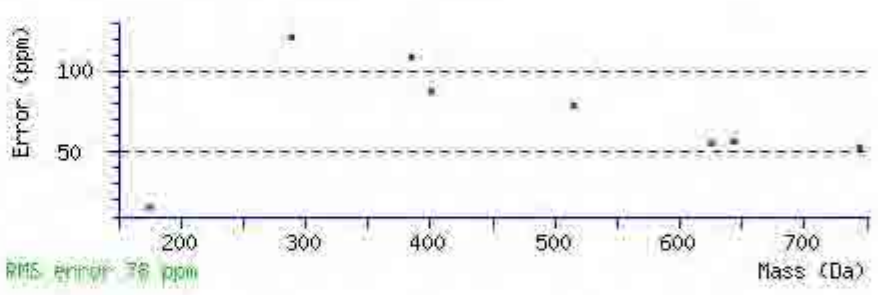
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 830.449768
Variable modifications:
P6 : Oxidation (P)
Ions Score: 47 **Expect:** 0.0098
Matches : 8/52 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	189.086983	95.047129	171.076418	86.041847	T	*744.425031*	372.716154	727.398482	364.202879	726.414466	363.710871	6
3	318.129576	159.568426	300.119011	150.563144	E	*643.377352*	322.192314	626.350803	313.679040	625.366787	313.187032	5
4	431.213640	216.110458	413.203075	207.105176	L	*514.334759*	257.671018	497.308210	249.157743			4
5	544.297704	272.652490	526.287139	263.647208	I	*401.250695*	201.128985	384.224146	192.615711			3
6	657.345383	329.176330	639.334818	320.171047	P	*288.166631*	144.586953	271.140082	136.073679			2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of STELIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	830.449768	0.005500	STELIPR
20.1	830.449768	0.005500	TSIEPIR
18.4	830.449768	0.005500	ETSPLIR
18.4	830.449768	0.005500	ETSPLLR
17.1	830.449783	0.005485	TTDPLIR
15.7	830.453796	0.001472	DATLLLW
15.3	830.460999	-0.005731	SKTNPIR
15.3	830.449768	0.005500	SLDDIIR
15.3	830.460999	-0.005731	SNQTLLR
15.3	830.460999	-0.005731	SQKSPIR

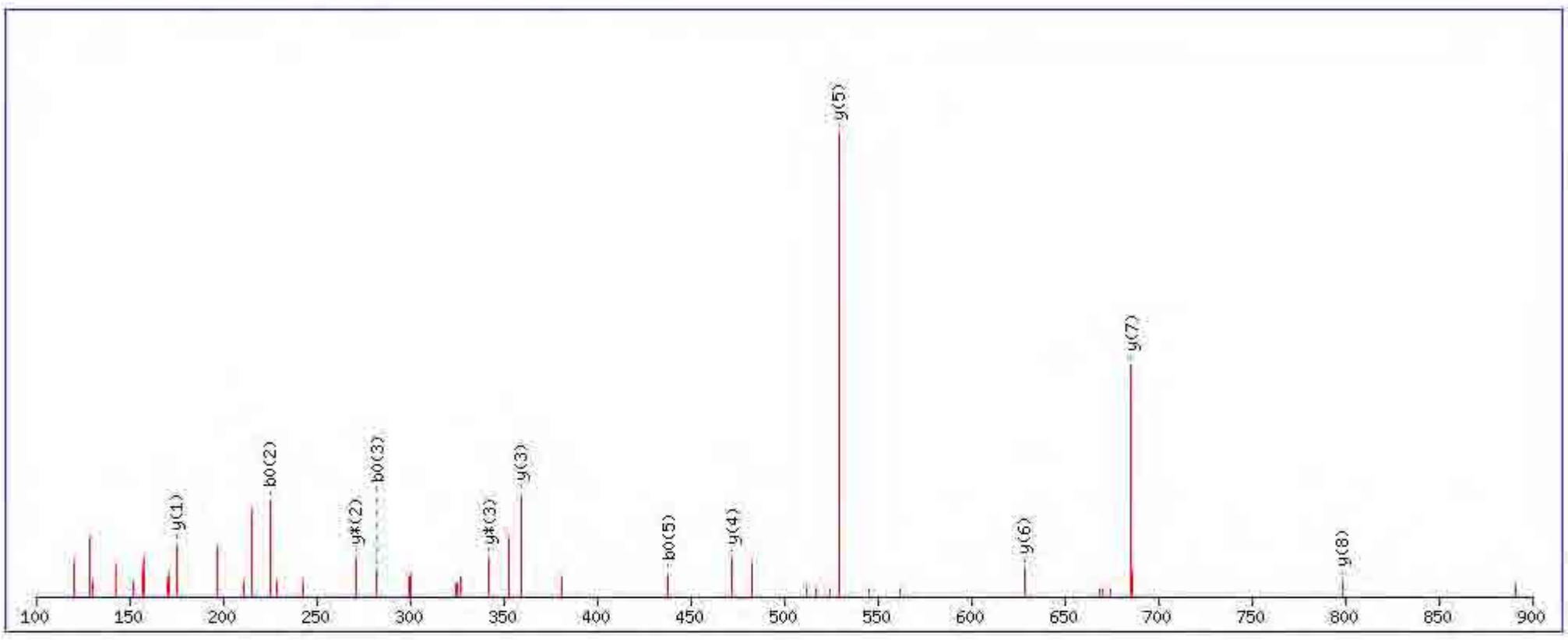
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGVGIALR**
Found in **FABP5_HUMAN**, Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3

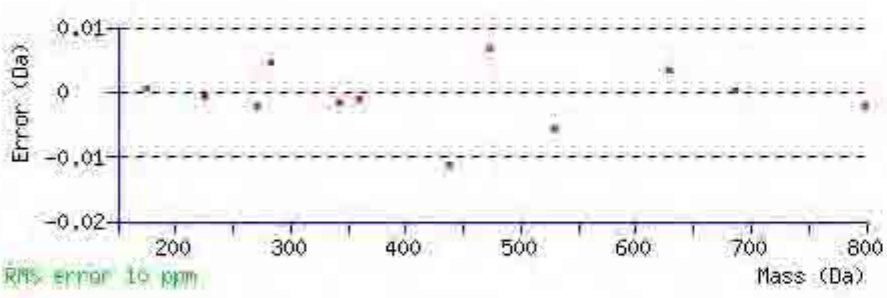
Match to Query 2675: 926.545688 from(464.280120,2+) rtinseconds(1751) index(13855)
Title: Locus:1.1.1.1802.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

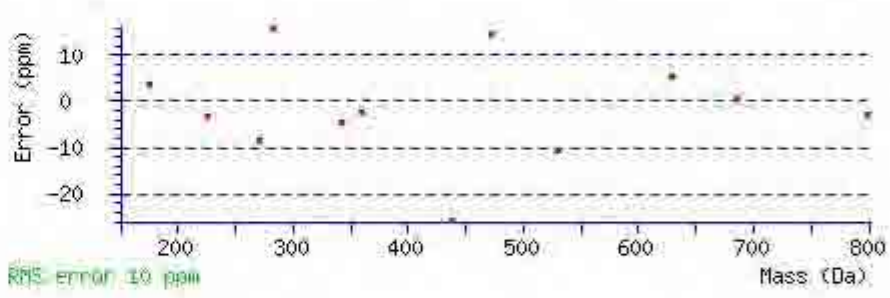
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 926.554901
Ions Score: 48 **Expect:** 0.0018
Matches : 12/64 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					9
2	243.133933	122.070605	225.123368	113.065322	L	*798.519600*	399.763438	781.493051	391.250163	8
3	300.155397	150.581336	282.144832	141.576054	G	*685.435536*	343.221406	668.408987	334.708131	7
4	399.223811	200.115544	381.213246	191.110261	V	*628.414072*	314.710674	611.387523	306.197400	6
5	456.245275	228.626275	438.234710	219.620993	G	*529.345658*	265.176467	512.319109	256.663192	5
6	569.329339	285.168308	551.318774	276.163025	I	*472.324194*	236.665735	455.297645	228.152460	4
7	640.366453	320.686865	622.355888	311.681582	A	*359.240130*	180.123703	342.213581	171.610428	3
8	753.450517	377.228897	735.439952	368.223614	L	288.203016	144.605146	271.176467	136.091871	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ELGVGIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	926.554901	-0.009213	ELGVGIALR
38.7	926.554901	-0.009213	ELRGLLQV
13.0	926.554901	-0.009213	ELVGRLGLA
11.7	926.554901	-0.009213	LREGPVLK
11.7	926.554901	-0.009213	RLEGILGGL
11.2	926.543686	0.002002	APTIGLAAVV
11.0	926.554901	-0.009213	EGVLGALLR
10.5	926.554901	-0.009213	ELVARVLQ
10.0	926.543671	0.002017	LTGSLPNLL
9.8	926.554901	-0.009213	KLTPPALR

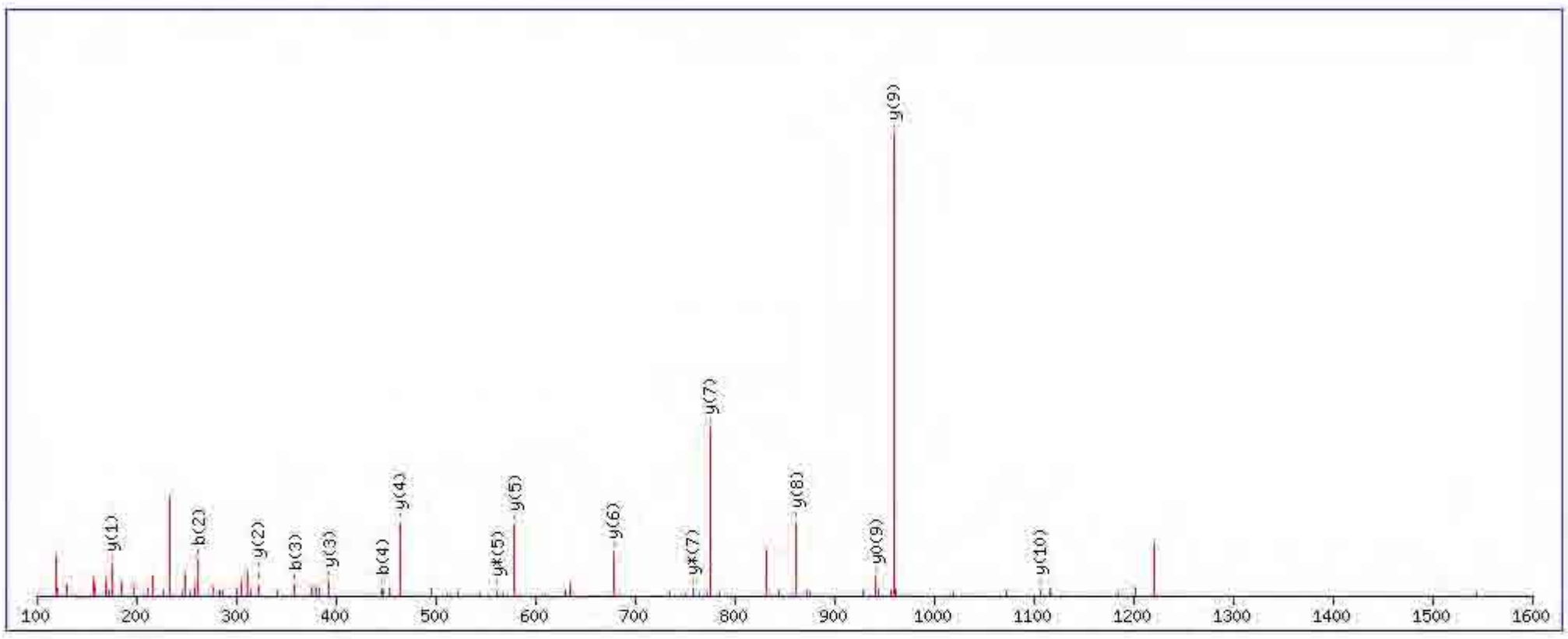
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFPSPVDAAFR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

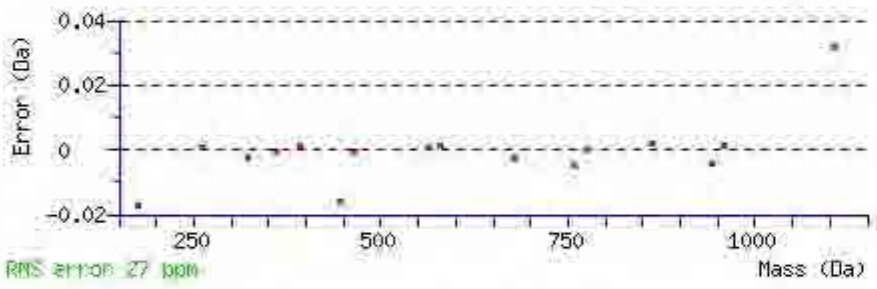
Match to Query 9984: 1219.594168 from(610.804360,2+) rtinseconds(1910) index(15273)
Title: Locus:1.1.1.1910.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

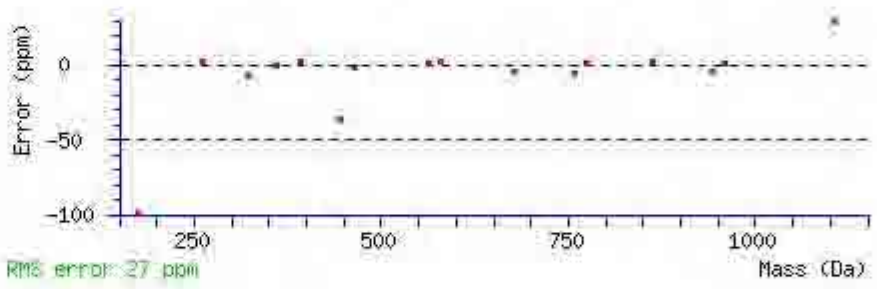
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1219.598572
Ions Score: 78 Expect: 3.5e-006
Matches : 16/106 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	262.118617	131.562946	245.092068	123.049672			F	1106.562921	553.785099	1089.536372	545.271824	1088.552356	544.779816	10
3	359.171381	180.089328	342.144832	171.576054			P	959.494507	480.250891	942.467958	471.737617	941.483942	471.245609	9
4	446.203409	223.605342	429.176860	215.092068	428.192844	214.600060	S	862.441743	431.724510	845.415194	423.211235	844.431178	422.719227	8
5	543.256173	272.131725	526.229624	263.618450	525.245608	263.126442	P	775.409715	388.208496	758.383166	379.695221	757.399150	379.203213	7
6	642.324587	321.665932	625.298038	313.152657	624.314022	312.660649	V	678.356951	339.682114	661.330402	331.168839	660.346386	330.676831	6
7	757.351530	379.179403	740.324981	370.666128	739.340965	370.174120	D	579.288537	290.147907	562.261988	281.634632	561.277972	281.142624	5
8	828.388644	414.697960	811.362095	406.184685	810.378079	405.692677	A	464.261594	232.634435	447.235045	224.121160			4
9	899.425758	450.216517	882.399209	441.703242	881.415193	441.211234	A	393.224480	197.115878	376.197931	188.602603			3
10	1046.494172	523.750724	1029.467623	515.237450	1028.483607	514.745441	F	322.187366	161.597321	305.160817	153.084047			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NFPSPVDAAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.2	1219.598572	-0.004404	NFPSPVDAAFR
30.6	1219.586685	0.007483	MNGSGQSPSVLK
19.7	1219.597916	-0.003748	KMVSQSQPGSR
17.4	1219.583313	0.010855	NFGDDIPSALR
14.5	1219.604431	-0.010263	SSSAADTNQVLK
13.9	1219.605286	-0.011118	CAALRMLLADQ
12.8	1219.601944	-0.007776	QVMQFVEPSR
12.4	1219.604431	-0.010263	SSSPVTELASRS
12.1	1219.583344	0.010824	FGGAPAGPAGTGKT
11.7	1219.586655	0.007513	GIEMAKESPSR

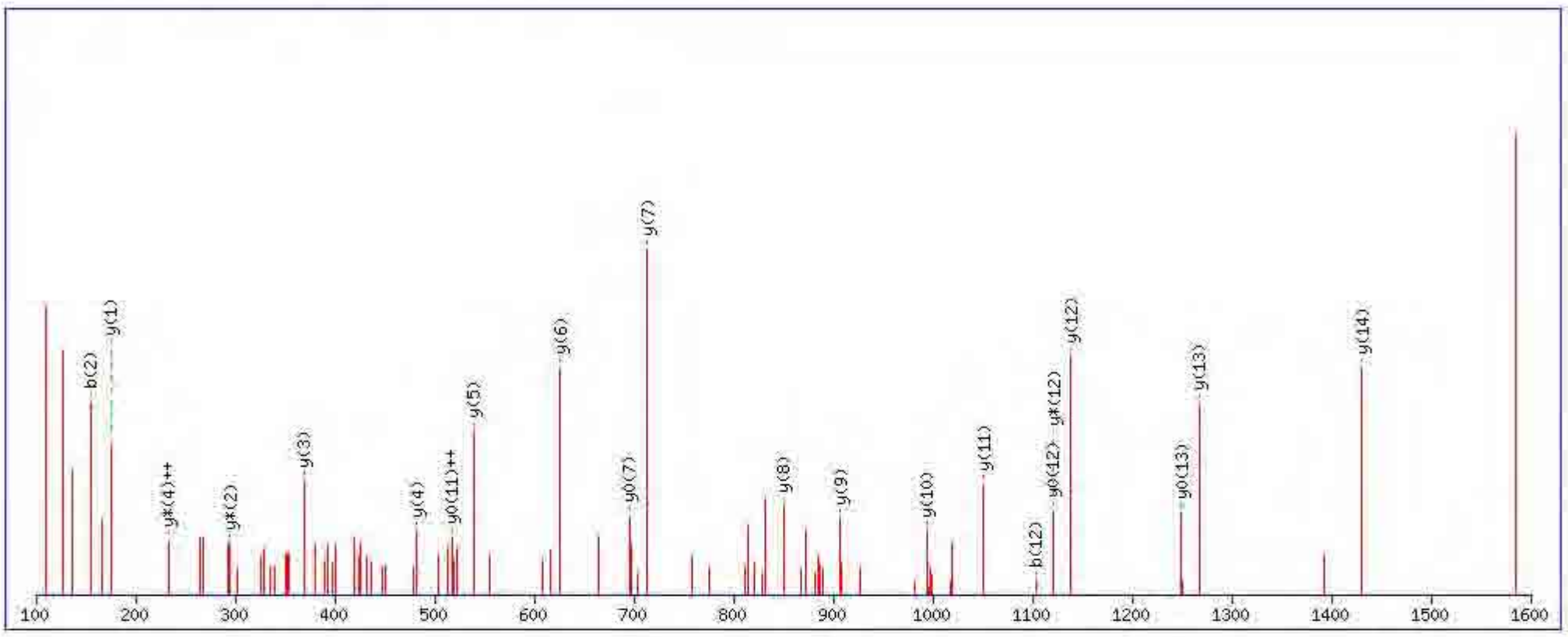
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPYESGSGHSSGLGHR**
Found in **HORN_HUMAN**, Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2

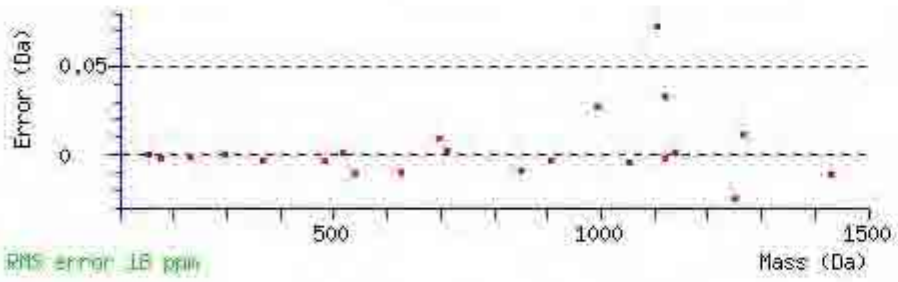
Match to Query 17319: 1583.699172 from(528.907000,3+) rtinseconds(573) index(1029)
Title: Locus:1.1.1.1162.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

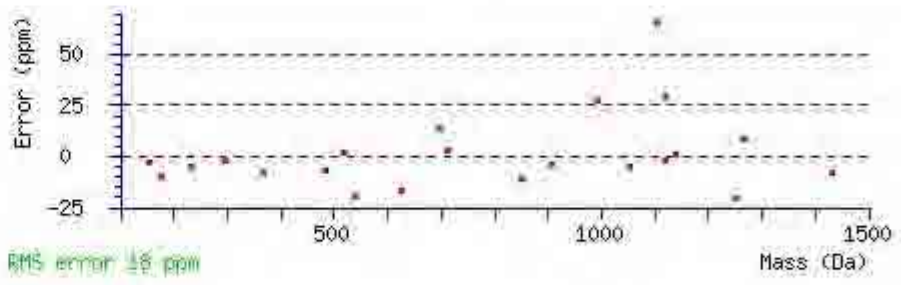
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1583.707687
Ions Score: 87 **Expect:** 1.4e-008
Matches : 22/134 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							16
2	155.081504	78.044390			P	1527.693494	764.350385	1510.666945	755.837110	1509.682929	755.345102	15
3	318.144833	159.576055			Y	1430.640730	715.824003	1413.614181	707.310728	1412.630165	706.818720	14
4	447.187426	224.097351	429.176861	215.092069	E	1267.577401	634.292338	1250.550852	625.779064	1249.566836	625.287056	13
5	534.219454	267.613365	516.208889	258.608083	S	1138.534808	569.771042	1121.508259	561.257767	1120.524243	560.765759	12
6	591.240918	296.124097	573.230353	287.118815	G	1051.502780	526.255028	1034.476231	517.741753	1033.492215	517.249745	11
7	678.272946	339.640111	660.262381	330.634829	S	994.481316	497.744296	977.454767	489.231021	976.470751	488.739013	10
8	735.294410	368.150843	717.283845	359.145561	G	907.449288	454.228282	890.422739	445.715007	889.438723	445.222999	9
9	872.353322	436.680299	854.342757	427.675017	H	850.427824	425.717550	833.401275	417.204275	832.417259	416.712267	8
10	959.385350	480.196313	941.374785	471.191031	S	713.368912	357.188094	696.342363	348.674819	695.358347	348.182811	7
11	1046.417378	523.712327	1028.406813	514.707045	S	626.336884	313.672080	609.310335	305.158805	608.326319	304.666797	6
12	1103.438842	552.223059	1085.428277	543.217777	G	539.304856	270.156066	522.278307	261.642791			5
13	1216.522906	608.765091	1198.512341	599.759808	L	482.283392	241.645334	465.256843	233.132059			4
14	1273.544370	637.275823	1255.533805	628.270540	G	369.199328	185.103302	352.172779	176.590027			3
15	1410.603282	705.805279	1392.592717	696.799996	H	312.177864	156.592570	295.151315	148.079295			2
16					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GPYESGSGHSSGLGHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.2	1583.707687	-0.008515	GPYESGSGHSSGLGHR
3.3	1583.688583	0.010589	PAFDSTTANMNLDR
1.6	1583.700027	-0.000855	FIDHLMVMFGETP
0.2	1583.710327	-0.011155	SELWVEKSSNYEN

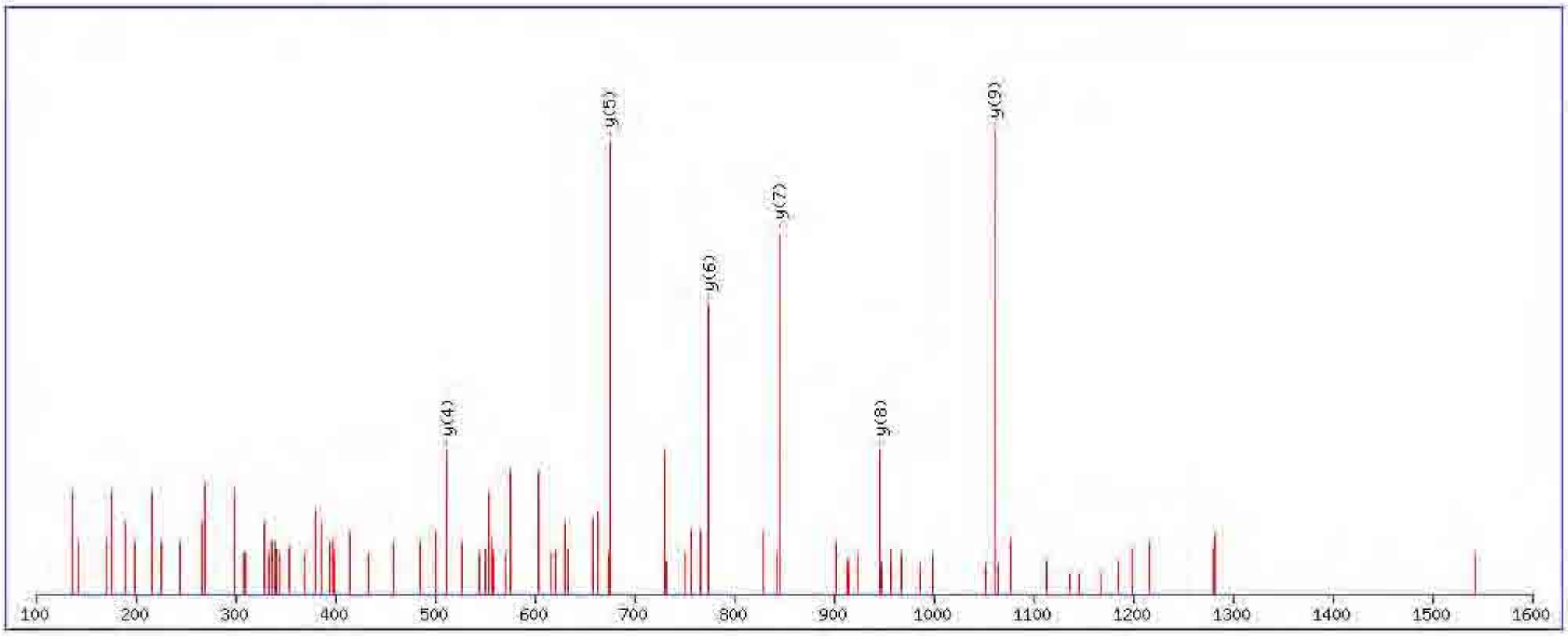
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEDTAVYYCAR**
Found in **HV102_HUMAN**, Ig heavy chain V-I region HG3 OS=Homo sapiens PE=4 SV=1

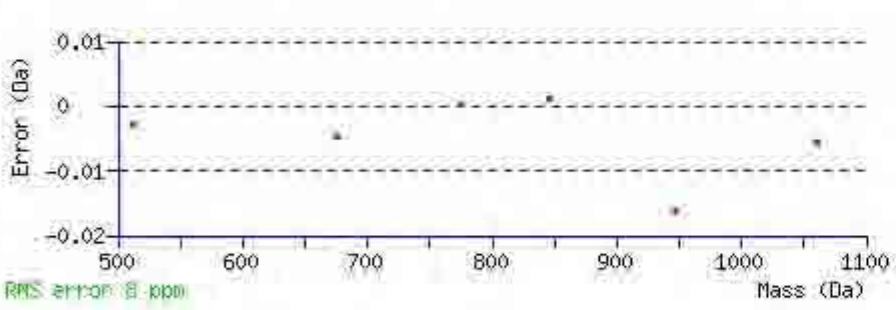
Match to Query 11391: 1276.537588 from(639.276070,2+) rtinseconds(1319) index(8407)
Title: Locus:1.1.1.1568.19
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

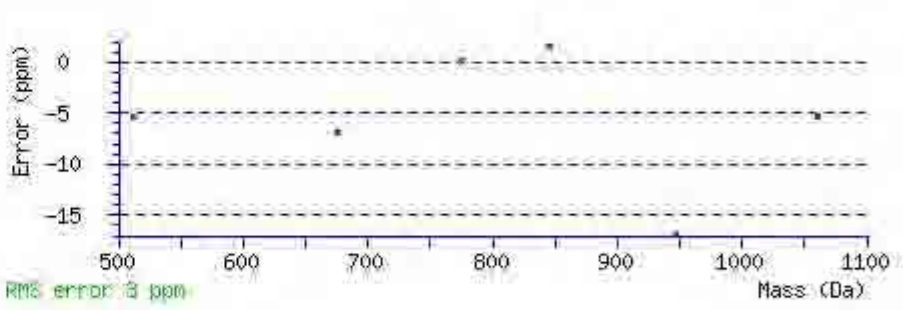
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1276.539383
Ions Score: 39 **Expect:** 0.00039
Matches : 6/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	217.081897	109.044586	199.071332	100.039304	E	1190.514652	595.760964	1173.488103	587.247689	1172.504087	586.755681	10
3	332.108840	166.558058	314.098275	157.552776	D	*1061.472059*	531.239668	1044.445510	522.726393	1043.461494	522.234385	9
4	433.156519	217.081898	415.145954	208.076615	T	*946.445116*	473.726196	929.418567	465.212921	928.434551	464.720913	8
5	504.193633	252.600455	486.183068	243.595172	A	*845.397437*	423.202356	828.370888	414.689082			7
6	603.262047	302.134662	585.251482	293.129379	V	*774.360323*	387.683799	757.333774	379.170525			6
7	766.325376	383.666326	748.314811	374.661044	Y	*675.291909*	338.149592	658.265360	329.636318			5
8	929.388705	465.197991	911.378140	456.192708	Y	*512.228580*	256.617928	495.202031	248.104653			4
9	1032.397890	516.702583	1014.387325	507.697300	C	349.165251	175.086263	332.138702	166.572989			3
10	1103.435004	552.221140	1085.424439	543.215857	A	246.156066	123.581671	229.129517	115.068396			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SEDTAVYYCAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1276.539383	-0.001795	SEDTAVYYCAR
2.1	1276.542770	-0.005182	CPSEAGAMTQPAV
2.0	1276.544098	-0.006510	VQASNCPCYHR
0.8	1276.529541	0.008047	DGAHFFVTSCGH

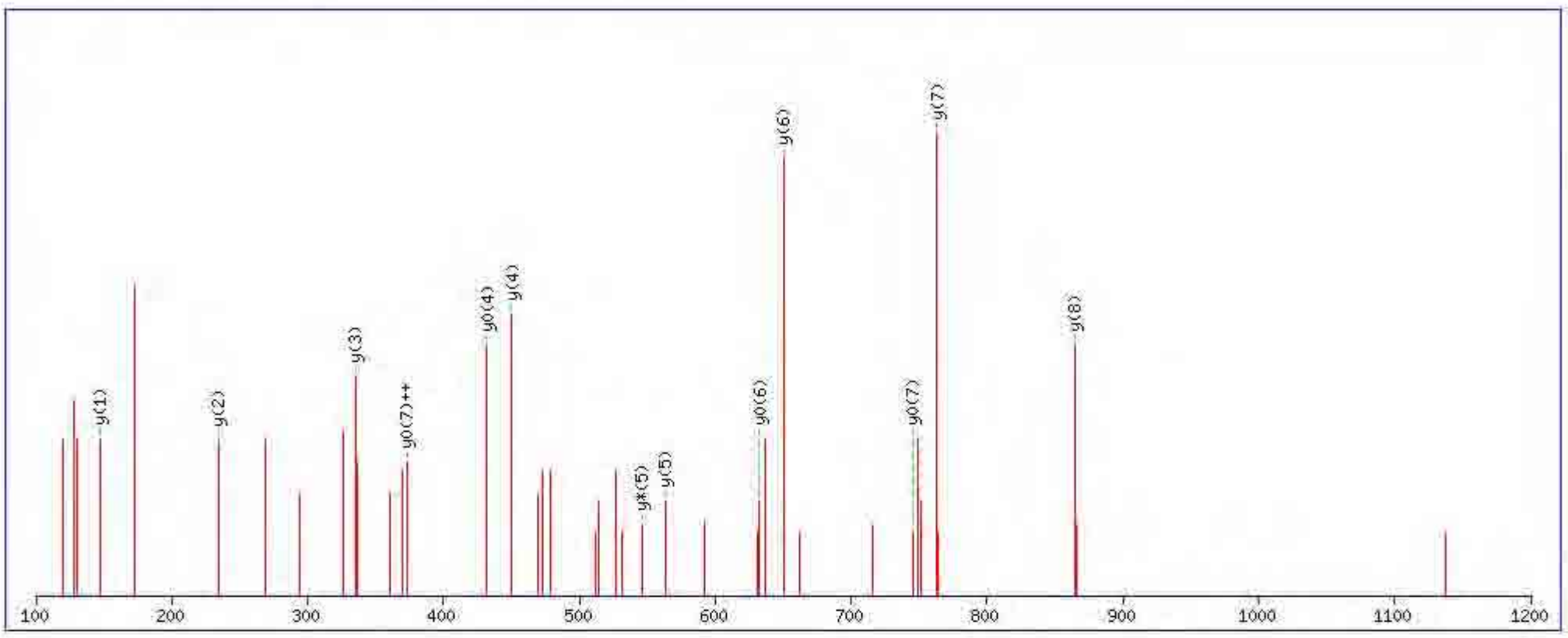
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTISLDTSK**
Found in **HV209_HUMAN**, Ig heavy chain V-II region ARH-77 OS=Homo sapiens PE=4 SV=1

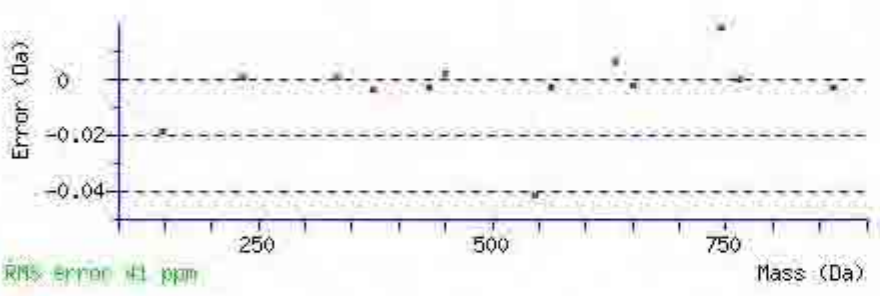
Match to Query 3474: 962.523868 from(482.269210,2+) rtinseconds(1295) index(8090)
Title: Locus:1.1.1.1556.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

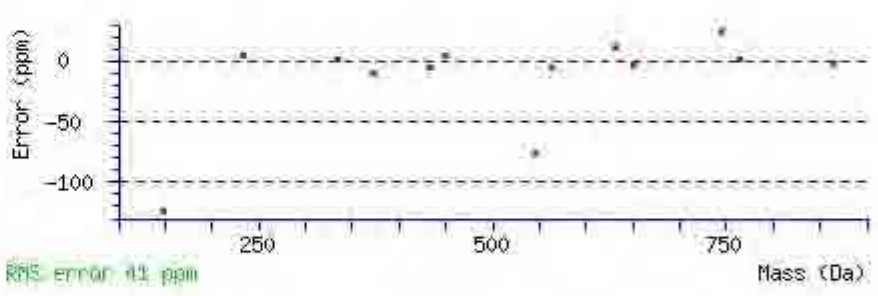
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 962.528427
Ions Score: 57 **Expect:** 0.00091
Matches : 13/76 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	201.123369	101.065322	183.112804	92.060040	T	*864.467289*	432.737283	847.440740	424.224008	846.456724	423.732000	8
3	314.207433	157.607354	296.196868	148.602072	I	*763.419610*	382.213443	746.393061	373.700169	745.409045	373.208161	7
4	401.239461	201.123368	383.228896	192.118086	S	*650.335546*	325.671411	633.308997	317.158137	632.324981	316.666129	6
5	514.323525	257.665401	496.312960	248.660118	L	*563.303518*	282.155397	546.276969	273.642123	545.292953	273.150115	5
6	629.350468	315.178872	611.339903	306.173589	D	*450.219454*	225.613365	433.192905	217.100090	432.208889	216.608082	4
7	730.398147	365.702712	712.387582	356.697429	T	*335.192511*	168.099893	318.165962	159.586619	317.181946	159.094611	3
8	817.430175	409.218726	799.419610	400.213443	S	*234.144832*	117.576054	217.118283	109.062779	216.134267	108.570771	2
9					K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTISLDTSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	962.528427	-0.004559	VTISLDTSK
30.5	962.528397	-0.004529	LSLSLESSK
19.9	962.521881	0.001987	PSLSRLMK
18.1	962.528397	-0.004529	SIISELSSK
14.2	962.521896	0.001972	VLDMRVSK
12.5	962.528442	-0.004574	VTTVSDLTK
12.4	962.529770	-0.005902	VTIPRPHQ
11.5	962.528427	-0.004559	VEVSITTSK
11.5	962.528397	-0.004529	LSLSSLSEK
11.4	962.521881	0.001987	SLPSMIRK

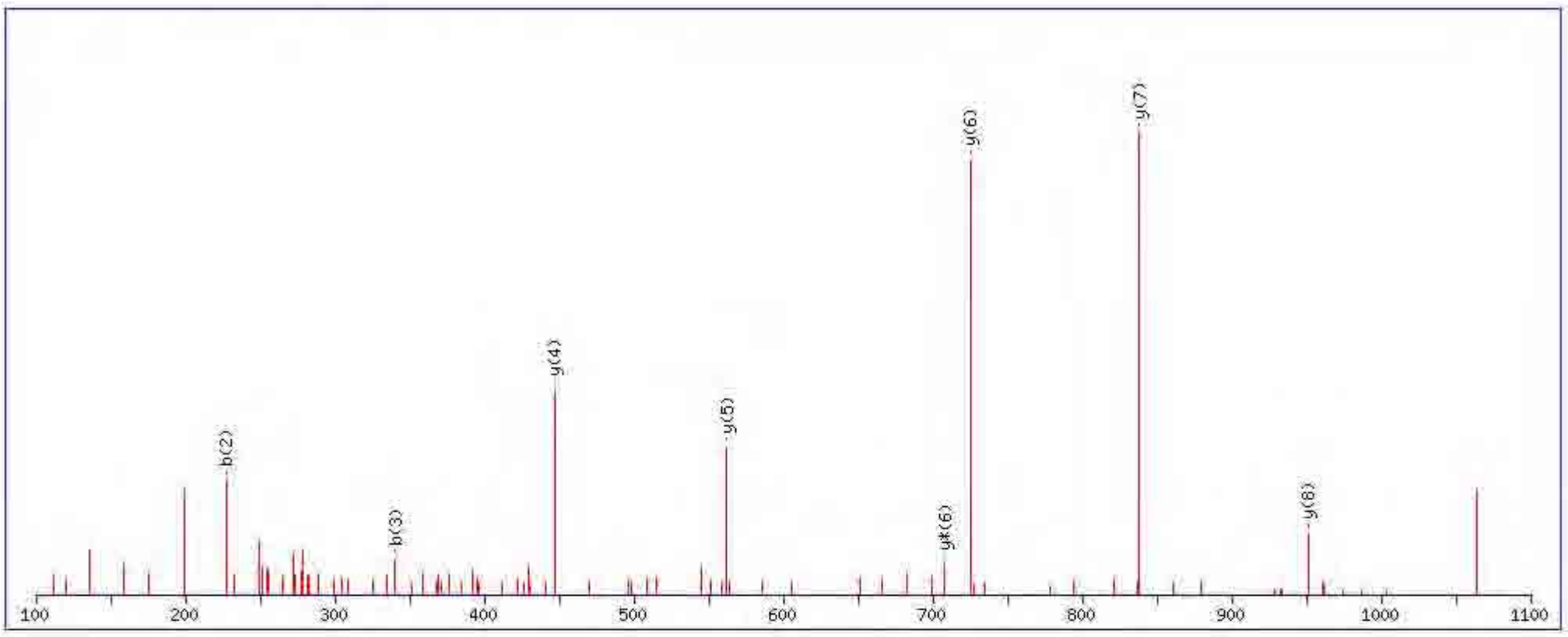
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

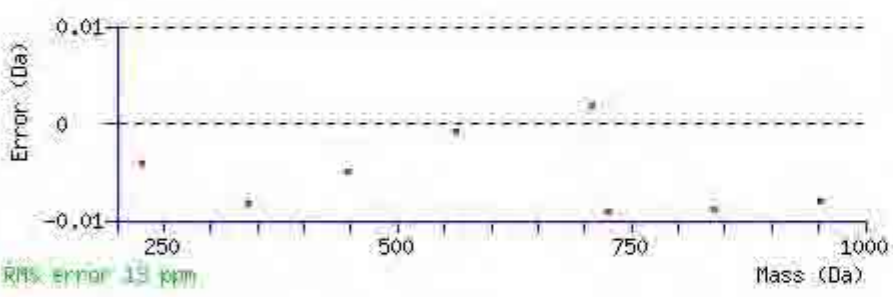
Match to Query 5686: 1063.559428 from(532.786990,2+) rtinseconds(1497) index(10647)
Title: Locus:1.1.1.1664.11
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

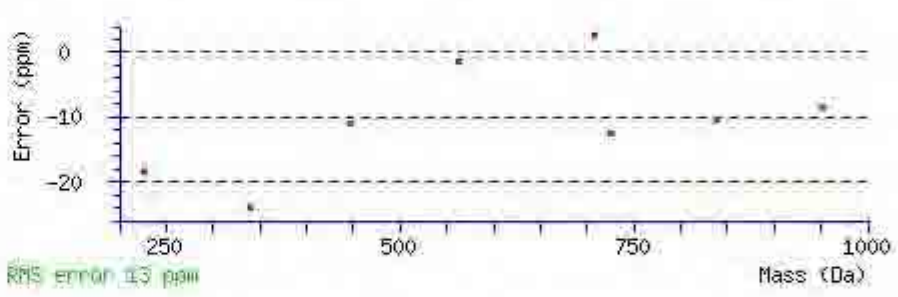
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 46 **Expect:** 0.0044
Matches : 8/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*951.489421*	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	*838.405357*	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	*725.321293*	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	*562.257964*	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	*447.231021*	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	1063.566177	-0.006749	LLIYDASNR
26.7	1063.566208	-0.006780	LPLAQVSAHP
19.8	1063.566208	-0.006780	LLLQHGADPT
17.2	1063.554947	0.004481	IIIADYDNK
17.2	1063.558334	0.001094	ILLTAGSDMK
17.2	1063.566208	-0.006780	ILPPDQRPP
17.2	1063.566208	-0.006780	ILPPDQRPP
17.2	1063.566208	-0.006780	ILPPDQRPP
17.2	1063.554947	0.004481	IPIANTEKY
17.2	1063.558334	0.001094	LLLATGSMDK

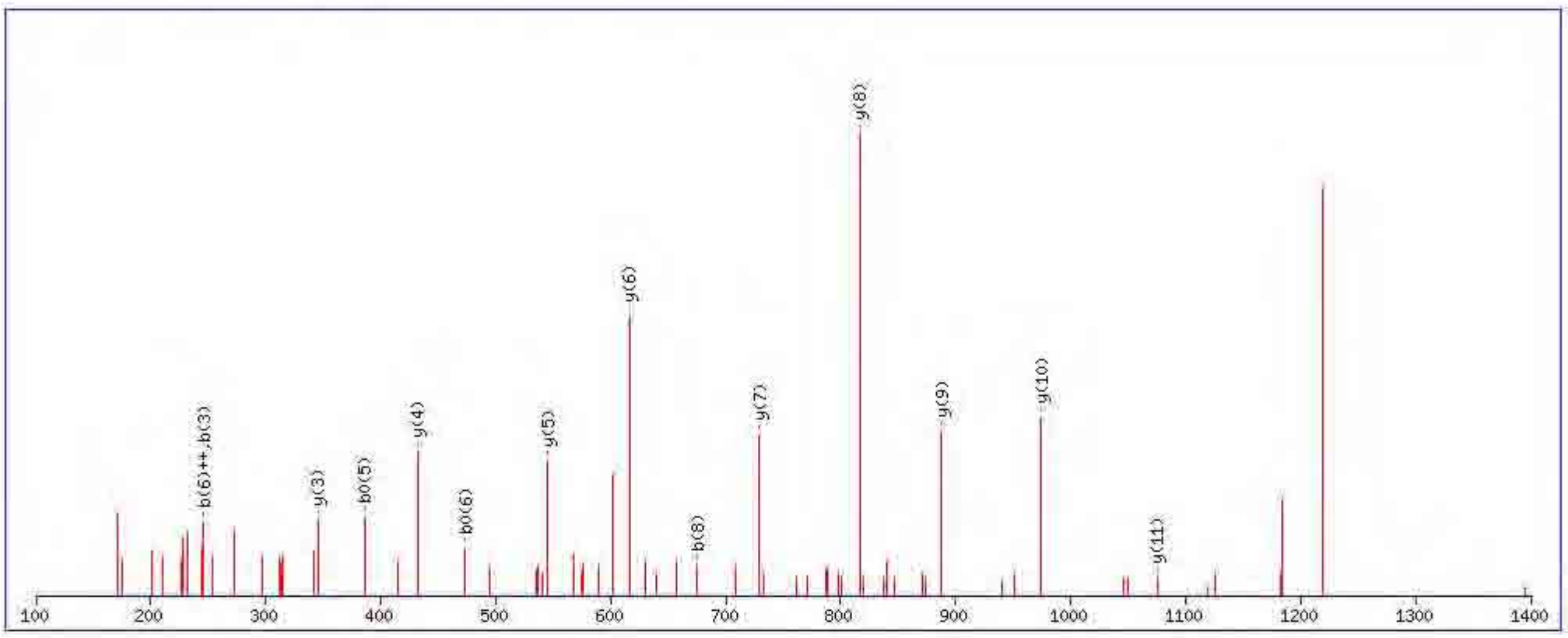
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGTSASLAISGLR**
Found in **LV102_HUMAN**, Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1

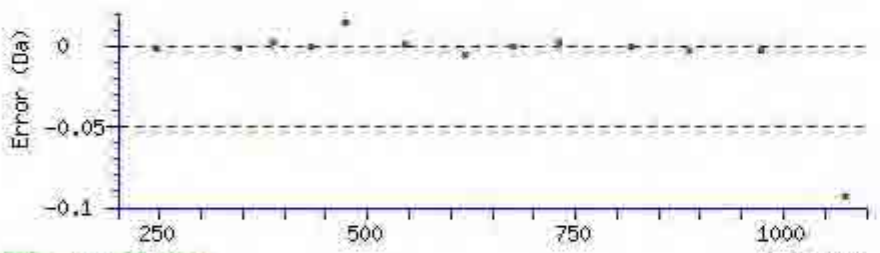
Match to Query 9968: 1218.652208 from(610.333380,2+) rtinseconds(1574) index(11651)
Title: Locus:1.1.1.1706.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

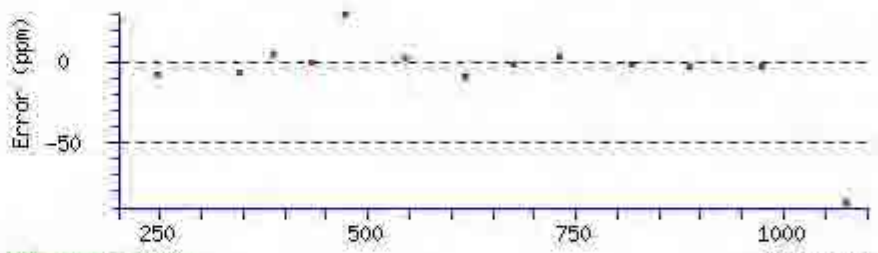
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1218.656799
Ions Score: 74 Expect: 6.9e-006
Matches : 14/114 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	145.060768	73.034022	127.050203	64.028740	G	1132.632063	566.819669	1115.605514	558.306395	1114.621498	557.814387	12
3	**246.108447**	123.557862	228.097882	114.552579	T	***1075.610599***	538.308937	1058.584050	529.795663	1057.600034	529.303655	11
4	333.140475	167.073875	315.129910	158.068593	S	***974.562920***	487.785098	957.536371	479.271823	956.552355	478.779815	10
5	404.177589	202.592432	386.167024	193.587150	A	***887.530892***	444.269084	870.504343	435.755809	869.520327	435.263801	9
6	491.209617	246.108446	473.199052	237.103164	S	***816.493778***	408.750527	799.467229	400.237252	798.483213	399.745244	8
7	604.293681	302.650479	586.283116	293.645196	L	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	7
8	**675.330795**	338.169036	657.320230	329.163753	A	***616.377686***	308.692481	599.351137	300.179206	598.367121	299.687198	6
9	788.414859	394.711068	770.404294	385.705785	I	***545.340572***	273.173924	528.314023	264.660649	527.330007	264.168641	5
10	875.446887	438.227082	857.436322	429.221799	S	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
11	932.468351	466.737814	914.457786	457.732531	G	***345.224480***	173.115878	328.197931	164.602603			3
12	1045.552415	523.279845	1027.541850	514.274563	L	288.203016	144.605146	271.176467	136.091871			2
13					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SGTSASLAISGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.6	1218.656799	-0.004591	SGTSASLAISGLR
17.7	1218.646912	0.005296	PARGSFLSAGTR
17.3	1218.645554	0.006654	QLLISSSSASNL
13.7	1218.656799	-0.004591	VATSVSNKSQAK
9.8	1218.664200	-0.011992	DAKTGVCITALK
8.7	1218.646881	0.005327	HEHSLKIEAR
8.7	1218.646896	0.005312	AFSGPRLASASR
8.6	1218.656799	-0.004591	LQTEGSLSTRK
8.6	1218.649567	0.002641	YLLEPISEKQ
8.3	1218.660828	-0.008620	PNGLAFISSGLK

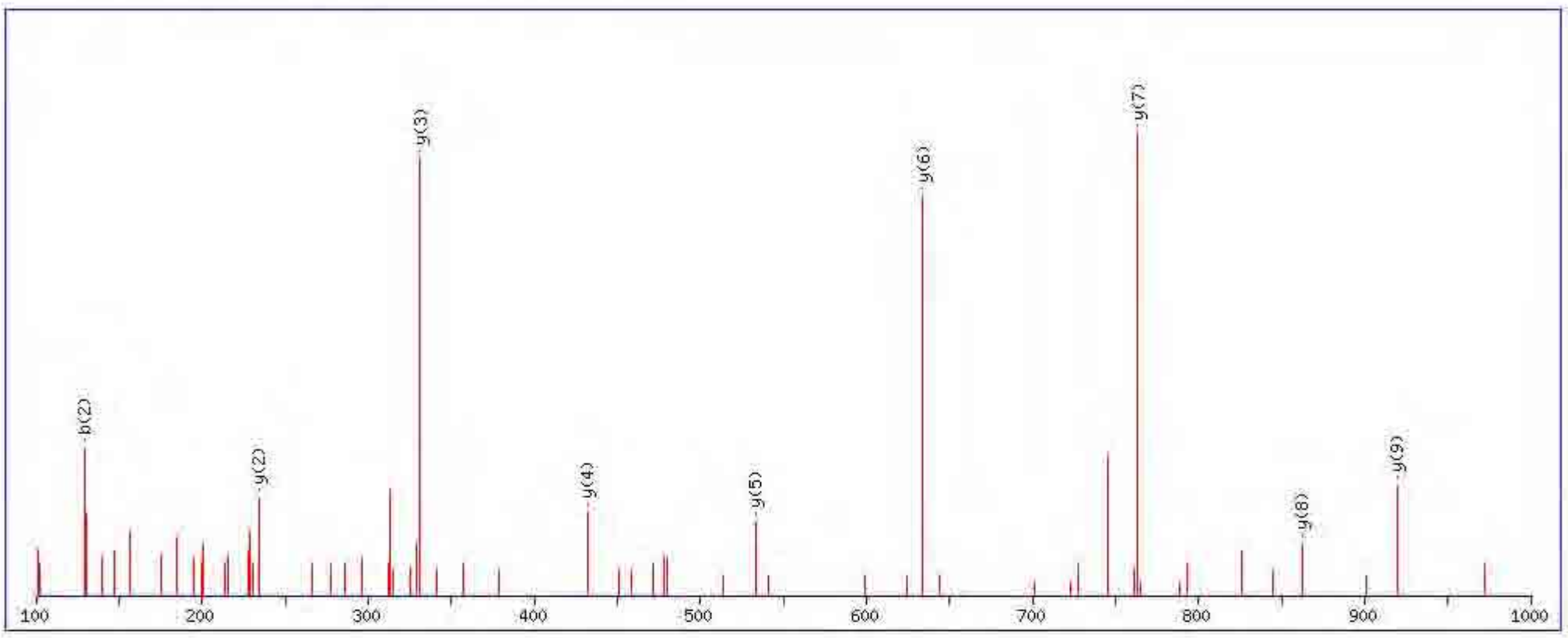
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVETTTPSK**
Found in **LAC2_HUMAN**, Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1

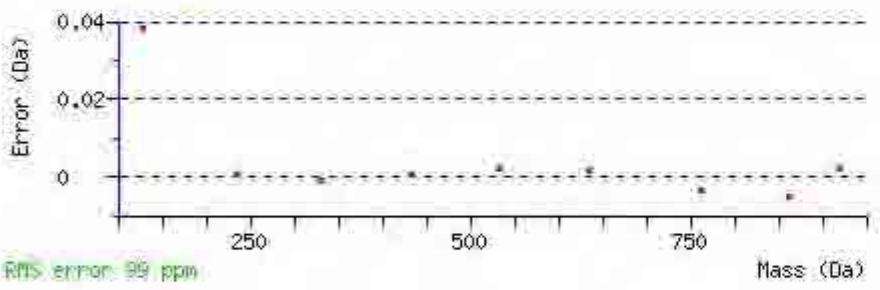
Match to Query 4022: 989.498328 from(495.756440,2+) rtinseconds(556) index(891)
Title: Locus:1.1.1.1153.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

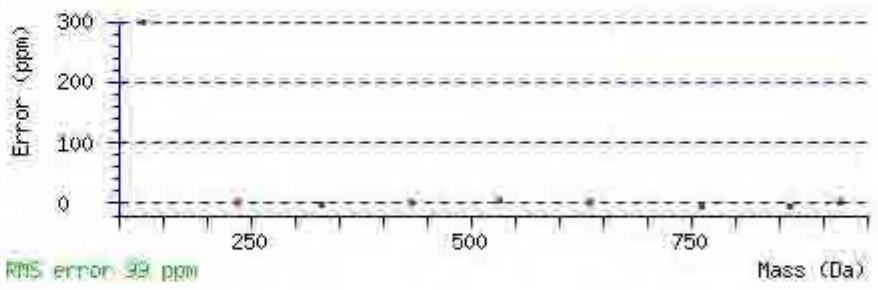
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 989.502945
Ions Score: 86 **Expect:** 5.6e-007
Matches : 9/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	129.065854	65.036565			G	*919.473104*	460.240190	902.446555	451.726916	901.462539	451.234908	9
3	228.134268	114.570772			V	*862.451640*	431.729458	845.425091	423.216184	844.441075	422.724176	8
4	357.176861	179.092069	339.166296	170.086786	E	*763.383226*	382.195251	746.356677	373.681977	745.372661	373.189969	7
5	458.224540	229.615908	440.213975	220.610626	T	*634.340633*	317.673955	617.314084	309.160680	616.330068	308.668672	6
6	559.272219	280.139748	541.261654	271.134465	T	*533.292954*	267.150115	516.266405	258.636841	515.282389	258.144833	5
7	660.319898	330.663587	642.309333	321.658305	T	*432.245275*	216.626275	415.218726	208.113001	414.234710	207.620993	4
8	757.372662	379.189969	739.362097	370.184687	P	*331.197596*	166.102436	314.171047	157.589161	313.187031	157.097153	3
9	844.404690	422.705983	826.394125	413.700701	S	*234.144832*	117.576054	217.118283	109.062779	216.134267	108.570771	2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AGVETTTPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.0	989.502945	-0.004617	AGVETTTPSK
25.1	989.502930	-0.004602	KSESTPDVK
21.2	989.502960	-0.004632	QPDTTSVVK
20.9	989.488998	0.009330	RATETGEAR
20.2	989.502930	-0.004602	NLETVLSQS
19.3	989.502914	-0.004586	KVESLSQEA
19.2	989.496399	0.001929	PNEMRTVK
18.5	989.496414	0.001914	AGVDICRVSA
18.5	989.496399	0.001929	QVEECRVK
15.7	989.493042	0.005286	QNQSWTVK

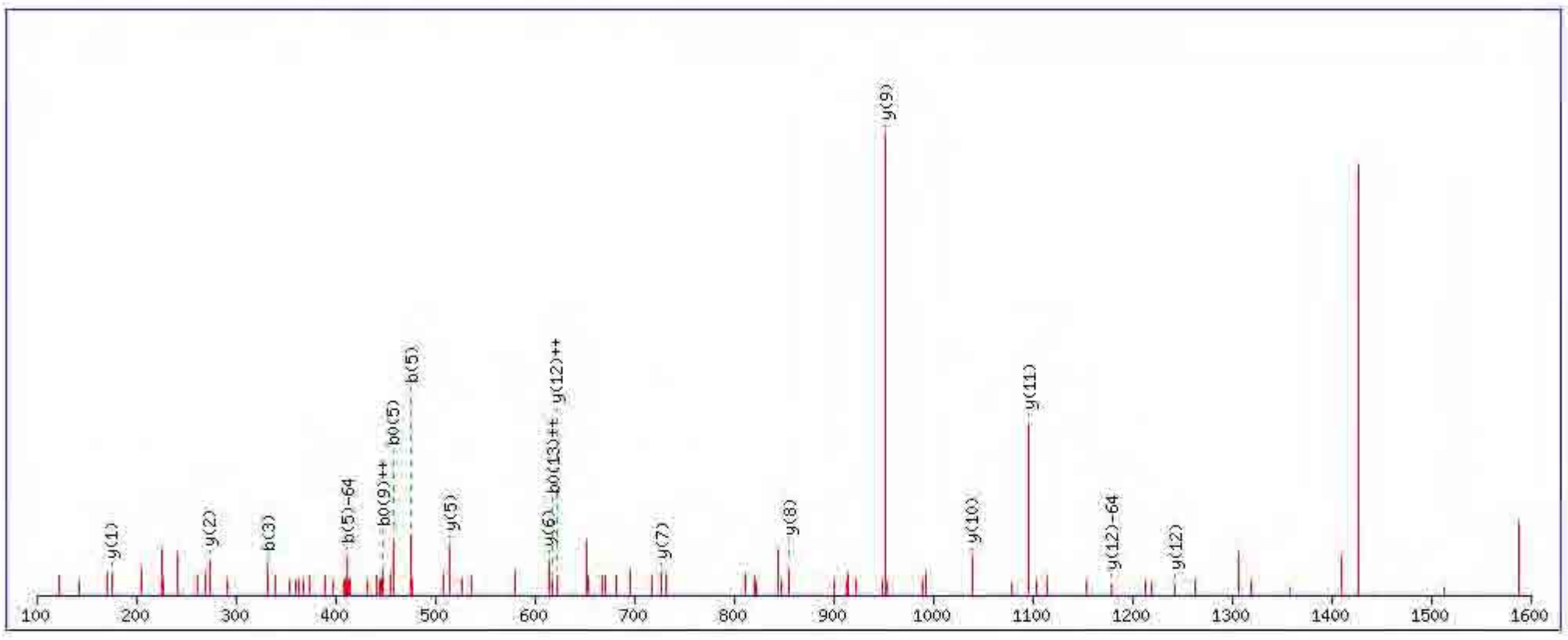
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALMGSPQLVAAVVR**
Found in **PLAK_HUMAN**, Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3

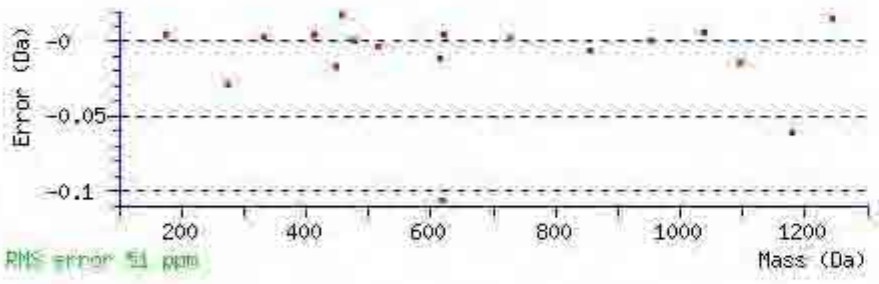
Match to Query 14346: 1426.787488 from(714.401020,2+) rtinseconds(1858) index(14829)
Title: Locus:1.1.1.1882.12
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

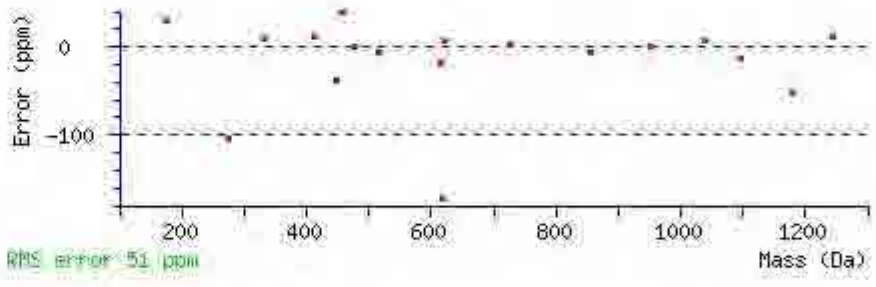
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1426.796616
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 50 **Expect:** 0.00012
Matches : 18/184 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							14
2	185.128454	93.067865					L	1356.766784	678.887030	1339.740235	670.373756	1338.756219	669.881748	13
3	332.163854	166.585565					M	*1243.682720*	622.344998	1226.656171	613.831724	1225.672155	613.339716	12
4	389.185318	195.096297					G	*1096.647320*	548.827298	1079.620771	540.314024	1078.636755	539.822016	11
5	476.217346	238.612311			458.206781	229.607028	S	*1039.625856*	520.316566	1022.599307	511.803292	1021.615291	511.311284	10
6	573.270110	287.138693			555.259545	278.133411	P	*952.593828*	476.800552	935.567279	468.287278			9
7	701.328688	351.167982	684.302139	342.654708	683.318123	342.162700	Q	*855.541064*	428.274170	838.514515	419.760896			8
8	814.412752	407.710014	797.386203	399.196740	796.402187	398.704732	L	*727.482486*	364.244881	710.455937	355.731607			7
9	913.481166	457.244221	896.454617	448.730947	895.470601	448.238939	V	*614.398422*	307.702849	597.371873	299.189575			6
10	984.518280	492.762778	967.491731	484.249504	966.507715	483.757496	A	*515.330008*	258.168642	498.303459	249.655368			5
11	1055.555394	528.281335	1038.528845	519.768061	1037.544829	519.276052	A	444.292894	222.650085	427.266345	214.136811			4
12	1154.623808	577.815542	1137.597259	569.302268	1136.613243	568.810260	V	373.255780	187.131528	356.229231	178.618254			3
13	1253.692222	627.349749	1236.665673	618.836475	1235.681657	618.344467	V	*274.187366*	137.597321	257.160817	129.084047			2
14							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ALMGSPQLVAAVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	1426.796616	-0.009128	ALMGSPQLVAAVVR
8.7	1426.796616	-0.009128	ALMGSPQLVAAVVR
7.7	1426.778000	0.009488	LQVAGEITTGPRVS
6.8	1426.777985	0.009503	QDITPKIVGGSNAK
4.4	1426.778824	0.008664	RPAQMAALLLAGIC
4.3	1426.796600	-0.009112	KPVSPLLTAAGMAR
4.3	1426.793259	-0.005771	FLQAQPIVPVQR
0.8	1426.789215	-0.001727	NAVGIEPVRLTSR
0.7	1426.785385	0.002103	APILCVLLPSPTR
0.6	1426.777969	0.009519	QLLQDPKLSQNK

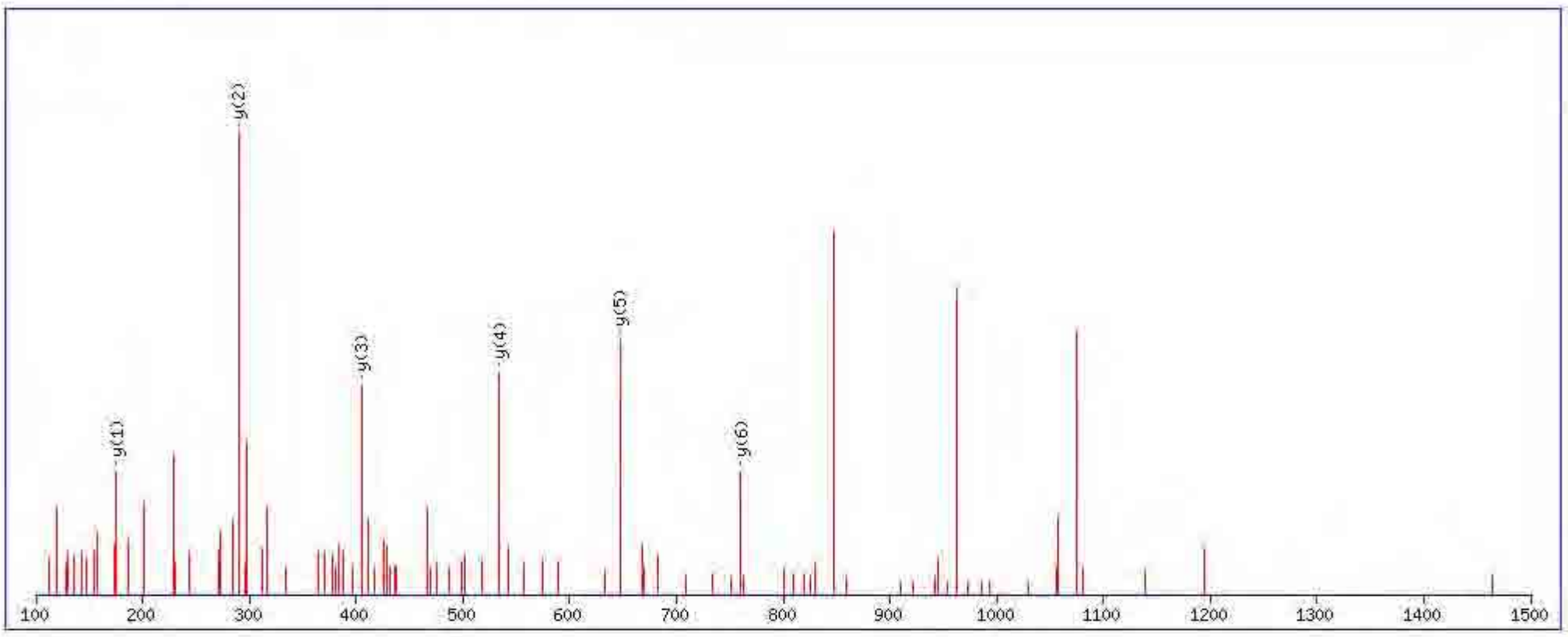
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTVIIEDDR**
Found in **PARD3_HUMAN**, Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2

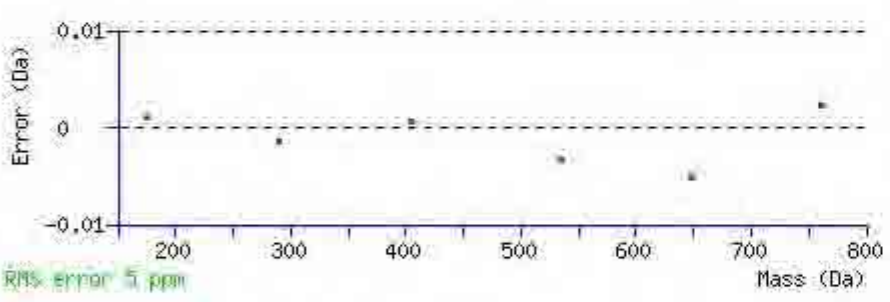
Match to Query 5952: 1074.516048 from(538.265300,2+) rtinseconds(1432) index(9910)
Title: Locus:1.1.1.1629.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

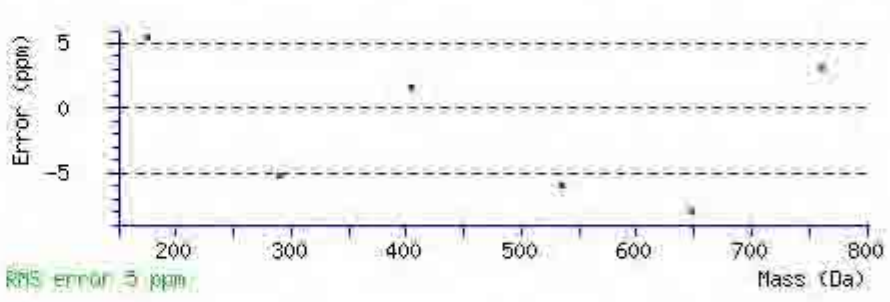
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.519318
Ions Score: 48 **Expect:** 0.0038
Matches : 6/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	217.081898	109.044587	199.071333	100.039304	T	960.499652	480.753464	943.473103	472.240190	942.489087	471.748182	8
3	316.150312	158.578794	298.139747	149.573512	V	859.451973	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	429.234376	215.120826	411.223811	206.115544	I	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
5	542.318440	271.662858	524.307875	262.657576	I	*647.299495*	324.153386	630.272946	315.640111	629.288930	315.148103	5
6	671.361033	336.184155	653.350468	327.178872	E	*534.215431*	267.611354	517.188882	259.098079	516.204866	258.606071	4
7	786.387976	393.697626	768.377411	384.692343	D	*405.172838*	203.090057	388.146289	194.576782	387.162273	194.084774	3
8	901.414919	451.211097	883.404354	442.205815	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DTVIIEDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1074.519318	-0.003270	DTVIIEDDR
33.0	1074.505386	0.010662	LDSAGREGDR
32.1	1074.519287	-0.003239	LEEGLEETR
29.3	1074.526688	-0.010640	LDSMAIEALP
26.6	1074.523331	-0.007283	EKLYPPSPP
19.6	1074.520645	-0.004597	LWTRNDDR
19.4	1074.526703	-0.010655	GSPMEISLPI
19.0	1074.523331	-0.007283	EKLYPPSPP
18.8	1074.509415	0.006633	PDSSWAPKR
18.8	1074.513443	0.002605	PEWLDFPR

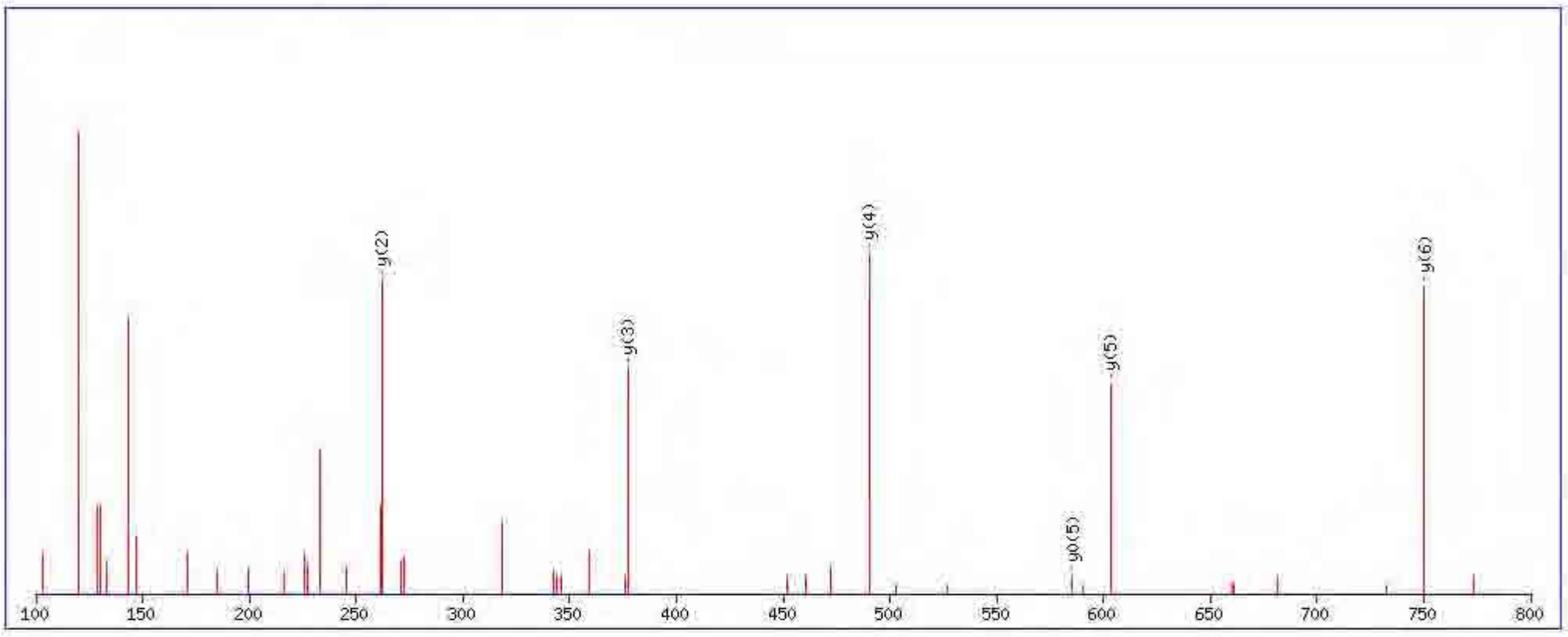
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVFLLDDK**
Found in **YE031_HUMAN**, Transmembrane protein ENSP00000382582 OS=Homo sapiens PE=4 SV=2

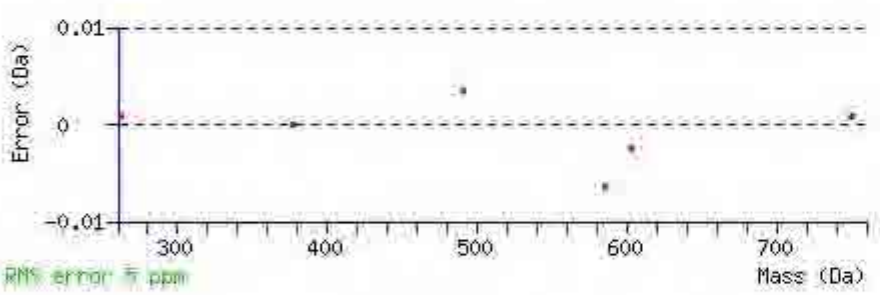
Match to Query 2517: 919.493768 from(460.754160,2+) rtinseconds(1963) index(15614)
Title: Locus:1.1.1.1938.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

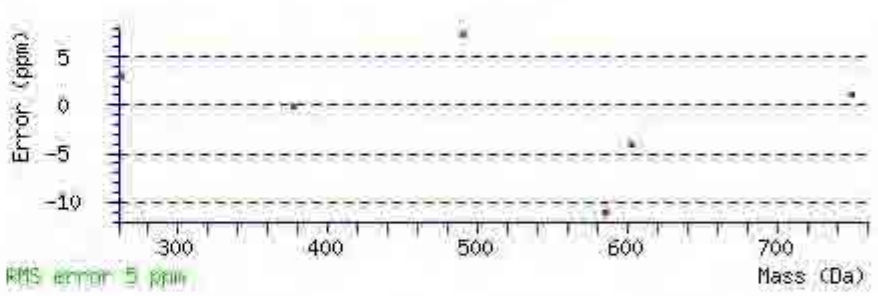
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 919.501480
Ions Score: 46 **Expect:** 0.004
Matches : 6/58 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							8
2	171.112804	86.060040			V	849.471646	425.239461	832.445097	416.726187	831.461081	416.234179	7
3	318.181218	159.594247			F	*750.403232*	375.705254	733.376683	367.191980	732.392667	366.699972	6
4	431.265282	216.136279			L	*603.334818*	302.171047	586.308269	293.657773	585.324253	293.165765	5
5	544.349346	272.678311			L	*490.250754*	245.629015	473.224205	237.115740	472.240189	236.623732	4
6	659.376289	330.191783	641.365724	321.186500	D	*377.166690*	189.086983	360.140141	180.573708	359.156125	180.081700	3
7	774.403232	387.705254	756.392667	378.699972	D	*262.139747*	131.573511	245.113198	123.060237	244.129182	122.568229	2
8					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AVFLLDDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	919.501480	-0.007712	AVFLLDDK
45.7	919.501480	-0.007712	GLFIIDDK
28.8	919.501480	-0.007712	GLFLPETK
18.3	919.501480	-0.007712	FLGLTPEK
17.2	919.494949	-0.001181	FILGMPSR
15.4	919.501511	-0.007743	GLFVGDLVT
15.4	919.487564	0.006204	LGFQGARAT
15.0	919.487091	0.006677	LMGPIVMK
14.9	919.501480	-0.007712	VAFPTEIK
14.7	919.491592	0.002176	LGFFPPSR

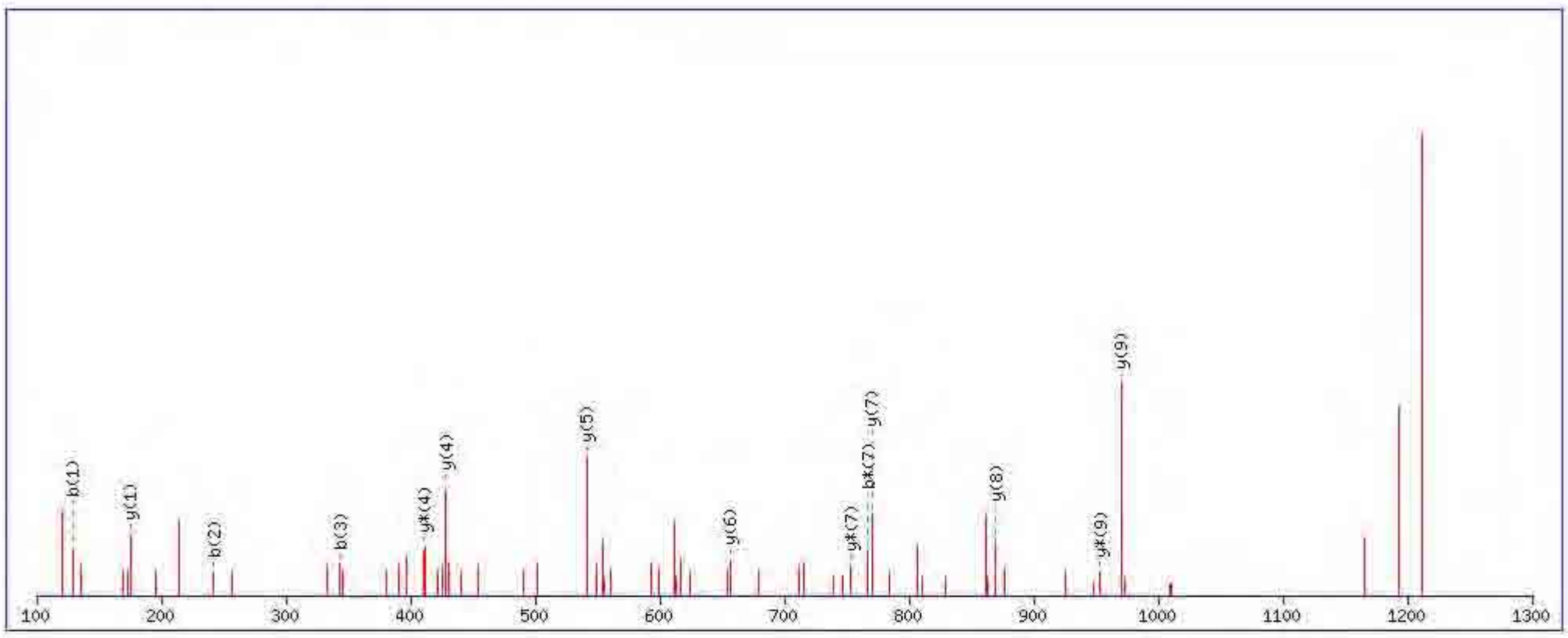
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QITVNDLPVGR**
Found in **PRDX1_HUMAN**, Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

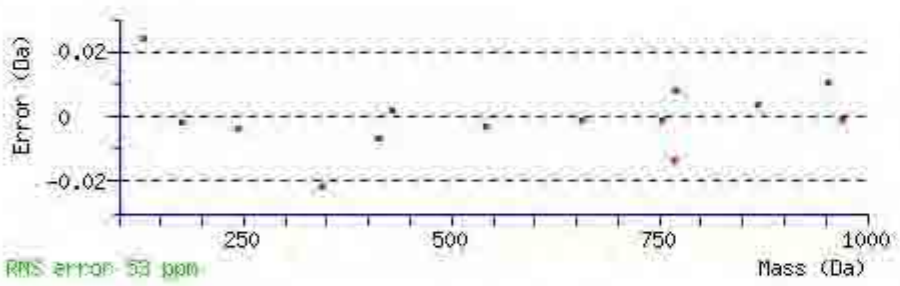
Match to Query 9716: 1210.656408 from(606.335480,2+) rtinseconds(1638) index(12359)
Title: Locus:1.1.1.1741.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

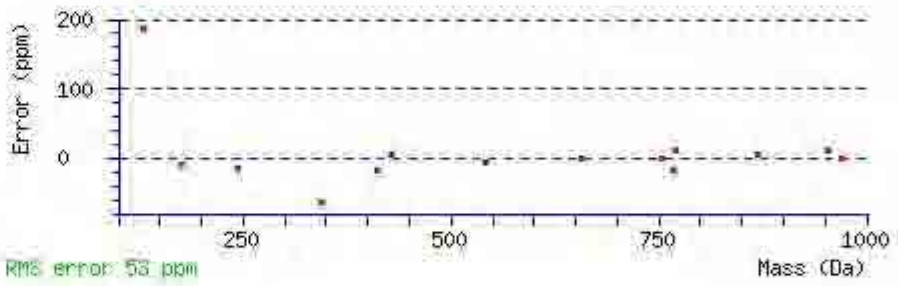
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1210.666992
Ions Score: 34 **Expect:** 0.035
Matches : 14/106 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	242.149918	121.578597	225.123369	113.065323			I	1083.615685	542.311481	1066.589136	533.798206	1065.605120	533.306198	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	*970.531621*	485.769449	953.505072	477.256174	952.521056	476.764166	9
4	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	V	*869.483942*	435.245609	852.457393	426.732335	851.473377	426.240327	8
5	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	N	*770.415528*	385.711402	753.388979	377.198128	752.404963	376.706120	7
6	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	D	*656.372601*	328.689939	639.346052	320.176664	638.362036	319.684656	6
7	784.419945	392.713611	767.393396	384.200336	766.409380	383.708328	L	*541.345658*	271.176467	524.319109	262.663193			5
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	P	*428.261594*	214.634435	411.235045	206.121160			4
9	980.541123	490.774200	963.514574	482.260925	962.530558	481.768917	V	331.208830	166.108053	314.182281	157.594778			3
10	1037.562587	519.284932	1020.536038	510.771657	1019.552022	510.279649	G	232.140416	116.573846	215.113867	108.060571			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QITVNDLPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.1	1210.666992	-0.010584	QITVNDLPVGR
17.4	1210.666992	-0.010584	QLTPGGGPLSLR
15.9	1210.645370	0.011038	LKGISICFSML
11.9	1210.653046	0.003362	PQDALARRPR
11.4	1210.655731	0.000677	QPGEIKPLDAK
10.5	1210.666977	-0.010569	ALGVSLSRPAPQ
10.5	1210.666977	-0.010569	ALGVSLSRPAPQ
9.0	1210.666992	-0.010584	KTLVPGPPGSSR
8.3	1210.659775	-0.003367	KLFIGGLSFET
8.0	1210.666992	-0.010584	KTLVPGPPGSSR

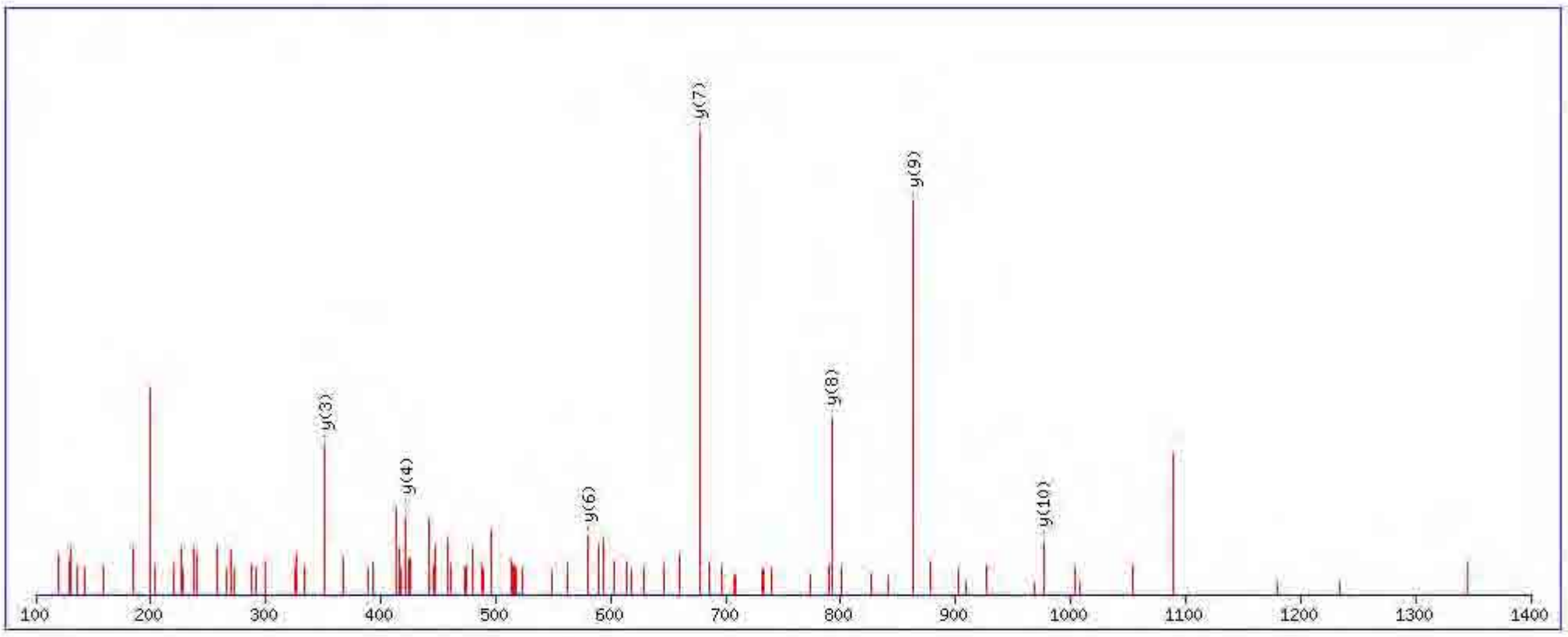
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLADPTGAFGK**
Found in **PRDX5_HUMAN**, Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4

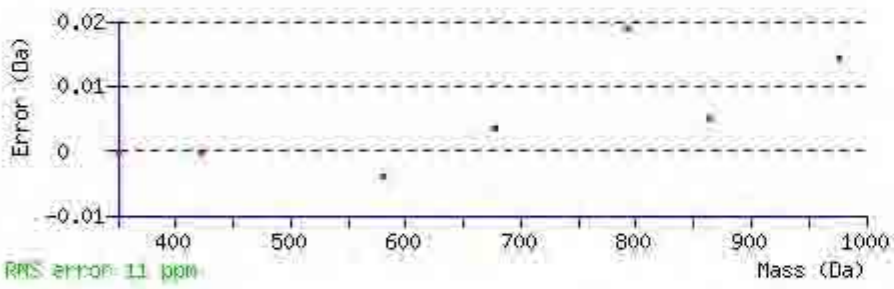
Match to Query 6329: 1088.585448 from(545.300000,2+) rtinseconds(1668) index(12756)
Title: Locus:1.1.1.1757.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

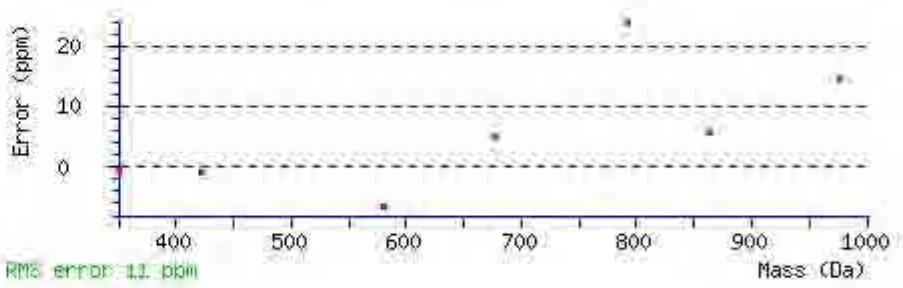
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1088.586609
Ions Score: 59 **Expect:** 0.00021
Matches : 7/84 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	227.175404	114.091340			L	*976.509824*	488.758550	959.483275	480.245276	958.499259	479.753268	10
3	298.212518	149.609897			A	*863.425760*	432.216518	846.399211	423.703244	845.415195	423.211236	9
4	413.239461	207.123369	395.228896	198.118086	D	*792.388646*	396.697961	775.362097	388.184687	774.378081	387.692679	8
5	510.292225	255.649750	492.281660	246.644468	P	*677.361703*	339.184490	660.335154	330.671215	659.351138	330.179207	7
6	611.339904	306.173590	593.329339	297.168308	T	*580.308939*	290.658108	563.282390	282.144833	562.298374	281.652825	6
7	668.361368	334.684322	650.350803	325.679040	G	479.261260	240.134268	462.234711	231.620994			5
8	739.398482	370.202879	721.387917	361.197597	A	*422.239796*	211.623536	405.213247	203.110261			4
9	886.466896	443.737086	868.456331	434.731804	F	*351.202682*	176.104979	334.176133	167.591704			3
10	943.488360	472.247818	925.477795	463.242536	G	204.134268	102.570772	187.107719	94.057498			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLADPTGAFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1088.586609	-0.001161	LLADPTGAFGK
19.6	1088.589951	-0.004503	LPAVEAAMKK
18.5	1088.589951	-0.004503	LLAALGEMQK
18.0	1088.575394	0.010054	LPADTVFTIP
10.8	1088.580078	0.005370	RPPKTPPCPP
10.1	1088.580078	0.005370	LVSLAMHFR
8.8	1088.586594	-0.001146	EPHISPIAPI
8.5	1088.589951	-0.004503	LLGLLEEMR
8.0	1088.578735	0.006713	ILGELAMVLD
7.7	1088.586594	-0.001146	LPDAERFLI

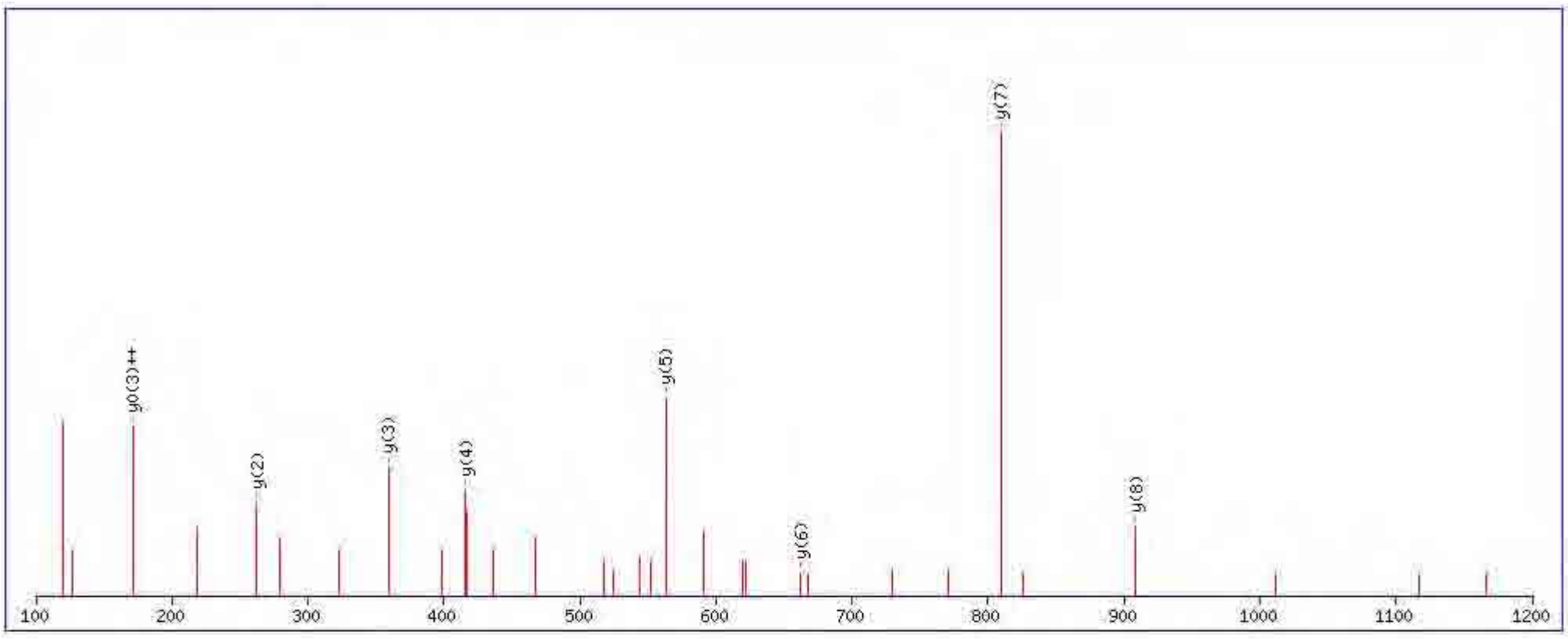
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVFVFGPDK**
Found in **PRDX6_HUMAN**, Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3

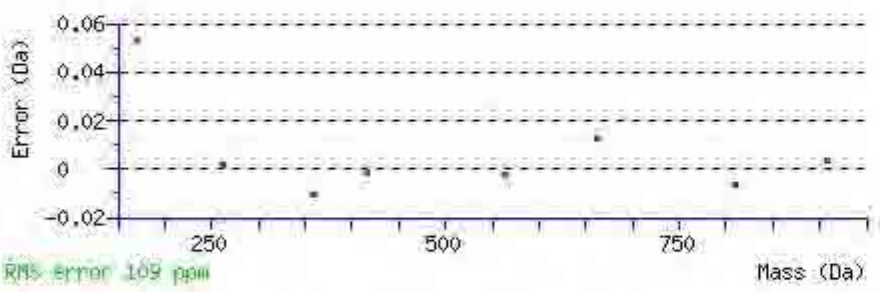
Match to Query 4411: 1006.547328 from(504.280940,2+) rtinseconds(1919) index(15343)
Title: Locus:1.1.1.1915.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

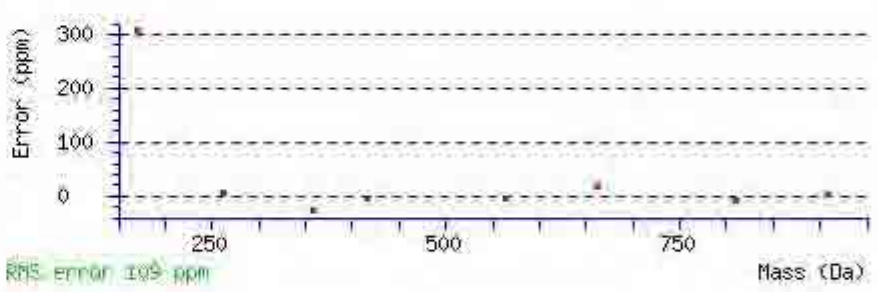
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1006.548798
Ions Score: 50 **Expect:** 2.6e-005
Matches : 8/64 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	199.144104	100.075690			V	*908.487631*	454.747454	891.461082	446.234179	890.477066	445.742171	8
3	346.212518	173.609897			F	*809.419217*	405.213247	792.392668	396.699972	791.408652	396.207964	7
4	445.280932	223.144104			V	*662.350803*	331.679040	645.324254	323.165765	644.340238	322.673757	6
5	592.349346	296.678311			F	*563.282389*	282.144833	546.255840	273.631558	545.271824	273.139550	5
6	649.370810	325.189043			G	*416.213975*	208.610626	399.187426	200.097351	398.203410	199.605343	4
7	746.423574	373.715425			P	*359.192511*	180.099893	342.165962	171.586619	341.181946	171.094611	3
8	861.450517	431.228897	843.439952	422.223614	D	*262.139747*	131.573511	245.113198	123.060237	244.129182	122.568229	2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVFVFGPDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1006.548798	-0.001470	VVFVFGPDK
0.9	1006.544739	0.002589	VVAVEAYTR
0.9	1006.552155	-0.004827	VVLGIFQTM
0.9	1006.544724	0.002604	AVARSIVEY
0.4	1006.555984	-0.008656	VVRTTFER
0.1	1006.552139	-0.004811	VVLDCFLAK
0.1	1006.548767	-0.001439	VVPYAAIQF
0.1	1006.544754	0.002574	VVTSEIFRG
0.1	1006.548752	-0.001424	VVYEWALK

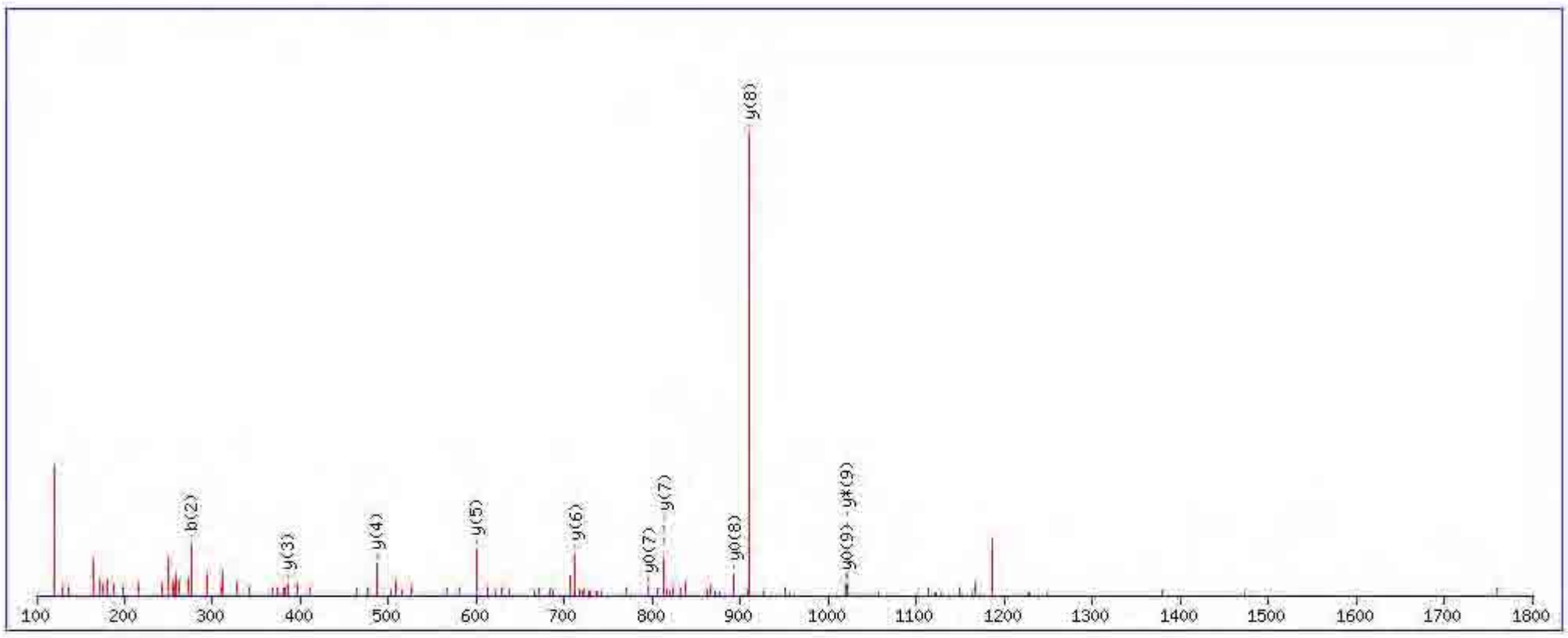
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQPTLLTLPR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

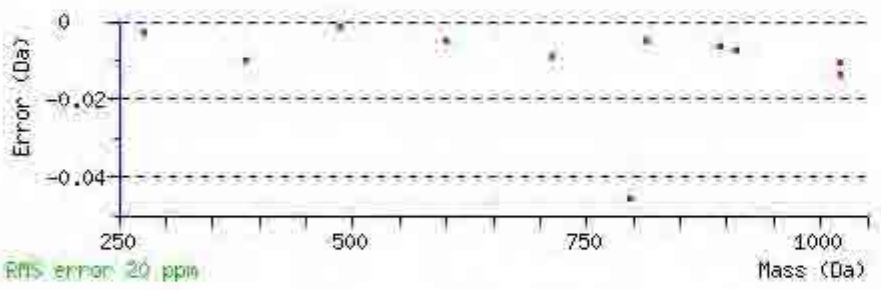
Match to Query 9013: 1184.685748 from(593.350150,2+) rtinseconds(3287) index(22210)
Title: Locus:1.1.1.2642.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

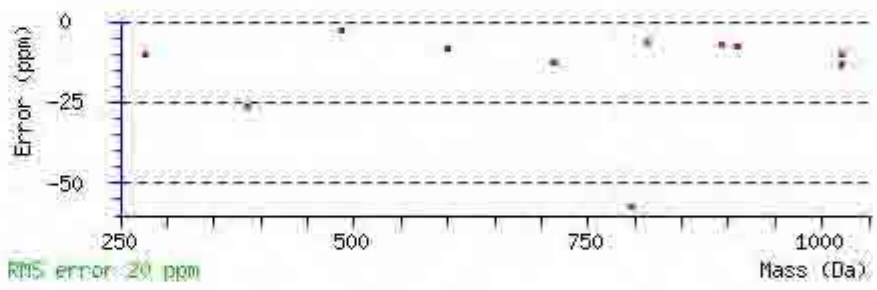
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.691742
Ions Score: 34 **Expect:** 0.0093
Matches : 11/94 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							10
2	276.134268	138.570772	259.107719	130.057497			Q	1038.630608	519.818942	1021.604059	511.305668	1020.620043	510.813660	9
3	373.187032	187.097154	356.160483	178.583879			P	*910.572030*	455.789653	893.545481	447.276379	892.561465	446.784371	8
4	474.234711	237.620994	457.208162	229.107719	456.224146	228.615711	T	*813.519266*	407.263271	796.492717	398.749997	795.508701	398.257989	7
5	587.318775	294.163026	570.292226	285.649751	569.308210	285.157743	L	*712.471587*	356.739432	695.445038	348.226157	694.461022	347.734149	6
6	700.402839	350.705058	683.376290	342.191783	682.392274	341.699775	L	*599.387523*	300.197400	582.360974	291.684125	581.376958	291.192117	5
7	801.450518	401.228897	784.423969	392.715623	783.439953	392.223615	T	*486.303459*	243.655368	469.276910	235.142093	468.292894	234.650085	4
8	914.534582	457.770929	897.508033	449.257655	896.524017	448.765647	L	*385.255780*	193.131528	368.229231	184.618254			3
9	1011.587346	506.297311	994.560797	497.784037	993.576781	497.292029	P	272.171716	136.589496	255.145167	128.076222			2
10							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FQPTLLTLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.2	1184.691742	-0.005994	FQPTLLTLPR
34.1	1184.676483	0.009265	TPSALILTPTR
11.8	1184.676483	0.009265	LTLTRLDPGSL
10.8	1184.676468	0.009280	KEDLTTLLPR
10.3	1184.683868	0.001880	TMPKLIPPLK
10.2	1184.695099	-0.009351	ICSAVLPLLTR
7.9	1184.677811	0.007937	FKPPRQLGAR
7.9	1184.691727	-0.005979	LGLRPFIPEK
6.5	1184.681839	0.003909	WRPFIIRPI
6.3	1184.676514	0.009234	TVLVIPVGDTR

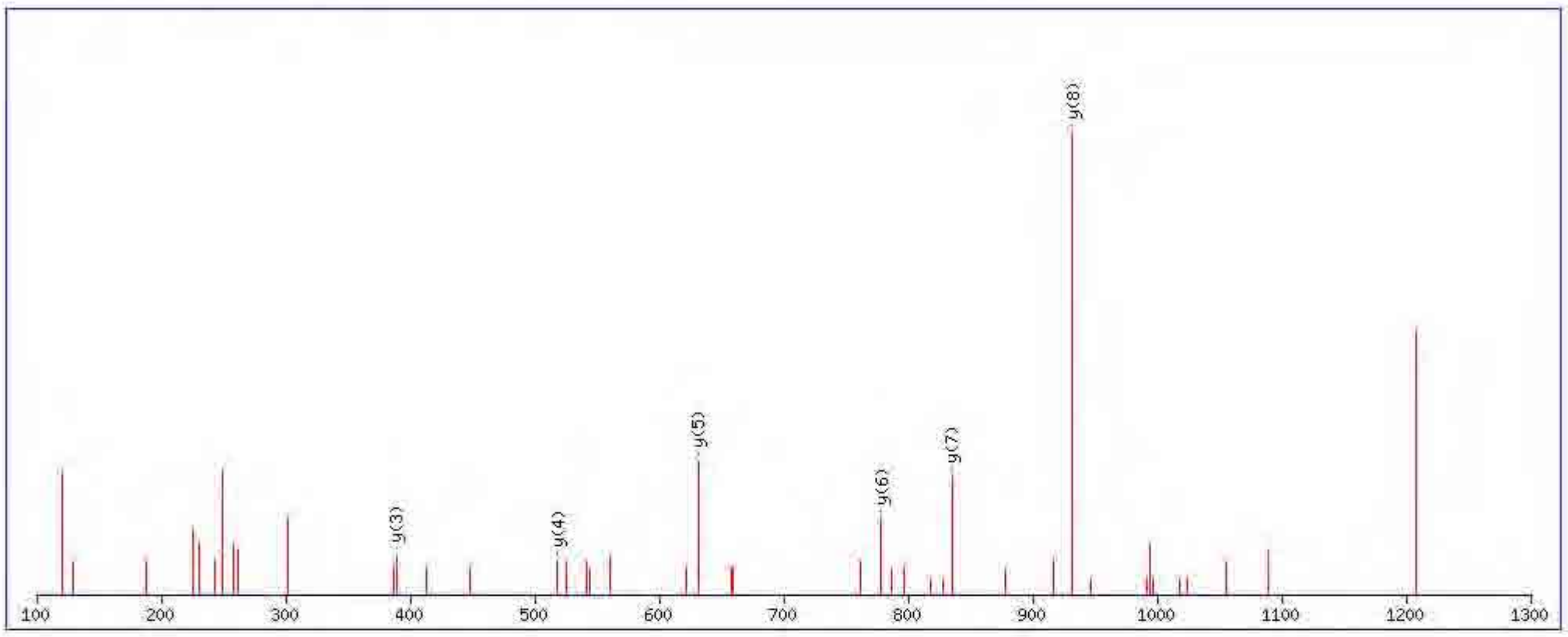
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFPGFLENQK**
Found in **S10AA_HUMAN**, Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

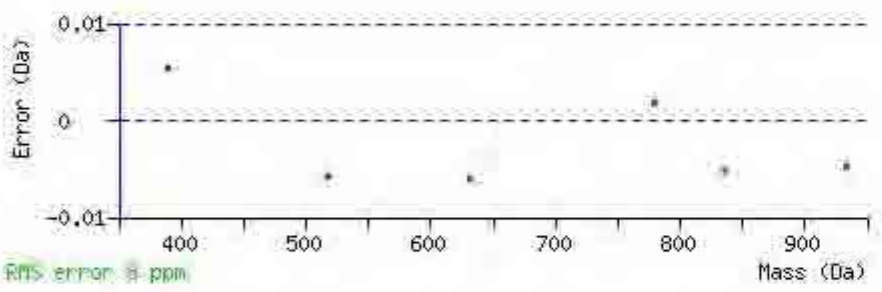
Match to Query 9634: 1207.590968 from(604.802760,2+) rtinseconds(1884) index(15052)
Title: Locus:1.1.1.1896.13
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

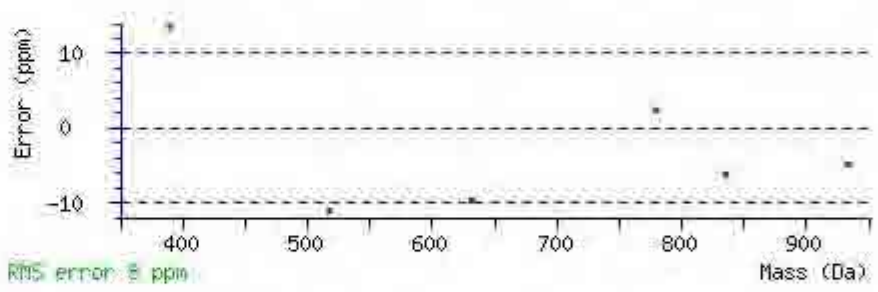
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1207.587326
Ions Score: 44 **Expect:** 0.0018
Matches : 6/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	277.118283	139.062779			259.107718	130.057497	F	1079.552022	540.279649	1062.525473	531.766375	1061.541457	531.274367	9
3	374.171047	187.589161			356.160482	178.583879	P	*932.483608*	466.745442	915.457059	458.232168	914.473043	457.740160	8
4	431.192511	216.099893			413.181946	207.094611	G	*835.430844*	418.219060	818.404295	409.705786	817.420279	409.213778	7
5	578.260925	289.634101			560.250360	280.628818	F	*778.409380*	389.708328	761.382831	381.195054	760.398815	380.703046	6
6	691.344989	346.176133			673.334424	337.170850	L	*631.340966*	316.174121	614.314417	307.660847	613.330401	307.168839	5
7	820.387582	410.697429			802.377017	401.692147	E	*518.256902*	259.632089	501.230353	251.118815	500.246337	250.626807	4
8	934.430509	467.718893	917.403960	459.205618	916.419944	458.713610	N	*389.214309*	195.110793	372.187760	186.597518			3
9	1062.489087	531.748182	1045.462538	523.234907	1044.478522	522.742899	Q	275.171382	138.089329	258.144833	129.576055			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EFPGFLENQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	1207.587326	0.003642	EFPGFLENQK
13.4	1207.580811	0.010157	TRMEPFHFK
10.6	1207.583313	0.007655	SATNGQPPAPAPT
8.4	1207.583313	0.007655	YIASTQRPDGT
6.7	1207.583313	0.007655	FTELSSPGAQR
5.8	1207.581985	0.008983	EPSTTILTTET
5.3	1207.594070	-0.003102	MTLCPIETLR
4.0	1207.598572	-0.007604	PFGLFGNAQNK
4.0	1207.600571	-0.009603	SLMTELEIEK
3.2	1207.579468	0.011500	FSMVLPEVEAA

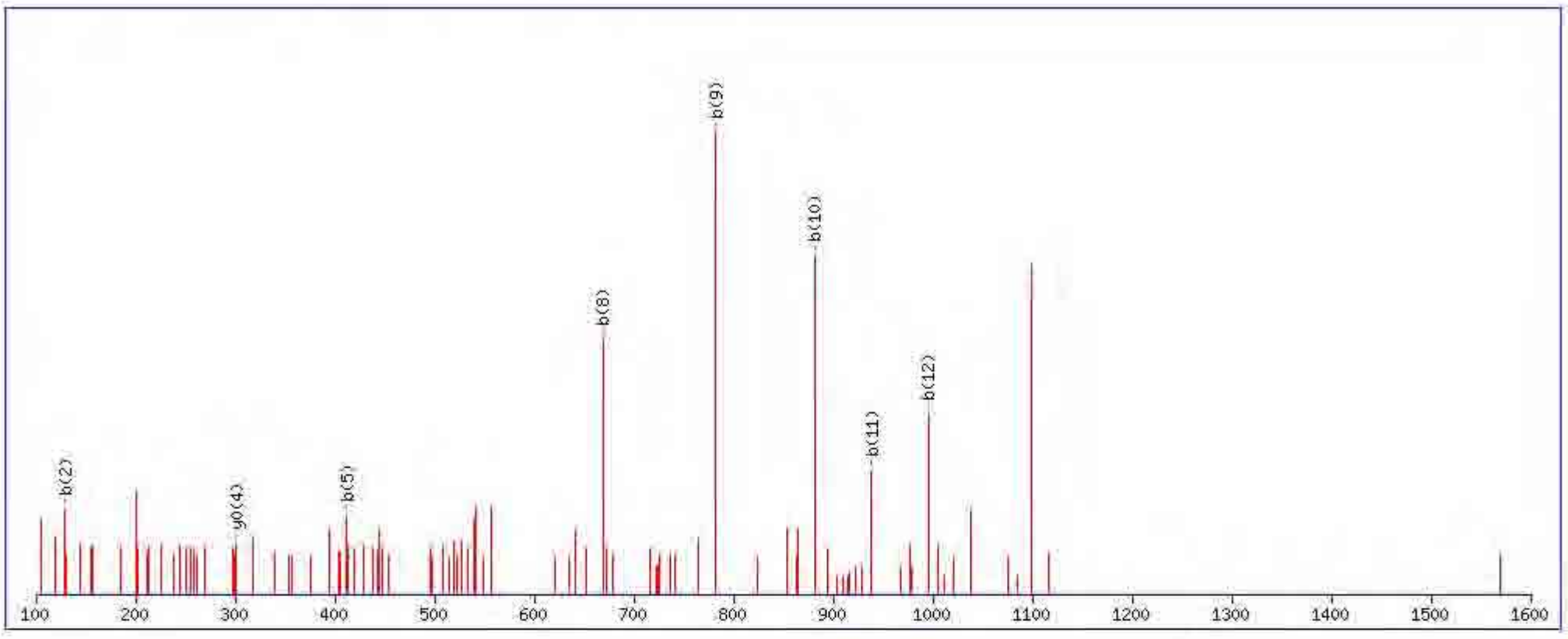
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGGPLGLSIVGGS**
Found in **SCRIB_HUMAN**, Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4

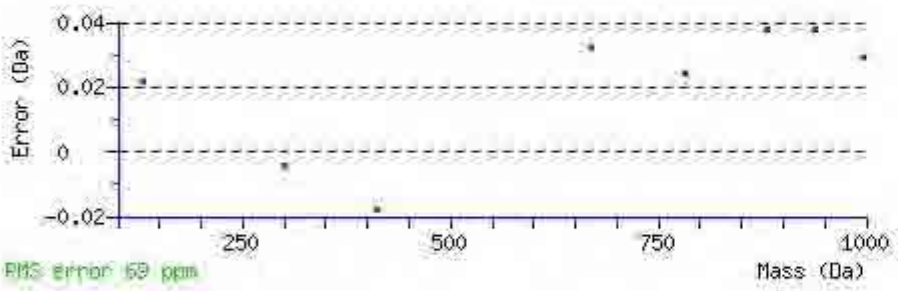
Match to Query 6588: 1099.591928 from(550.803240,2+) rtinseconds(1862) index(14862)
Title: Locus:1.1.1.1884.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

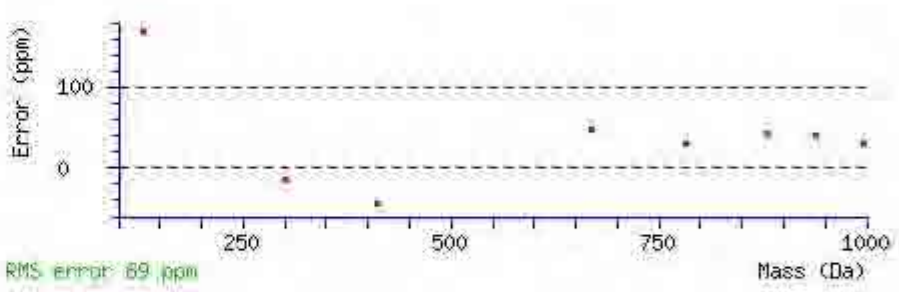
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1099.587357
Variable modifications:
P4 : Oxidation (P)
Ions Score: 32 **Expect:** 0.0045
Matches : 8/82 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A					13
2	*129.065854*	65.036565			G	1029.557502	515.282389	1011.546937	506.277107	12
3	186.087318	93.547297			G	972.536038	486.771657	954.525473	477.766375	11
4	299.134997	150.071136			P	915.514574	458.260925	897.504009	449.255643	10
5	*412.219061*	206.613169			L	802.466895	401.737086	784.456330	392.731803	9
6	469.240525	235.123900			G	689.382831	345.195054	671.372266	336.189771	8
7	582.324589	291.665933			L	632.361367	316.684322	614.350802	307.679039	7
8	*669.356617*	335.181947	651.346052	326.176664	S	519.277303	260.142290	501.266738	251.137007	6
9	*782.440681*	391.723979	764.430116	382.718696	I	432.245275	216.626275	414.234710	207.620993	5
10	*881.509095*	441.258186	863.498530	432.252903	V	319.161211	160.084243	301.150646	151.078961	4
11	*938.530559*	469.768918	920.519994	460.763635	G	220.092797	110.550037	202.082232	101.544754	3
12	*995.552023*	498.279650	977.541458	489.274367	G	163.071333	82.039304	145.060768	73.034022	2
13					S	106.049869	53.528572	88.039304	44.523290	1





NCBI **BLAST** search of AGGPLGLSIVGGS
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.1	1099.587357	0.004571	AGGPLGLSIVGGS
6.6	1099.598541	-0.006613	NSLPEIKGSR
5.3	1099.598572	-0.006644	SLPDKQVTGR
5.2	1099.587326	0.004602	GEISPGKINSV
5.1	1099.587326	0.004602	QAPVEKVADK
5.0	1099.587341	0.004587	SGTTPKPVTNS
4.5	1099.587311	0.004617	SIPNIIKNDS
4.5	1099.598557	-0.006629	VTPNLNRSLS
2.9	1099.598541	-0.006613	ISLLNQRQE
2.1	1099.598557	-0.006629	KPRSVEVAAGS

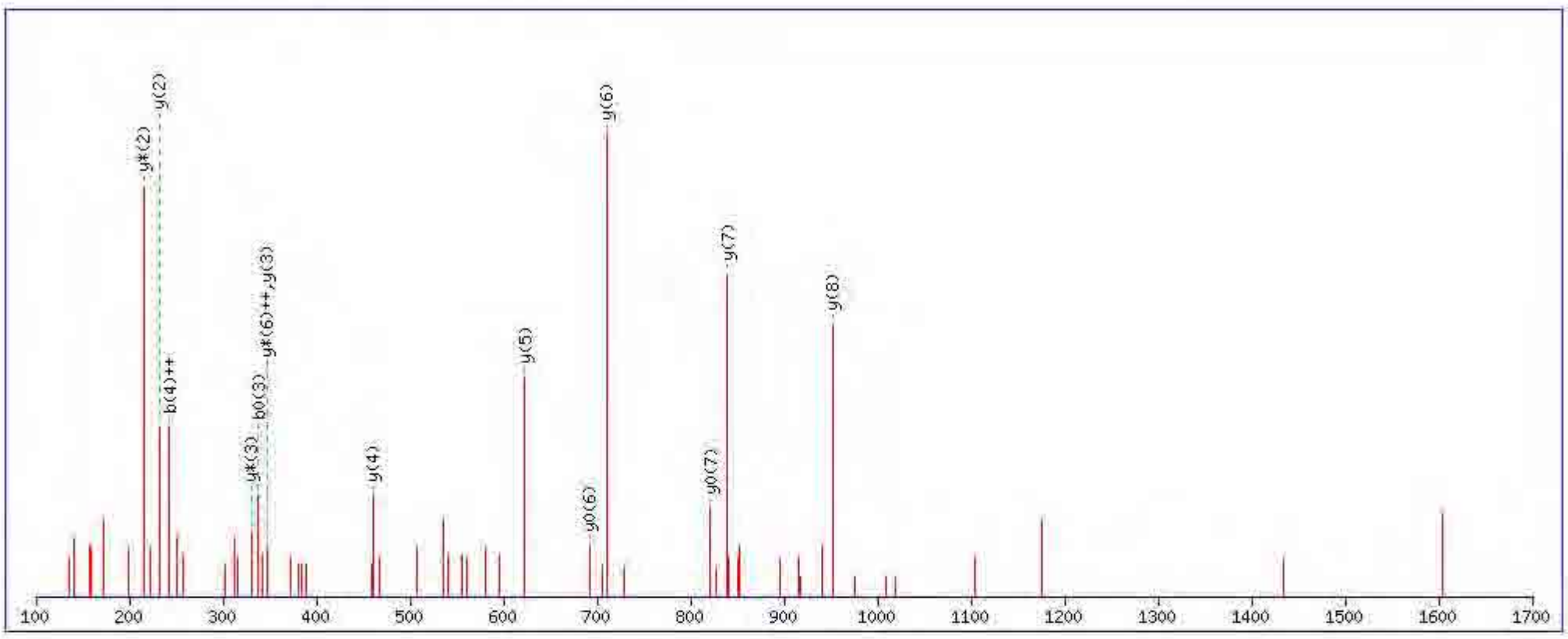
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLESYIDGR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

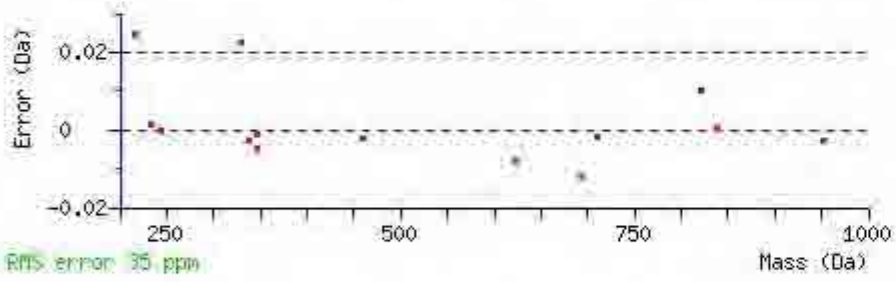
Match to Query 9269: 1193.587388 from(597.800970,2+) rtinseconds(1898) index(15172)
Title: Locus:1.1.1.1903.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

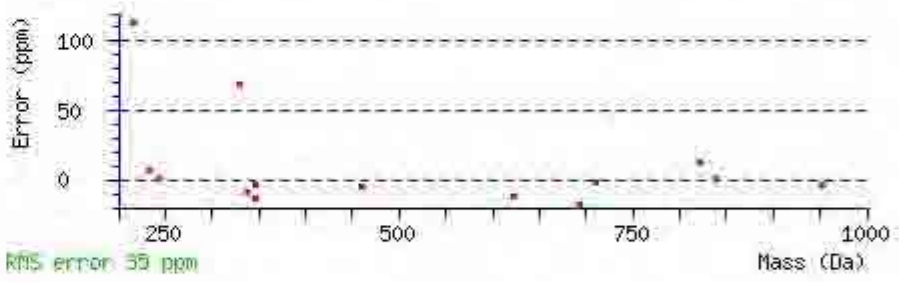
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1193.592789
Ions Score: 51 **Expect:** 0.00029
Matches : 15/86 fragment ions using 20 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572	112.039304	56.523290	E							10
2	243.133933	122.070605	225.123368	113.065322	L	1065.557501	533.282389	1048.530952	524.769114	1047.546936	524.277106	9
3	356.217997	178.612637	338.207432	169.607354	L	*952.473437*	476.740357	935.446888	468.227082	934.462872	467.735074	8
4	485.260590	243.133933	467.250025	234.128651	E	*839.389373*	420.198325	822.362824	411.685050	821.378808	411.193042	7
5	572.292618	286.649947	554.282053	277.644665	S	*710.346780*	355.677028	693.320231	347.163754	692.336215	346.671746	6
6	735.355947	368.181612	717.345382	359.176329	Y	*623.314752*	312.161014	606.288203	303.647740	605.304187	303.155732	5
7	848.440011	424.723644	830.429446	415.718361	I	*460.251423*	230.629350	443.224874	222.116075	442.240858	221.624067	4
8	963.466954	482.237115	945.456389	473.231833	D	*347.167359*	174.087318	330.140810	165.574043	329.156794	165.082035	3
9	1020.488418	510.747847	1002.477853	501.742565	G	*232.140416*	116.573846	215.113867	108.060572			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ELLESYIDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.6	1193.592789	-0.005401	ELLESYIDGR
12.2	1193.580231	0.007157	HHLPSHRSHS
10.9	1193.582916	0.004472	EPPEVHWLR
10.8	1193.582932	0.004456	TPPYQVHISH
10.8	1193.592804	-0.005416	INQESGSLSFL
8.3	1193.592789	-0.005401	IEQNYSSKPI
7.1	1193.592789	-0.005401	IELYQSSQNL
6.2	1193.586960	0.000428	WKTFFETVH
5.9	1193.589645	-0.002257	NLPIKMSMGR
4.6	1193.589630	-0.002242	ELIMSGKNMR

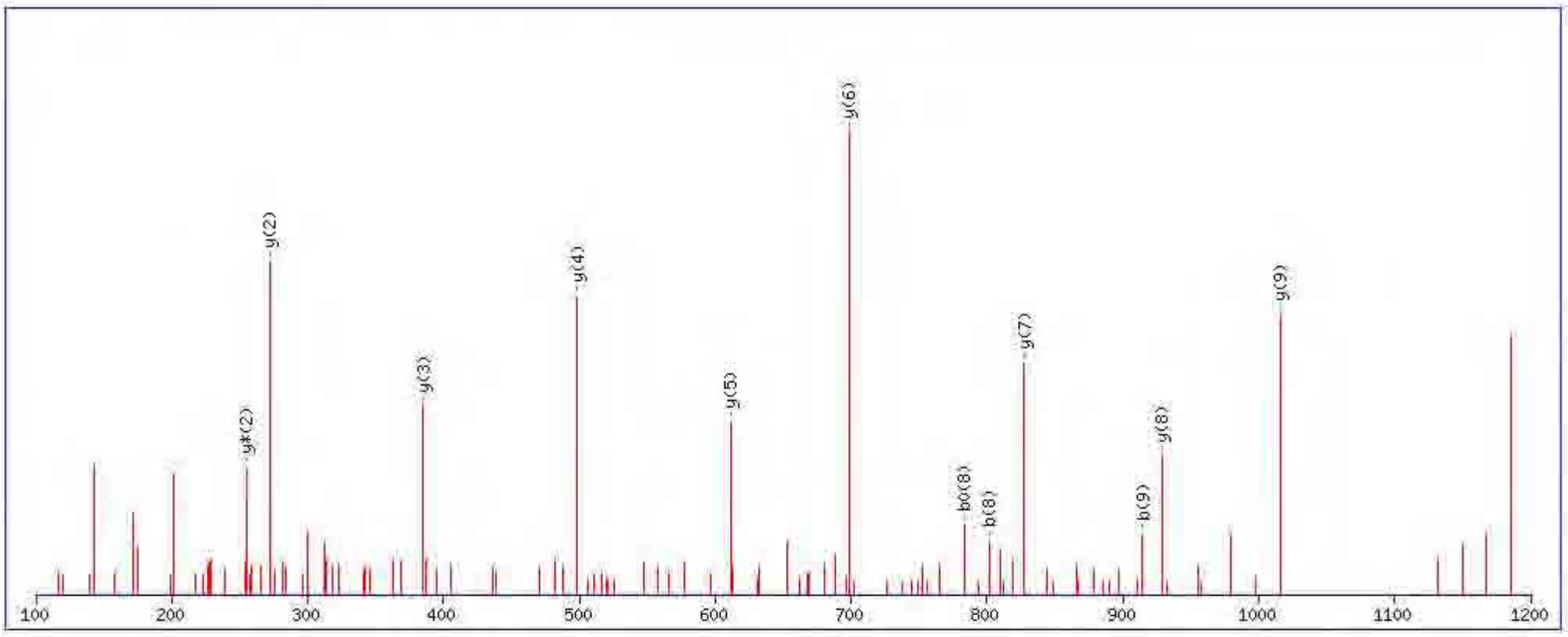
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

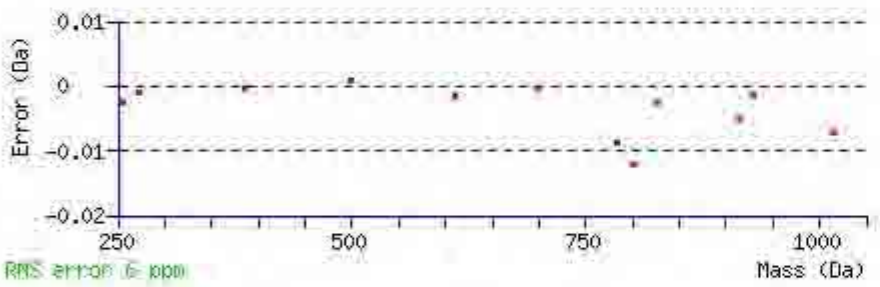
Match to Query 9012: 1184.669908 from(593.342230,2+) rtinseconds(1890) index(15105)
Title: Locus:1.1.1.1899.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

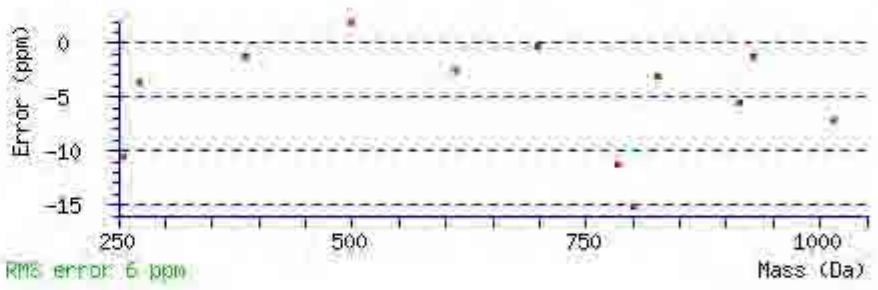
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 67 **Expect:** 2.1e-005
Matches : 12/86 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	*1015.578236*	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	*928.546208*	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	*827.498529*	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	*698.455936*	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	*611.423908*	306.215592	594.397359	297.702318			5
8	**801.435260**	401.221268	783.424695	392.215986	L	*498.339844*	249.673560	481.313295	241.160285			4
9	**914.519324**	457.763300	896.508759	448.758018	I	*385.255780*	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	*272.171716*	136.589496	255.145167	128.076221			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.5	1184.676468	-0.006560	GLSTESILIPR
19.7	1184.677795	-0.007887	PRHPEALLPR
18.7	1184.665237	0.004671	SSPIIIQLLSD
15.6	1184.676468	-0.006560	KEDLTTLLPR
14.6	1184.676483	-0.006575	GPVVEISLISR
12.6	1184.662552	0.007356	RGQTSASILPR
12.5	1184.680527	-0.010619	GLTLPPVPFTK
10.7	1184.666580	0.003328	SISLFRPPPR
10.4	1184.680527	-0.010619	GLTLPPVPFTK
9.7	1184.680527	-0.010619	GLTLPPVPFTK

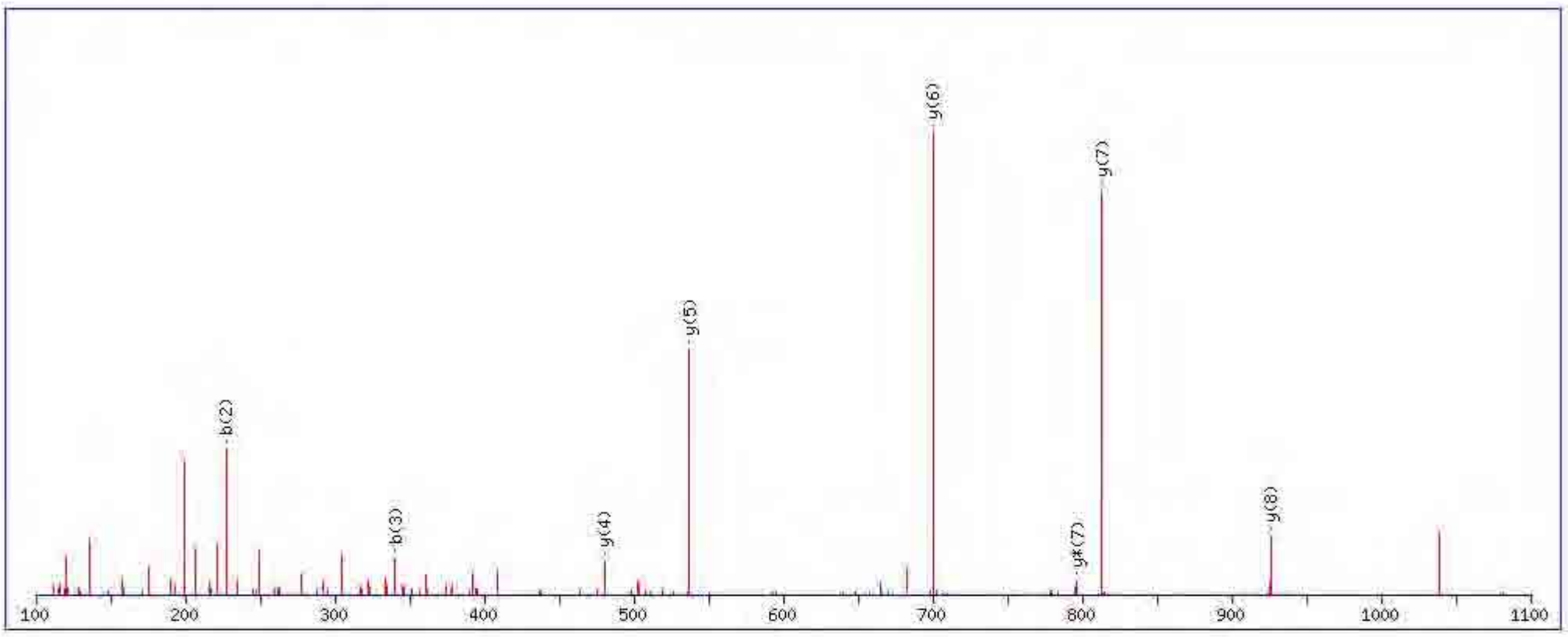
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIYGNISF**
Found in **RMI1_HUMAN**, RecQ-mediated genome instability protein 1 OS=Homo sapiens GN=RMI1 PE=1 SV=3

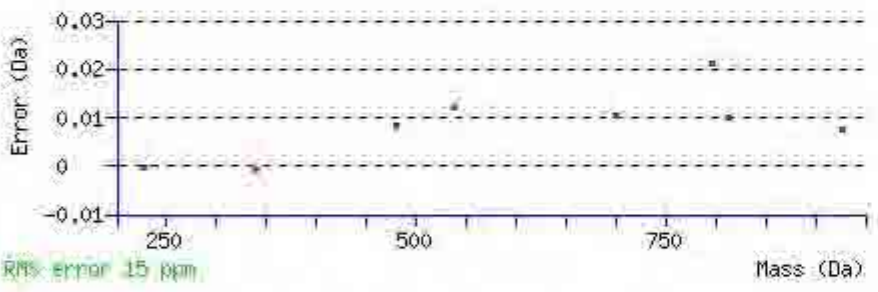
Match to Query 5092: 1038.581368 from(520.297960,2+) rtinseconds(1938) index(15446)
Title: Locus:1.1.1.1925.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

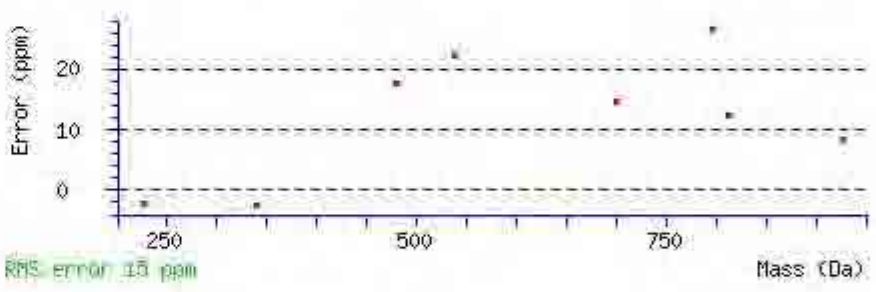
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1038.574966
Ions Score: 46 **Expect:** 0.0019
Matches : 8/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							9
2	227.175404	114.091340					L	*926.498195*	463.752736	909.471646	455.239461	908.487630	454.747453	8
3	340.259468	170.633372					I	*813.414131*	407.210704	796.387582	398.697429	795.403566	398.205421	7
4	503.322797	252.165036					Y	*700.330067*	350.668672	683.303518	342.155397	682.319502	341.663389	6
5	560.344261	280.675769					G	*537.266738*	269.137007	520.240189	260.623733	519.256173	260.131725	5
6	674.387188	337.697232	657.360639	329.183958			N	*480.245274*	240.626275	463.218725	232.113000	462.234709	231.620992	4
7	787.471252	394.239264	770.444703	385.725990			I	366.202347	183.604811			348.191782	174.599529	3
8	874.503280	437.755278	857.476731	429.242004	856.492715	428.749996	S	253.118283	127.062779			235.107718	118.057497	2
9							F	166.086255	83.546765					1





NCBI **BLAST** search of ILIYGNISF
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1038.574966	0.006402	ILIYGNISF
20.6	1038.578339	0.003029	LLLGTYMTK
19.5	1038.582184	-0.000816	PPLPTRQAK
18.3	1038.582184	-0.000816	PLPGATPAKR
17.8	1038.582184	-0.000816	IPLQNGRLP
17.8	1038.586227	-0.004859	LIPHVQVFA
17.8	1038.582153	-0.000785	LLLNAENPR
17.8	1038.586197	-0.004829	LLPAQPAWK
17.8	1038.589584	-0.008216	PILVCPPLR
17.8	1038.589584	-0.008216	PILVCPPLR

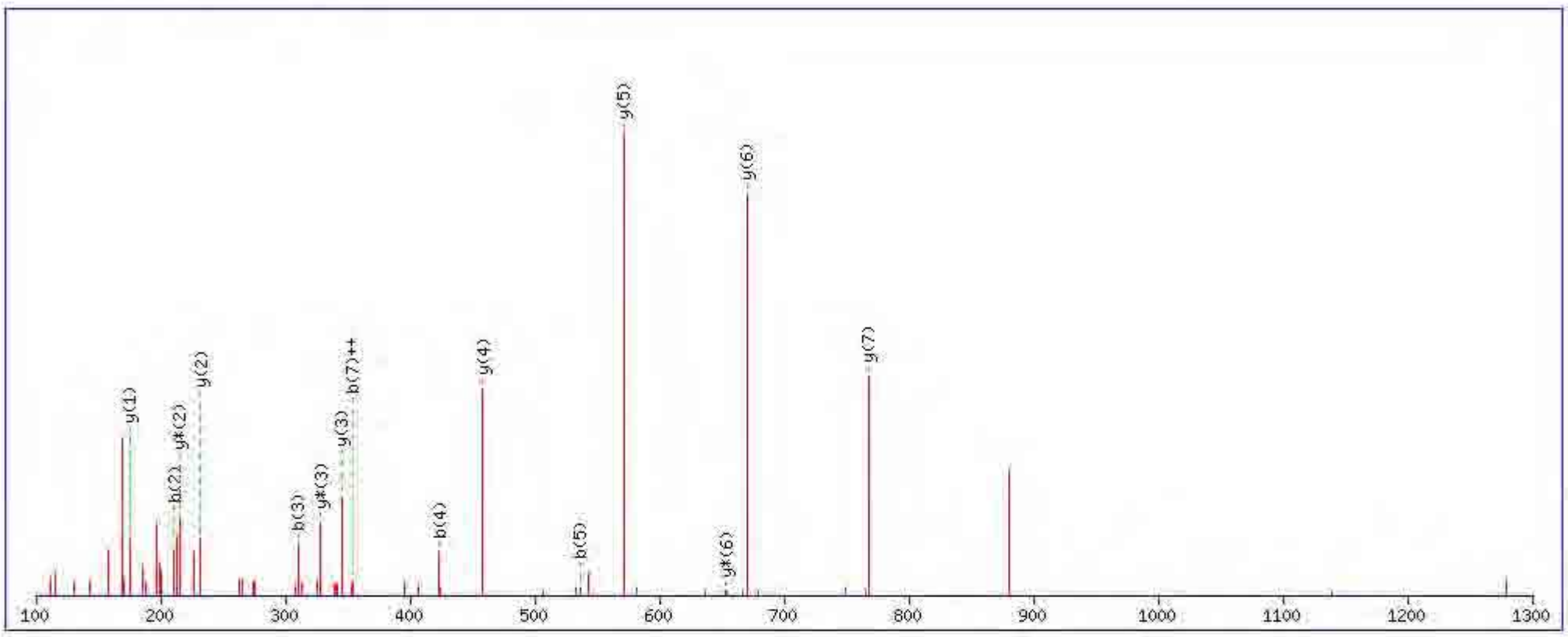
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVLLLGR**
Found in **HTRA1_HUMAN**, Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1

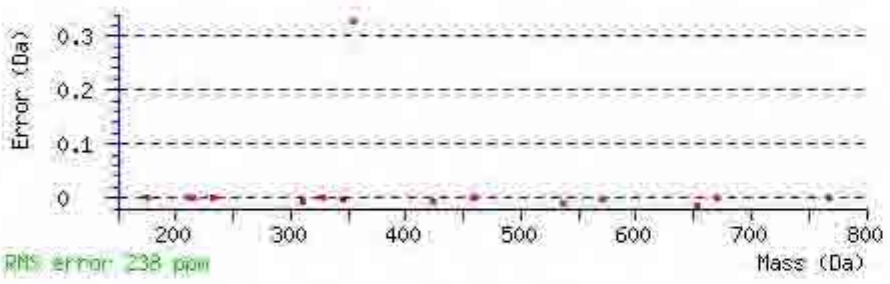
Match to Query 1744: 879.586388 from(440.800470,2+) rtinseconds(2088) index(16286)
Title: Locus:1.1.1.2006.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

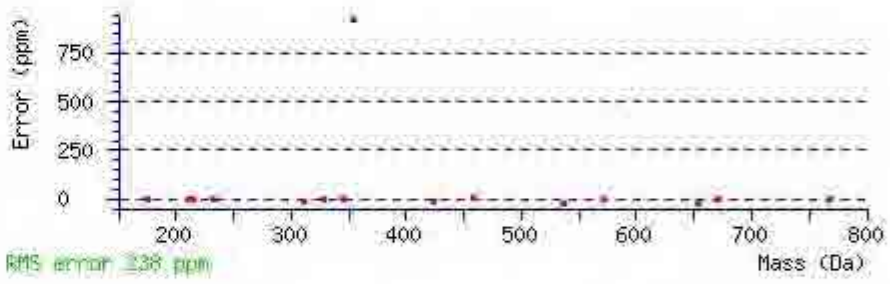
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 879.590561
Ions Score: 52 **Expect:** 3.3e-005
Matches : 15/42 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308	L					8
2	211.144104	106.075690	P	767.513786	384.260531	750.487237	375.747257	7
3	310.212518	155.609897	V	670.461022	335.734149	653.434473	327.220875	6
4	423.296582	212.151929	L	571.392608	286.199942	554.366059	277.686668	5
5	536.380646	268.693961	L	458.308544	229.657910	441.281995	221.144635	4
6	649.464710	325.235993	L	345.224480	173.115878	328.197931	164.602603	3
7	706.486174	353.746725	G	232.140416	116.573846	215.113867	108.060571	2
8			R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of LPVLLLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.0	879.590561	-0.004173	LPVLLLGR
31.1	879.590561	-0.004173	ILVPLIGR
28.2	879.579330	0.007058	IPVIPITK
27.1	879.590561	-0.004173	LVPILVAR
26.8	879.590561	-0.004173	IPLVLAVR
22.1	879.579330	0.007058	VIPLLVNI
19.4	879.590561	-0.004173	LVLPLGRL
15.0	879.579346	0.007042	PPVVVILK
14.4	879.579346	0.007042	LPVVIGGLL
11.0	879.590561	-0.004173	VLLPLGLR

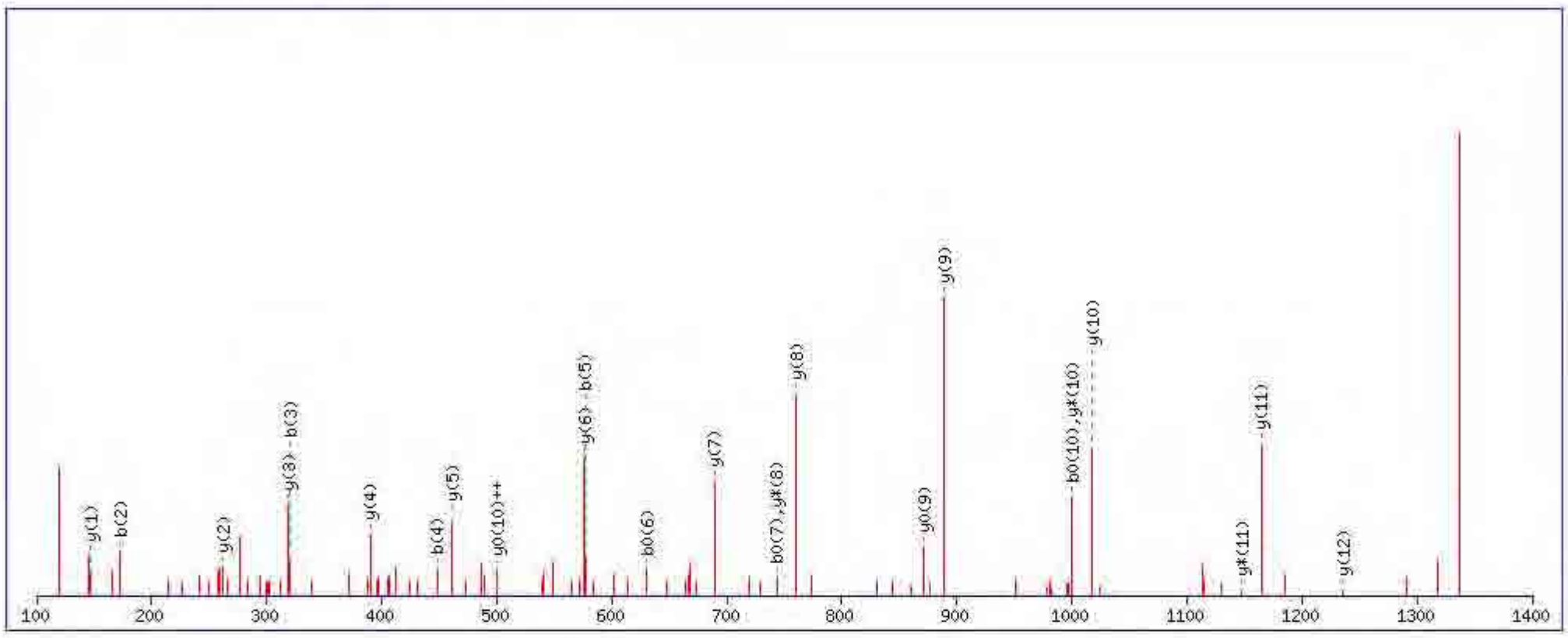
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

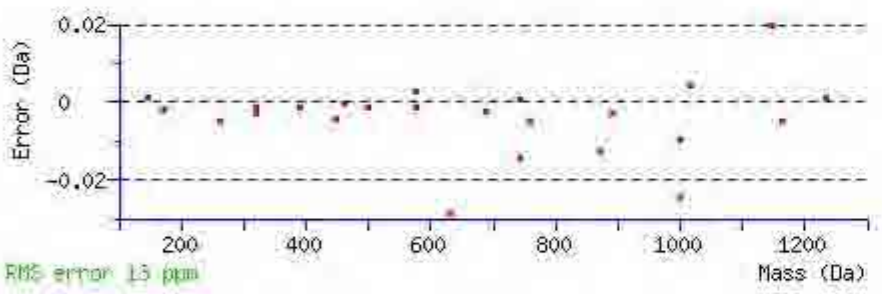
Match to Query 12884: 1335.632388 from(668.823470,2+) rtinseconds(1755) index(13917)
Title: Locus:1.1.1.1804.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

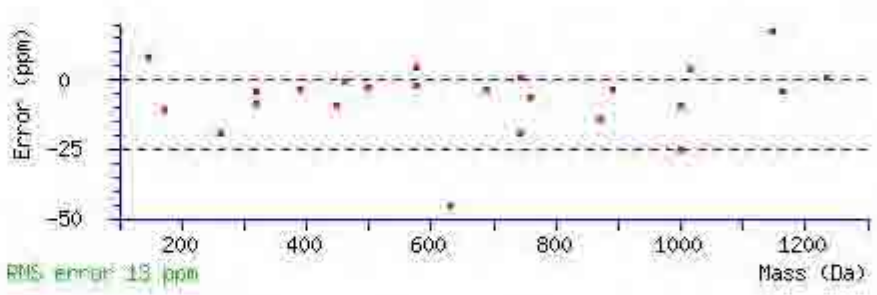
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 88 Expect: 1.8e-007
Matches : 24/136 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	*1235.590259*	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	*319.161211*	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	*262.139747*	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.9	1335.630646	0.001742	TAFQEALDAAGDK
15.0	1335.638031	-0.005643	FIDISPAEMANL
6.7	1335.634033	-0.001645	TQTANMLSGPIST
6.5	1335.645233	-0.012845	STMQELNSRLAS
6.4	1335.630661	0.001727	TVTAWDSQTAEK
5.7	1335.635376	-0.002988	MGDKPPGFRGSR
5.7	1335.635376	-0.002988	MGDKPPGFRGSR
5.0	1335.626633	0.005755	TASSSTEPSVSRQ
5.0	1335.641861	-0.009473	QENFEEVARSK
5.0	1335.634033	-0.001645	SLTVVQNMEGDK

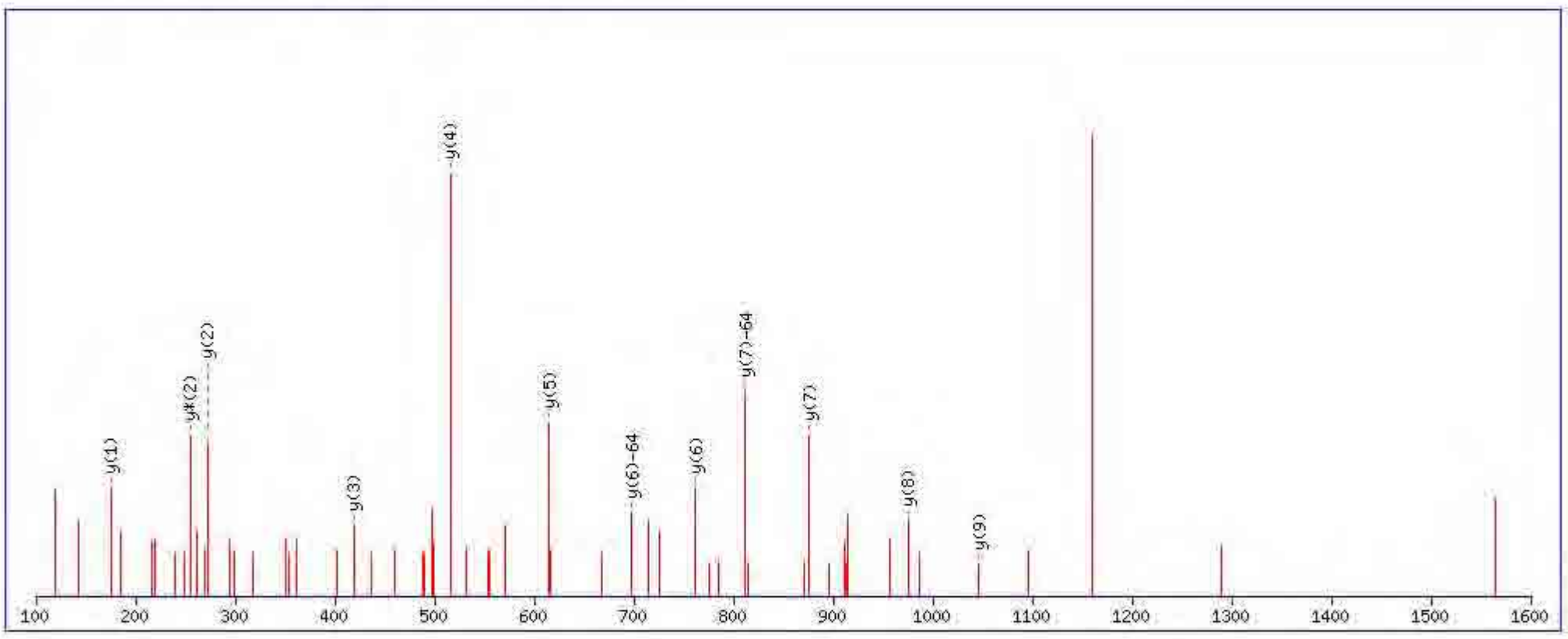
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVNMVPFPR**
Found in **TBB1_HUMAN**, Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1

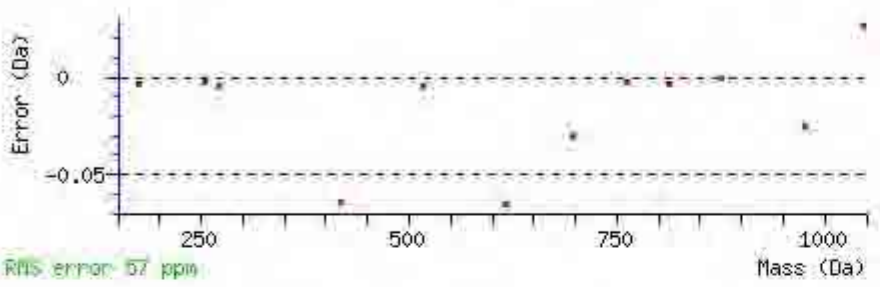
Match to Query 8275: 1158.615568 from(580.315060,2+) rtinseconds(1747) index(13808)
Title: Locus:1.1.1.1800.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

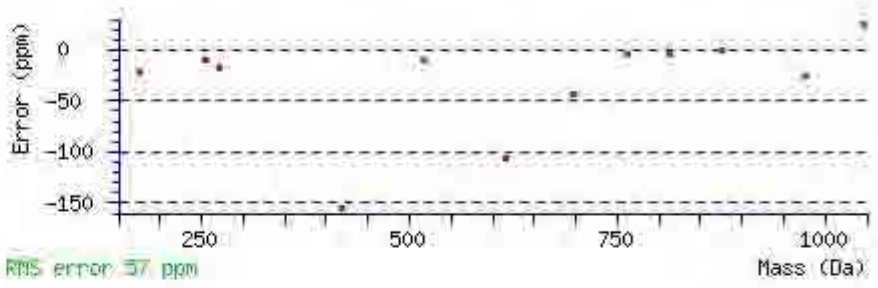
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1158.621948
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 77 **Expect:** 2.1e-006
Matches : 12/102 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			L					10
2	185.128454	93.067865			A	*1046.545163*	523.776220	1029.518614	515.262945	9
3	284.196868	142.602072			V	*975.508049*	488.257663	958.481500	479.744388	8
4	398.239795	199.623536	381.213246	191.110261	N	*876.439635*	438.723456	859.413086	430.210181	7
5	545.275195	273.141236	528.248646	264.627961	M	*762.396708*	381.701992	745.370159	373.188718	6
6	644.343609	322.675443	627.317060	314.162168	V	*615.361308*	308.184292	598.334759	299.671018	5
7	741.396373	371.201825	724.369824	362.688550	P	*516.292894*	258.650085	499.266345	250.136811	4
8	888.464787	444.736032	871.438238	436.222757	F	*419.240130*	210.123703	402.213581	201.610429	3
9	985.517551	493.262414	968.491002	484.749139	P	*272.171716*	136.589496	255.145167	128.076222	2
10					R	*175.118952*	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of LAVNMVPFPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.1	1158.621948	-0.006380	LAVNMVPFPR
37.0	1158.621948	-0.006380	LAVNMVPFPR
15.7	1158.614548	0.001020	PAHLPLNPPR
15.7	1158.617920	-0.002352	PATGCVKLAQR
11.6	1158.621948	-0.006380	LAVNMVPFPR
10.7	1158.606689	0.008879	PAVGCSLLQQK
10.4	1158.617905	-0.002337	LAELTGRPMR
10.4	1158.614548	0.001020	TVFAPERSPR
9.9	1158.606689	0.008879	ISMPTTKPRP
9.8	1158.608002	0.007566	LAHLHAACAPR

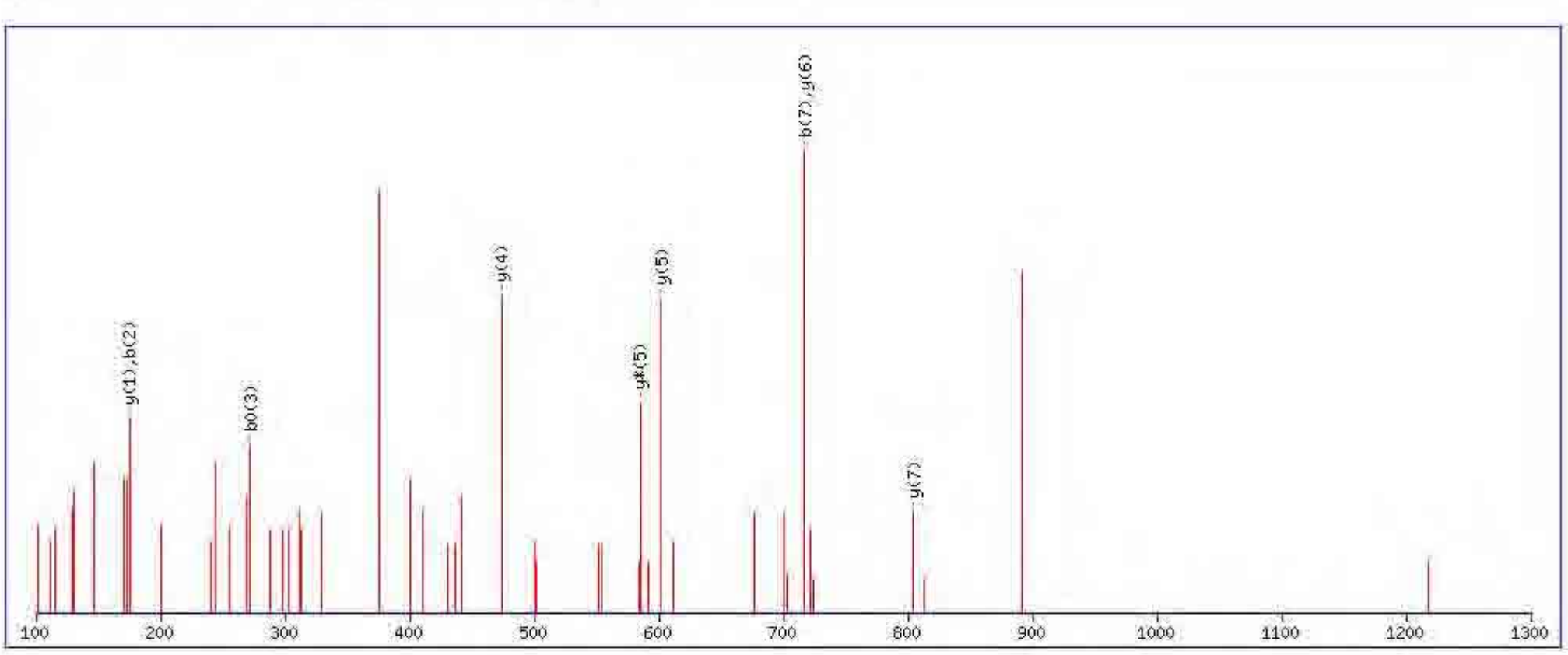
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSDKQNGR**
Found in **CR025_HUMAN**, Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=2

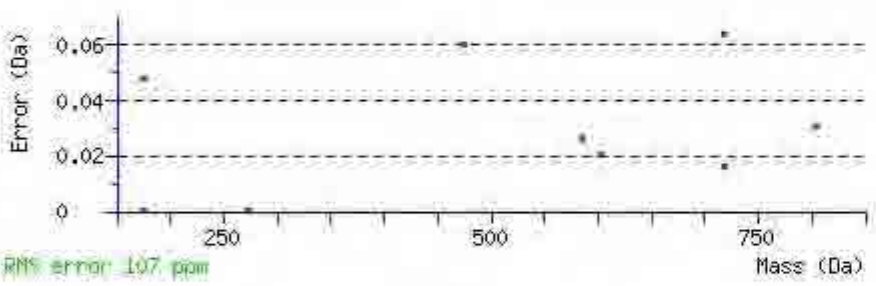
Match to Query 1956: 890.429468 from(446.222010,2+) rtinseconds(822) index(2877)
Title: Locus:1.1.1.1298.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_1.mgf

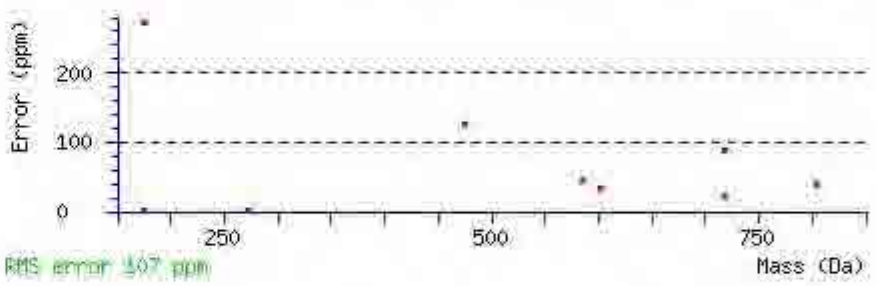
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 890.420593
Ions Score: 45 **Expect:** 0.0062
Matches : 9/68 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	175.071332	88.039304			157.060767	79.034021	S	804.395855	402.701566	787.369306	394.188291	786.385290	393.696283	7
3	290.098275	145.552776			272.087710	136.547493	D	717.363827	359.185552	700.337278	350.672277	699.353262	350.180269	6
4	418.193238	209.600257	401.166689	201.086983	400.182673	200.594975	K	602.336884	301.672080	585.310335	293.158806			5
5	546.251816	273.629546	529.225267	265.116272	528.241251	264.624264	Q	474.241921	237.624598	457.215372	229.111324			4
6	660.294743	330.651010	643.268194	322.137735	642.284178	321.645727	N	346.183343	173.595309	329.156794	165.082035			3
7	717.316207	359.161742	700.289658	350.648467	699.305642	350.156459	G	232.140416	116.573846	215.113867	108.060571			2
8							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SSDKQNGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	890.420593	0.008875	SSDKQNGR
27.6	890.427994	0.001474	SSPQVMSR
23.2	890.420593	0.008875	SDSAPSRR
23.2	890.420593	0.008875	SDSSPSRR
22.9	890.427979	0.001489	SSMKPADR
22.9	890.420593	0.008875	SSSSRPDR
21.1	890.420593	0.008875	SSGRESPR
20.7	890.424606	0.004862	SSENWIR
19.4	890.424622	0.004846	SSPNPFSR
17.0	890.434525	-0.005057	STTKPDDK

Control – technical replicate # 2

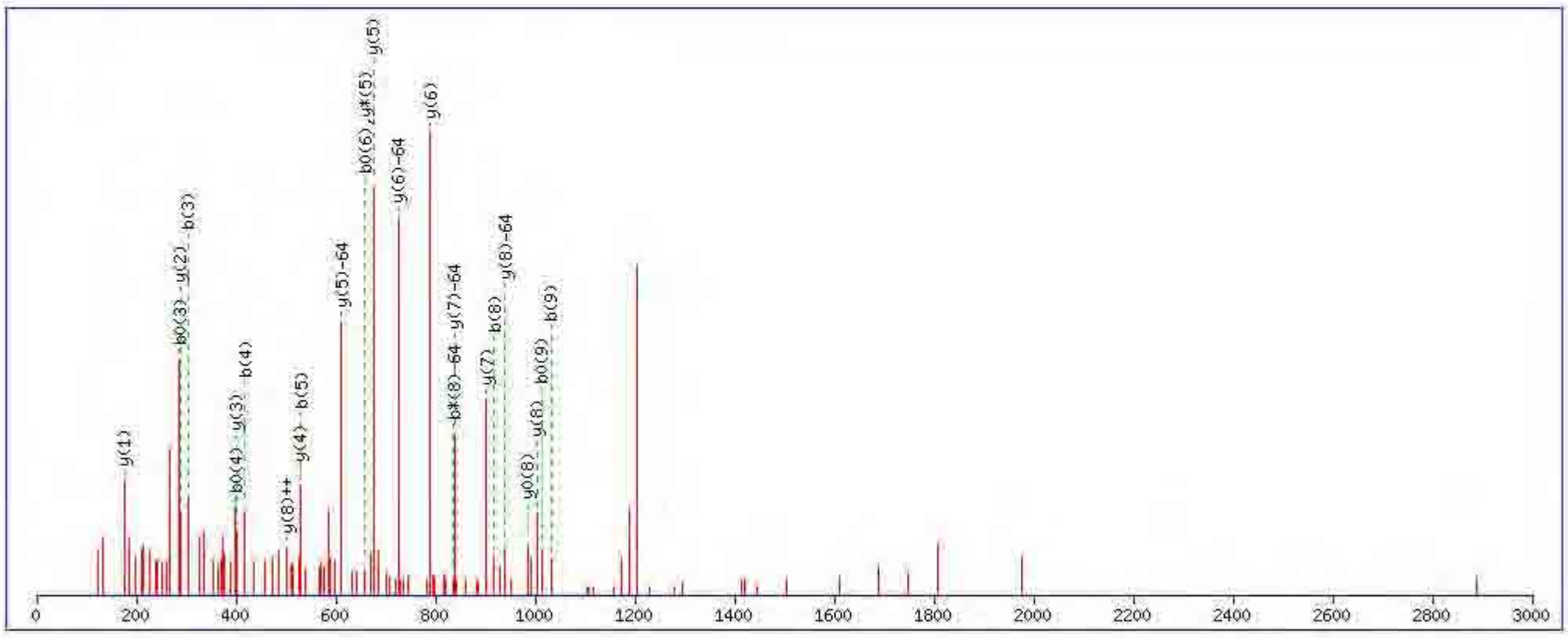
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSTLIMQLLR**
Found in **1433B_HUMAN**, 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

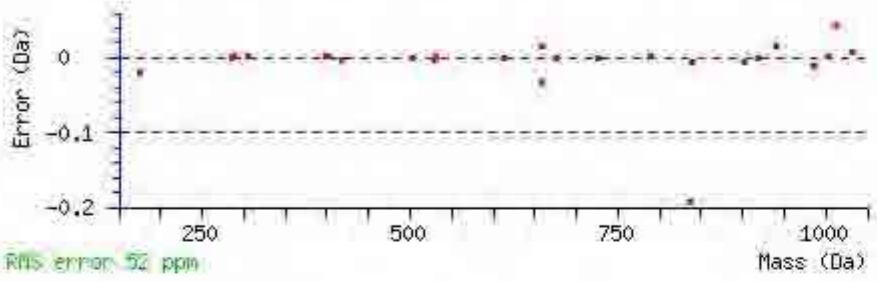
Match to Query 8931: 1204.642388 from(603.328470,2+) rtinseconds(2650) index(22219)
Title: Locus:1.1.1.2538.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

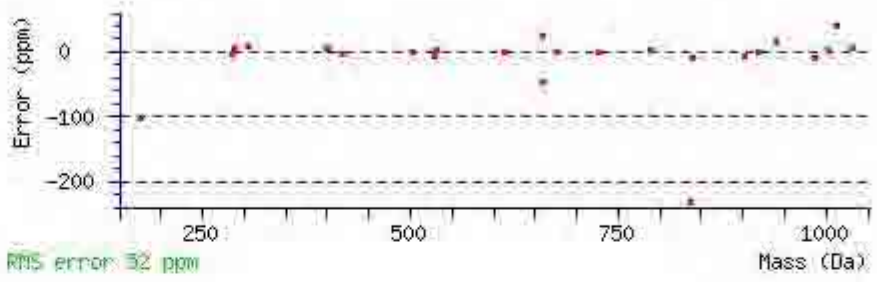
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1204.648544
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 52 **Expect:** 0.0012
Matches : 25/128 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1090.628893	545.818084	1073.602344	537.304810	1072.618328	536.812802	9
3	**304.113926**	152.560601			286.103361	143.555319	T	***1003.596865***	502.302071	986.570316	493.788796	985.586300	493.296788	8
4	**417.197990**	209.102633			399.187425	200.097351	L	***902.549186***	451.778231	885.522637	443.264956			7
5	**530.282054**	265.644665			512.271489	256.639383	I	***789.465122***	395.236199	772.438573	386.722924			6
6	677.317454	339.162365			659.306889	330.157083	M	***676.381058***	338.694167	659.354509	330.180892			5
7	805.376032	403.191654	788.349483	394.678380	787.365467	394.186372	Q	***529.345658***	265.176467	512.319109	256.663192			4
8	**918.460096**	459.733686	901.433547	451.220412	900.449531	450.728404	L	***401.287080***	201.147178	384.260531	192.633903			3
9	**1031.544160**	516.275718	1014.517611	507.762443	1013.533595	507.270435	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DSTLIMQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1204.648544	-0.006156	DSTLIMQLLR
25.1	1204.630783	0.011605	CTVLLQIMER
20.5	1204.635269	0.007119	DFWARLLER
18.4	1204.641129	0.001259	ANSTSSKLLER
18.1	1204.631256	0.011132	HDGRPLPIER
18.1	1204.645187	-0.002799	LTLPPPGPPER
18.1	1204.648544	-0.006156	VCTLINKPSSK
17.5	1204.645187	-0.002799	SVGAVDFELLR
16.6	1204.645187	-0.002799	LLFVGGEVSER
16.1	1204.648529	-0.006141	ASSGLLLMIER

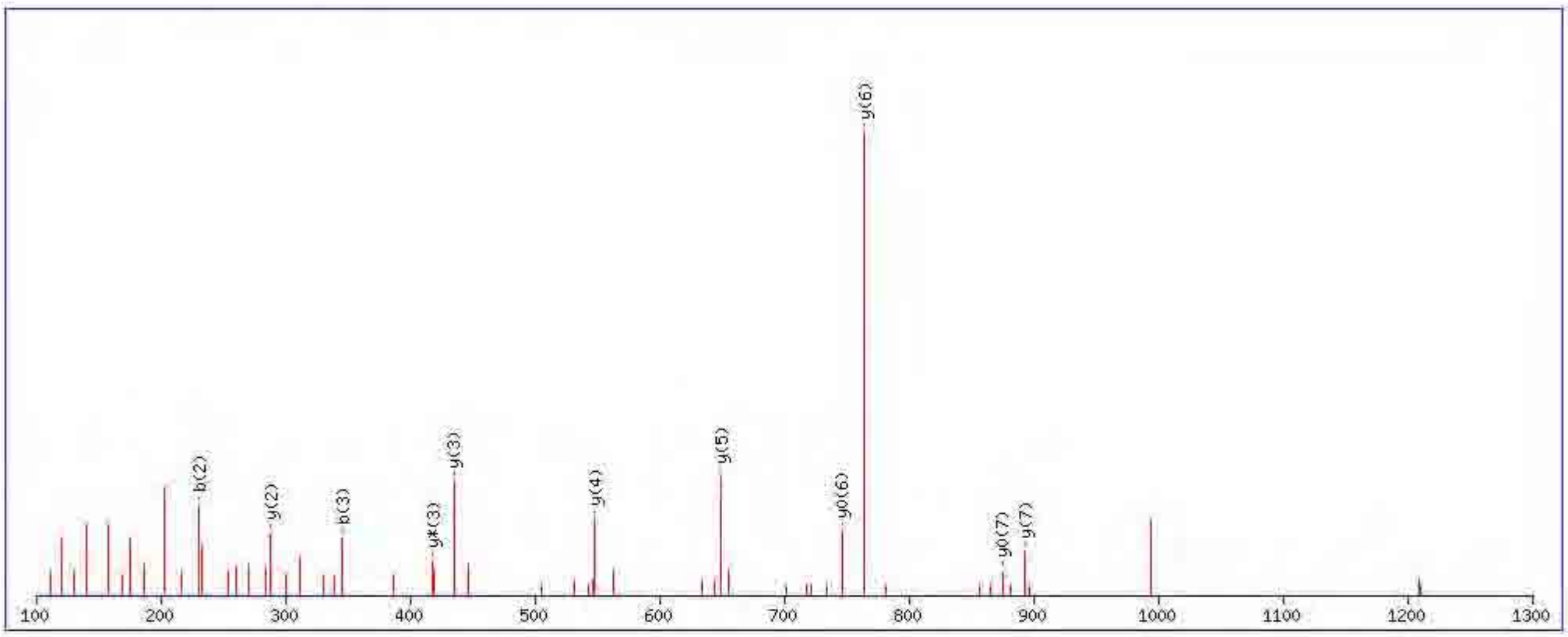
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEDTIFLR**
Found in **A1AG1_HUMAN**, Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

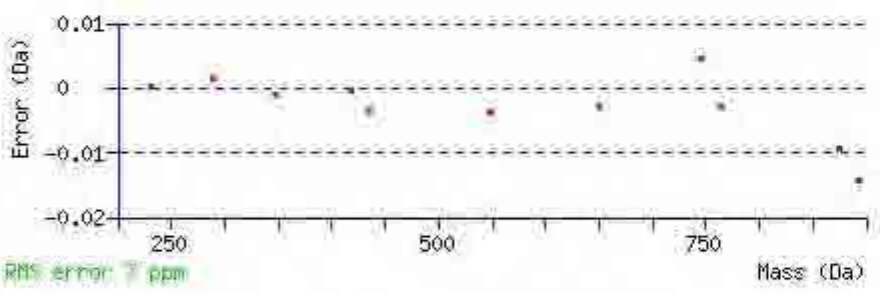
Match to Query 3602: 993.506588 from(497.760570,2+) rtinseconds(1819) index(13341)
Title: Locus:1.1.1.2096.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

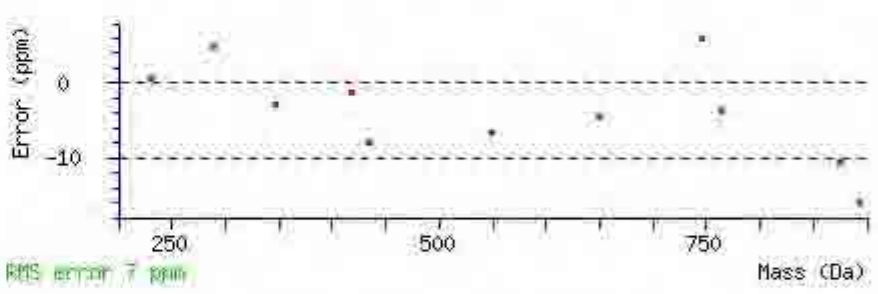
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 993.513107
Ions Score: 48 **Expect:** 0.00057
Matches : 11/62 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	231.097548	116.052412	213.086983	107.047130	E	*893.472709*	447.239993	876.446160	438.726718	875.462144	438.234710	7
3	346.124491	173.565884	328.113926	164.560601	D	*764.430116*	382.718696	747.403567	374.205422	746.419551	373.713414	6
4	447.172170	224.089723	429.161605	215.084441	T	*649.403173*	325.205225	632.376624	316.691950	631.392608	316.199942	5
5	560.256234	280.631755	542.245669	271.626473	I	*548.355494*	274.681385	531.328945	266.168111			4
6	707.324648	354.165962	689.314083	345.160680	F	*435.271430*	218.139353	418.244881	209.626079			3
7	820.408712	410.707994	802.398147	401.702712	L	*288.203016*	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TEDTIFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	993.513107	-0.006519	TEDTIFLR
12.8	993.506561	0.000027	AAFAAKMPR
12.8	993.503220	0.003368	FVNAQFPR
10.2	993.513092	-0.006504	TEIISYPR
9.6	993.513107	-0.006519	TTRFEEVL
9.5	993.506561	0.000027	ECQKAFIR
9.2	993.513077	-0.006489	TEELAYLR
8.8	993.509949	-0.003361	CGLTGKMIR
7.8	993.513107	-0.006519	AFSQKSDLV
7.8	993.513107	-0.006519	NFTSAKDVL

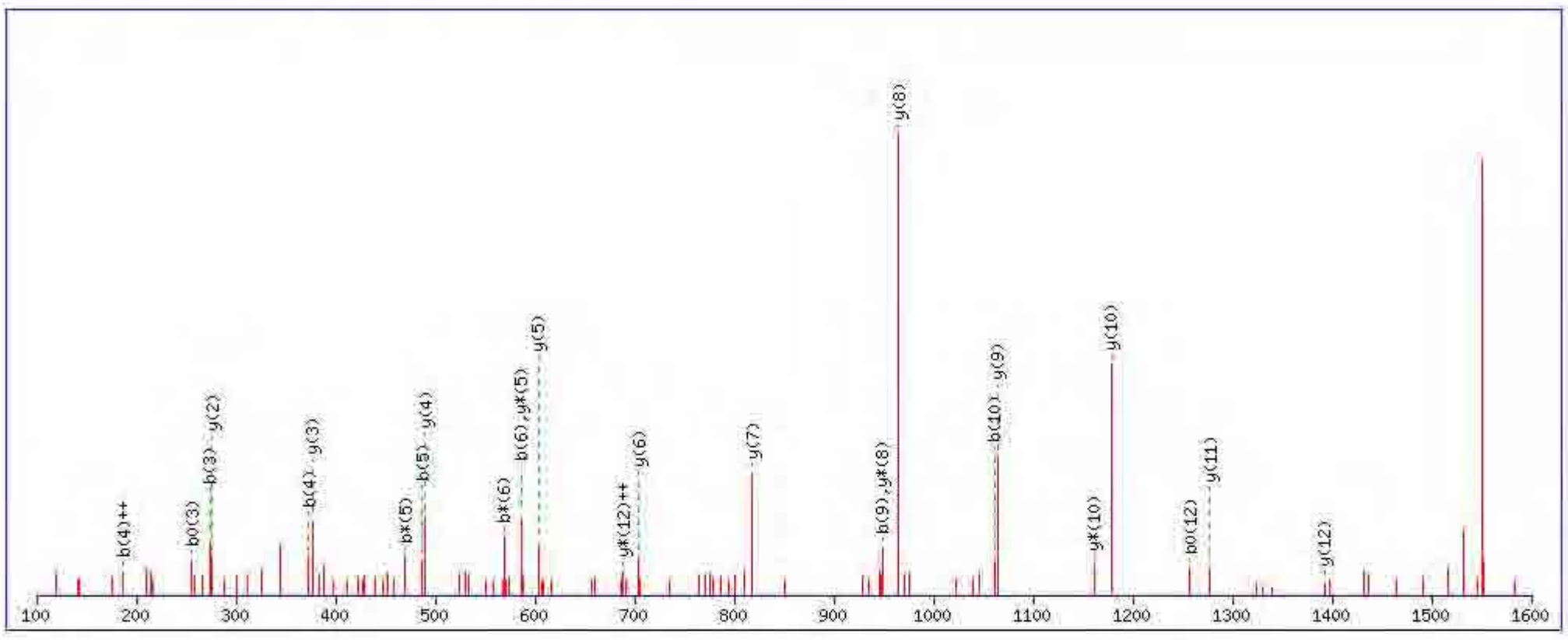
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTDVNVFNTILTTR**
Found in **ANXA1_HUMAN**, Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2

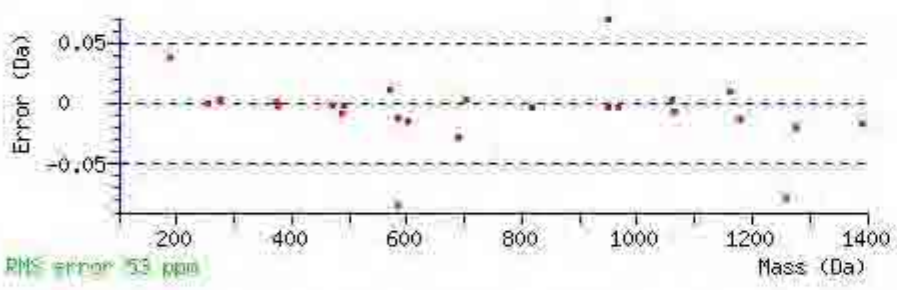
Match to Query 17126: 1549.795828 from(775.905190,2+) rtinseconds(2541) index(21696)
Title: Locus:1.1.1.2481.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

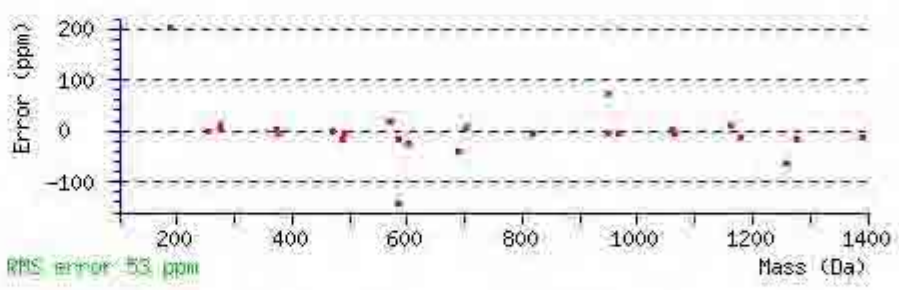
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1549.810043
Ions Score: 84 **Expect:** 2.3e-007
Matches : 26/144 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	159.076419	80.041847			141.065854	71.036565	T	1493.795835	747.401555	1476.769286	738.888281	1475.785270	738.396273	13
3	**274.103362**	137.555319			256.092797	128.550037	D	*1392.748156*	696.877716	1375.721607	688.364442	1374.737591	687.872433	12
4	**373.171776**	187.089526			355.161211	178.084244	V	*1277.721213*	639.364244	1260.694664	630.850970	1259.710648	630.358962	11
5	**487.214703**	244.110990	470.188154	235.597715	469.204138	235.105707	N	*1178.652799*	589.830037	1161.626250	581.316763	1160.642234	580.824755	10
6	**586.283117**	293.645197	569.256568	285.131922	568.272552	284.639914	V	*1064.609872*	532.808574	1047.583323	524.295299	1046.599307	523.803291	9
7	733.351531	367.179404	716.324982	358.666129	715.340966	358.174121	F	*965.541458*	483.274367	948.514909	474.761092	947.530893	474.269084	8
8	847.394458	424.200867	830.367909	415.687592	829.383893	415.195585	N	*818.473044*	409.740160	801.446495	401.226885	800.462479	400.734877	7
9	**948.442137**	474.724707	931.415588	466.211432	930.431572	465.719424	T	*704.430117*	352.718696	687.403568	344.205422	686.419552	343.713414	6
10	**1061.526201**	531.266738	1044.499652	522.753464	1043.515636	522.261456	I	*603.382438*	302.194857	586.355889	293.681582	585.371873	293.189574	5
11	1174.610265	587.808770	1157.583716	579.295496	1156.599700	578.803488	L	*490.298374*	245.652825	473.271825	237.139550	472.287809	236.647542	4
12	1275.657944	638.332610	1258.631395	629.819335	1257.647379	629.327327	T	*377.214310*	189.110793	360.187761	180.597518	359.203745	180.105510	3
13	1376.705623	688.856449	1359.679074	680.343175	1358.695058	679.851167	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GTDVNVFNTILTTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.2	1549.810043	-0.014215	GTDVNVFNTILTTR
12.6	1549.792267	0.003561	NVGLCEAIVQFTRT
7.7	1549.806168	-0.010340	PKLDVSYEPMIVK
7.6	1549.792267	0.003561	GTAQSNYLPMVVVR
5.0	1549.781006	0.014822	NAVSCPYLPSNLLK
2.9	1549.807526	-0.011698	LLHYLGHVMVNGPT
2.9	1549.785736	0.010092	YRGLLHCMVTSVR
2.2	1549.788223	0.007605	NSMGTLRTSISVER
2.1	1549.810028	-0.014200	STITSLQSVFGPAAR
1.2	1549.796295	-0.000467	LPVVLFNGMPFER

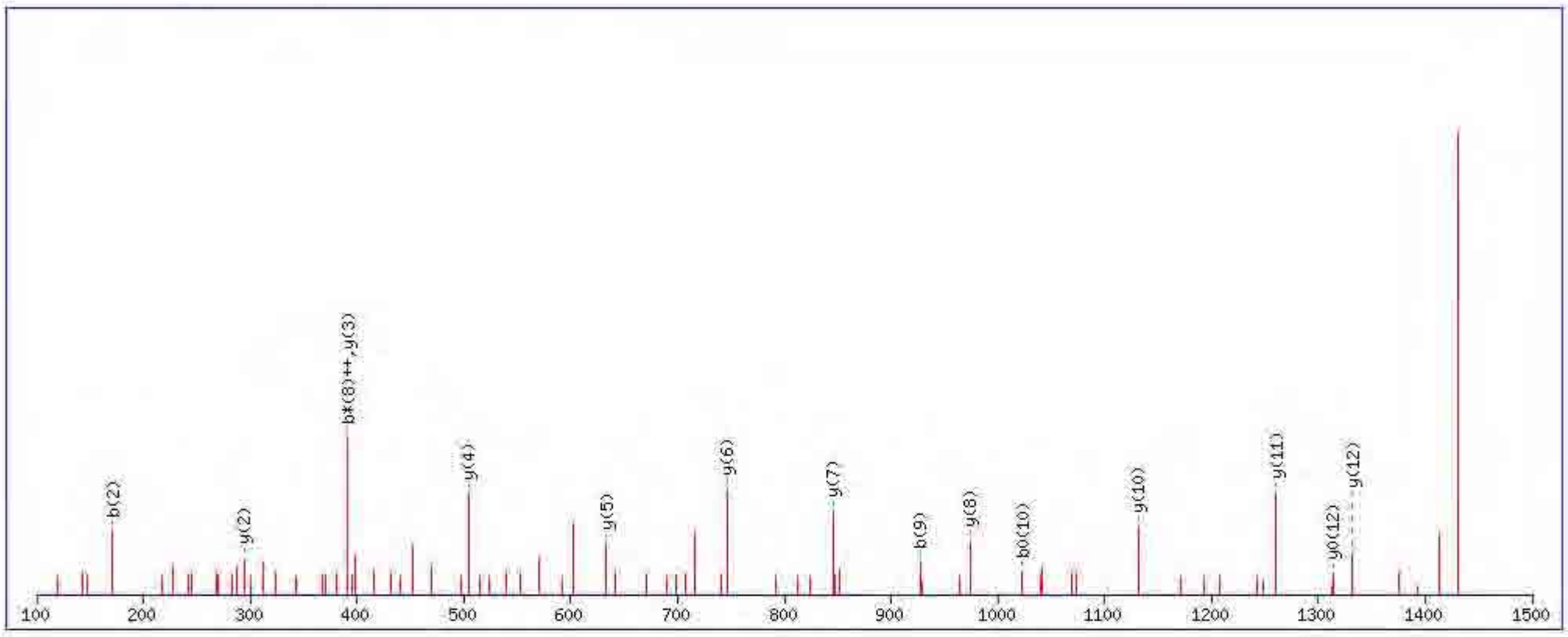
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAEGTQVLELPFK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

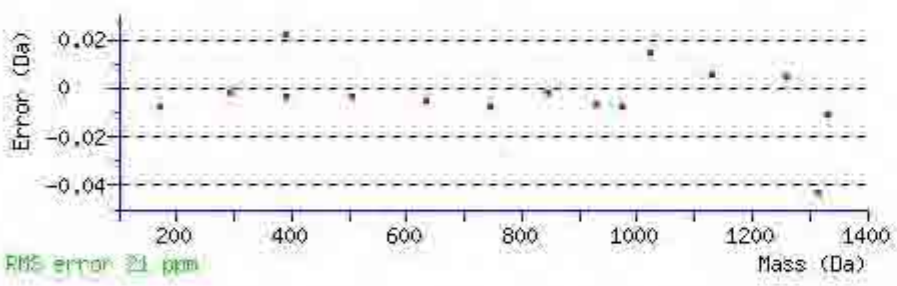
Match to Query 14480: 1429.775848 from(715.895200,2+) rtinseconds(2345) index(20140)
Title: Locus:1.1.1.2378.11
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

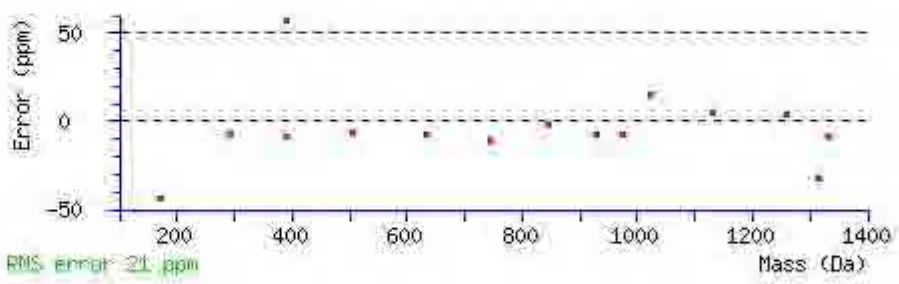
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1429.781677
Ions Score: 76 **Expect:** 9e-007
Matches : 15/122 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							13
2	171.112804	86.060040					A	*1331.720545*	666.363911	1314.693996	657.850636	1313.709980	657.358628	12
3	300.155397	150.581336			282.144832	141.576054	E	*1260.683431*	630.845354	1243.656882	622.332079	1242.672866	621.840071	11
4	357.176861	179.092068			339.166296	170.086786	G	*1131.640838*	566.324057	1114.614289	557.810783	1113.630273	557.318775	10
5	458.224540	229.615908			440.213975	220.610626	T	1074.619374	537.813325	1057.592825	529.300051	1056.608809	528.808043	9
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	Q	*973.571695*	487.289486	956.545146	478.776211	955.561130	478.284203	8
7	685.351532	343.179404	668.324983	334.666130	667.340967	334.174122	V	*845.513117*	423.260197	828.486568	414.746922	827.502552	414.254914	7
8	798.435596	399.721436	781.409047	391.208162	780.425031	390.716154	L	*746.444703*	373.725990	729.418154	365.212715	728.434138	364.720707	6
9	927.478189	464.242733	910.451640	455.729458	909.467624	455.237450	E	*633.360639*	317.183958	616.334090	308.670683	615.350074	308.178675	5
10	1040.562253	520.784765	1023.535704	512.271490	1022.551688	511.779482	L	*504.318046*	252.662661	487.291497	244.149387			4
11	1137.615017	569.311147	1120.588468	560.797872	1119.604452	560.305864	P	*391.233982*	196.120629	374.207433	187.607355			3
12	1284.683431	642.845354	1267.656882	634.332079	1266.672866	633.840071	F	*294.181218*	147.594247	277.154669	139.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VAEGTQVLELPFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.8	1429.781677	-0.005829	VAEGTQVLELPFK
10.6	1429.788895	-0.013047	SVLASQSVGITNVR
8.6	1429.785049	-0.009201	VKIVEALSTVPQM
7.7	1429.766388	0.009460	QKELSVLEEDIK
7.5	1429.767746	0.008102	GLYGPEGILPARR
7.3	1429.781647	-0.005799	VAEQLEKLGYPAI
5.8	1429.788895	-0.013047	VATTSTPGIVRNSK
4.5	1429.783020	-0.007172	VAWFLEGTPVRR
4.0	1429.763931	0.011917	VDFILQPLGMGPK
0.7	1429.775146	0.000702	YQVLLCPRPKDV

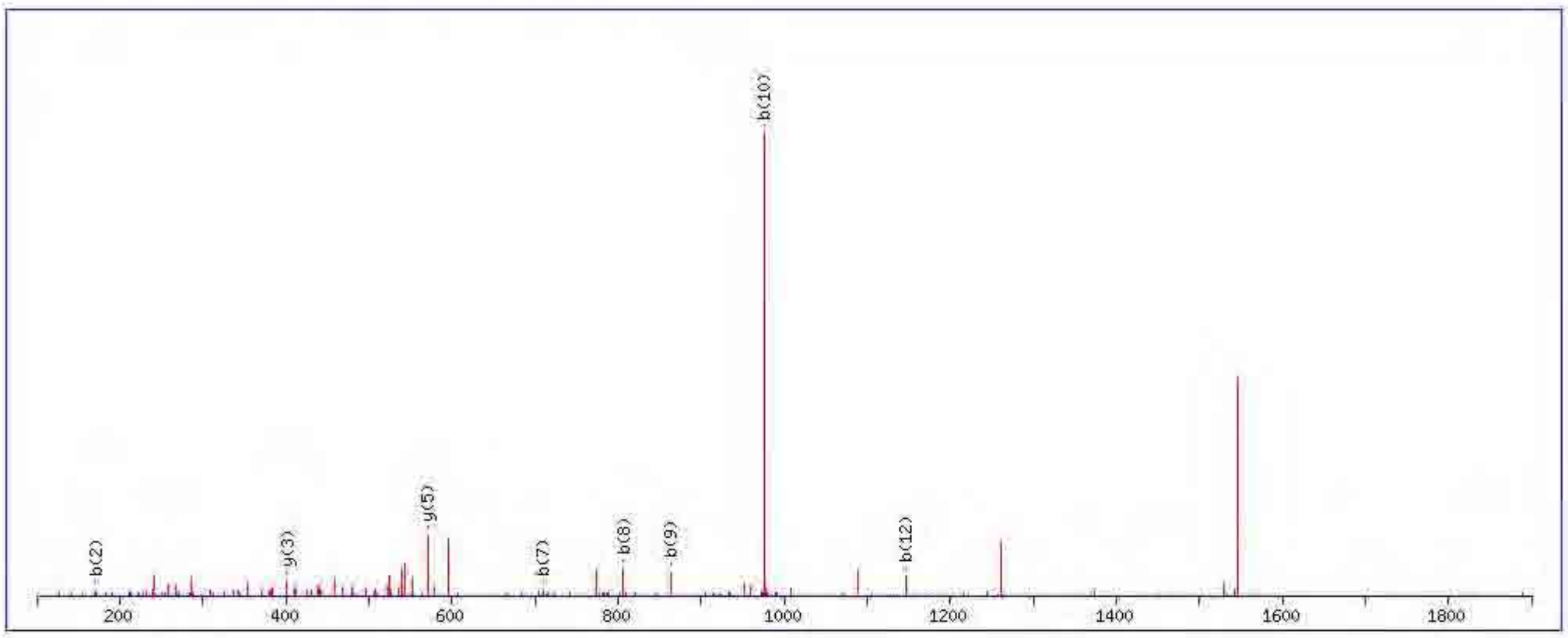
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAQPLEPGPGPPER**
Found in **KCTD2_HUMAN**, BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens GN=KCTD2 PE=1 SV=3

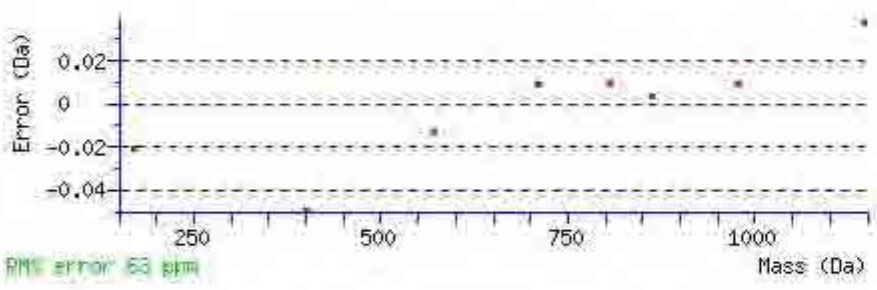
Match to Query 17005: 1545.773588 from(773.894070,2+) rtinseconds(1774) index(12760)
Title: Locus:1.1.1.2072.22
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

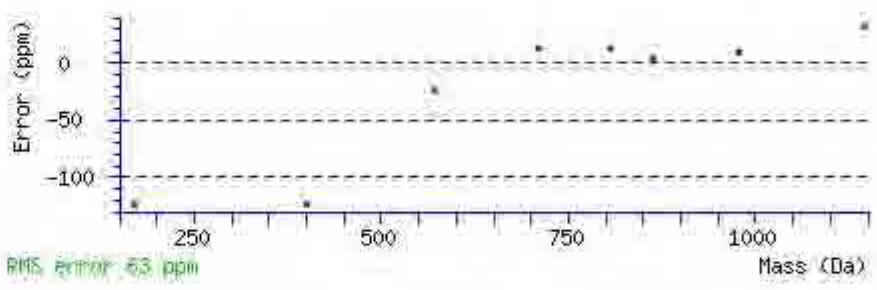
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1545.778717
Variable modifications:
P10 : Oxidation (P)
P12 : Oxidation (P)
Ions Score: 37 **Expect:** 0.021
Matches : 8/148 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	*171.112804*	86.060040					V	1475.748886	738.378081	1458.722337	729.864807	1457.738321	729.372799	14
3	242.149918	121.578597					A	1376.680472	688.843874	1359.653923	680.330600	1358.669907	679.838592	13
4	370.208496	185.607886	353.181947	177.094612			Q	1305.643358	653.325317	1288.616809	644.812043	1287.632793	644.320035	12
5	467.261260	234.134268	450.234711	225.620994			P	1177.584780	589.296028	1160.558231	580.782754	1159.574215	580.290746	11
6	580.345324	290.676300	563.318775	282.163026			L	1080.532016	540.769646	1063.505467	532.256372	1062.521451	531.764364	10
7	*709.387917*	355.197597	692.361368	346.684322	691.377352	346.192314	E	967.447952	484.227614	950.421403	475.714340	949.437387	475.222332	9
8	*806.440681*	403.723979	789.414132	395.210704	788.430116	394.718696	P	838.405359	419.706318	821.378810	411.193043	820.394794	410.701035	8
9	*863.462145*	432.234711	846.435596	423.721436	845.451580	423.229428	G	741.352595	371.179936	724.326046	362.666661	723.342030	362.174653	7
10	*976.509824*	488.758550	959.483275	480.245276	958.499259	479.753268	P	684.331131	342.669204	667.304582	334.155929	666.320566	333.663921	6
11	1033.531288	517.269282	1016.504739	508.756008	1015.520723	508.264000	G	571.283452	286.145364	554.256903	277.632090	553.272887	277.140082	5
12	*1146.578967*	573.793122	1129.552418	565.279847	1128.568402	564.787839	P	514.261988	257.634632	497.235439	249.121358	496.251423	248.629350	4
13	1243.631731	622.319504	1226.605182	613.806229	1225.621166	613.314221	P	401.214309	201.110793	384.187760	192.597518	383.203744	192.105510	3
14	1372.674324	686.840800	1355.647775	678.327526	1354.663759	677.835518	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVAQPLEPGPGPPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1545.778717	-0.005129	AVAQPLEPGPGPPER
21.6	1545.778717	-0.005129	AVAQPLEPGPGPPER
18.0	1545.776047	-0.002459	GGRARPGPGPGPGPER
17.0	1545.782761	-0.009173	VDWGLPIPSPSPIH
17.0	1545.782761	-0.009173	VDWGLPIPSPSPIH
17.0	1545.782761	-0.009173	VDWGLPIPSPSPIH
16.3	1545.778717	-0.005129	ESALAVPRLPPHDP
16.3	1545.778717	-0.005129	ESALAVPRLPPHDP
16.3	1545.778717	-0.005129	AVAQPLEPGPGPPER
11.1	1545.778717	-0.005129	AVAQPLEPGPGPPER

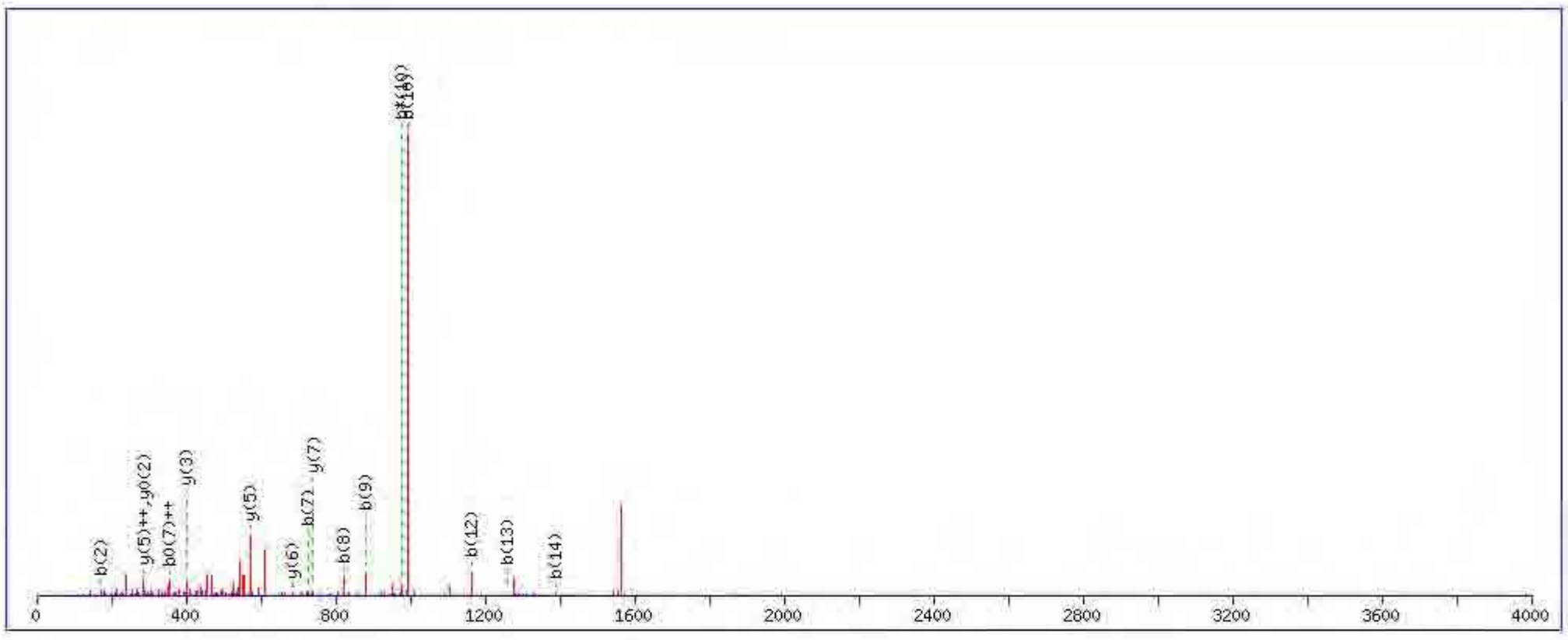
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAQPLEPGPGPPER**
Found in **KCTD2_HUMAN**, BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens GN=KCTD2 PE=1 SV=3

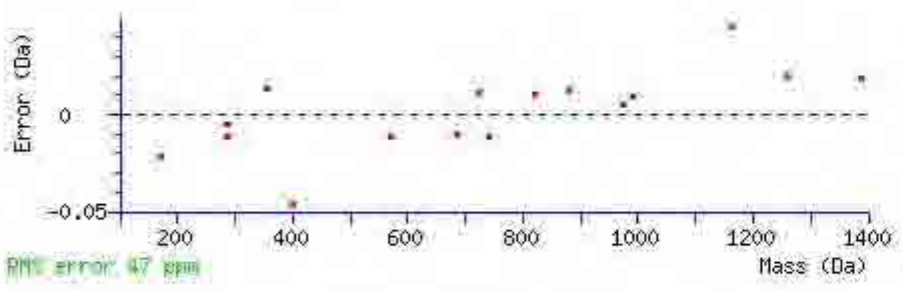
Match to Query 17370: 1561.769528 from(781.892040,2+) rtinseconds(1784) index(12886)
Title: Locus:1.1.1.2077.23
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

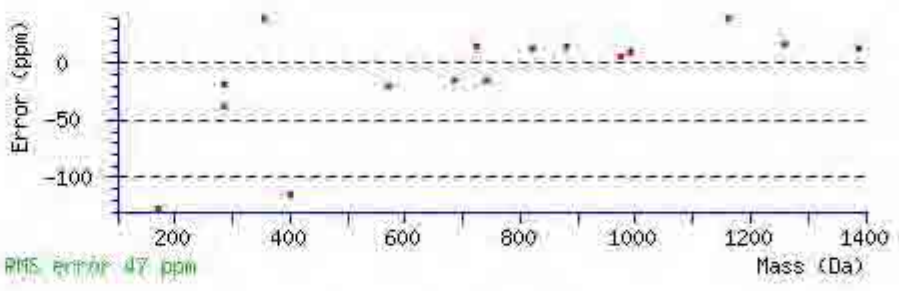
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1561.773636
Variable modifications:
P5 : Oxidation (P)
P10 : Oxidation (P)
P12 : Oxidation (P)
Ions Score: 47 **Expect:** 0.005
Matches : 16/148 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	*171.112804*	86.060040					V	1491.743801	746.375539	1474.717252	737.862264	1473.733236	737.370256	14
3	242.149918	121.578597					A	1392.675387	696.841332	1375.648838	688.328057	1374.664822	687.836049	13
4	370.208496	185.607886	353.181947	177.094612			Q	1321.638273	661.322775	1304.611724	652.809500	1303.627708	652.317492	12
5	483.256175	242.131726	466.229626	233.618451			P	1193.579695	597.293486	1176.553146	588.780211	1175.569130	588.288203	11
6	596.340239	298.673758	579.313690	290.160483			L	1080.532016	540.769646	1063.505467	532.256372	1062.521451	531.764363	10
7	*725.382832*	363.195054	708.356283	354.681780	707.372267	354.189772	E	967.447952	484.227614	950.421403	475.714339	949.437387	475.222332	9
8	*822.435596*	411.721436	805.409047	403.208162	804.425031	402.716154	P	838.405359	419.706318	821.378810	411.193043	820.394794	410.701035	8
9	*879.457060*	440.232168	862.430511	431.718894	861.446495	431.226886	G	741.352595	371.179936	724.326046	362.666661	723.342030	362.174653	7
10	*992.504739*	496.756008	975.478190	488.242733	974.494174	487.750725	P	684.331131	342.669203	667.304582	334.155929	666.320566	333.663921	6
11	1049.526203	525.266740	1032.499654	516.753465	1031.515638	516.261457	G	571.283452	286.145364	554.256903	277.632089	553.272887	277.140081	5
12	*1162.573882*	581.790579	1145.547333	573.277305	1144.563317	572.785297	P	514.261988	257.634632	497.235439	249.121357	496.251423	248.629349	4
13	*1259.626646*	630.316961	1242.600097	621.803687	1241.616081	621.311679	P	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
14	*1388.669239*	694.838258	1371.642690	686.324983	1370.658674	685.832975	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVAQPLEPGPGPPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	1561.773636	-0.004108	AVAQPLEPGPGPPER
34.6	1561.773636	-0.004108	AVAQPLEPGPGPPER
34.5	1561.773636	-0.004108	AVAQPLEPGPGPPER
28.8	1561.770981	-0.001453	PTARGGQHGGGPGPLR
26.1	1561.770966	-0.001438	GGRARPGPGPGPGPER
26.1	1561.770966	-0.001438	GGRARPGPGPGPGPER
23.8	1561.773636	-0.004108	AVAQPLEPGPGPPER
23.8	1561.773636	-0.004108	AVAQPLEPGPGPPER
21.3	1561.784897	-0.015369	KGLNGPTGPPGPPGPR
20.4	1561.770966	-0.001438	GGRARPGPGPGPGPER

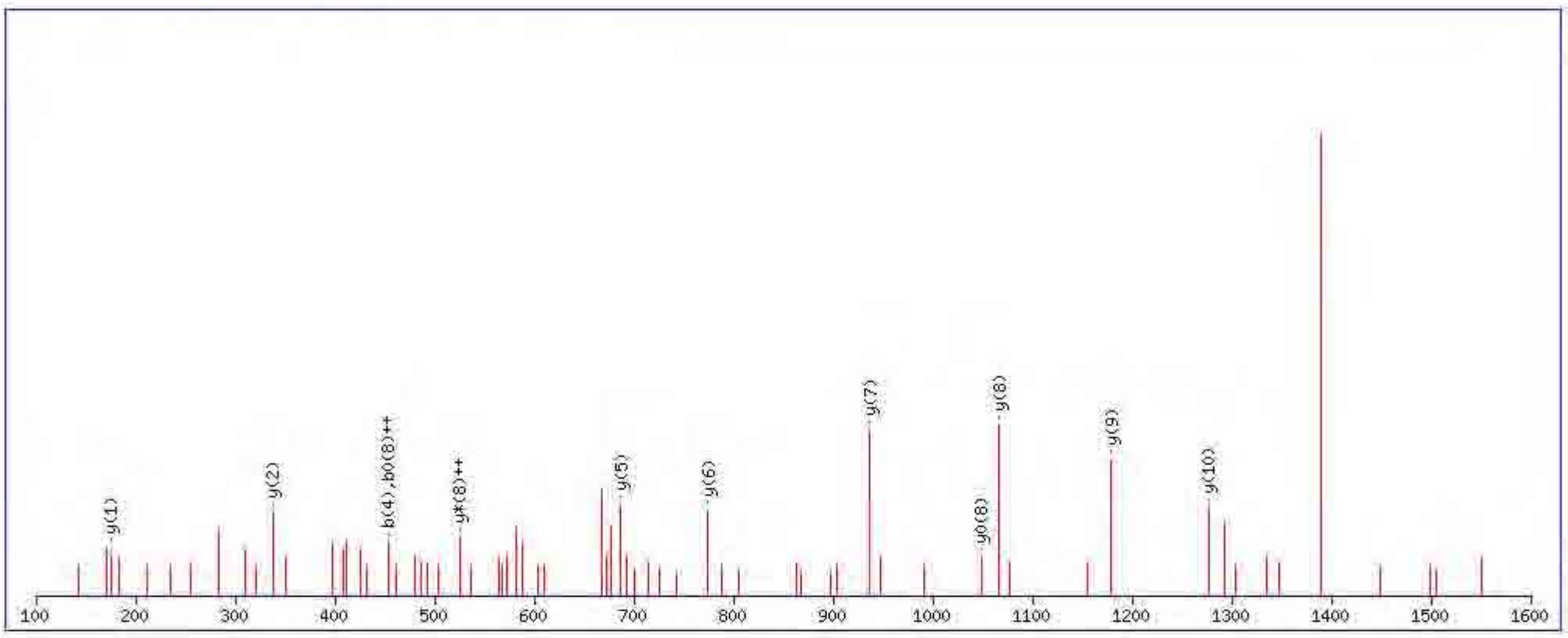
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

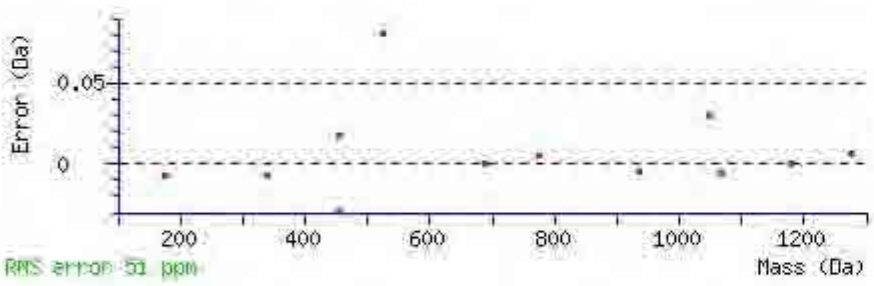
Match to Query 13751: 1388.655368 from(695.334960,2+) rtinseconds(1913) index(14587)
Title: Locus:1.1.1.2147.14
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

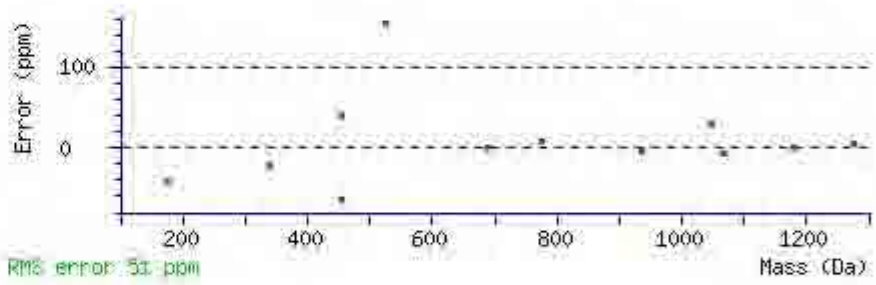
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 42 **Expect:** 0.0023
Matches : 12/90 fragment ions using 25 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	*1276.584445*	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	*1179.531681*	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	*1066.447617*	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	*937.405024*	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	*774.341695*	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	*687.309667*	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	524.246338	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	*338.182281*	169.594778	321.155732	161.081504			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	1388.661194	-0.005826	LPLEYSYGEYR
13.3	1388.667114	-0.011746	PPPELTDTATSTK
11.4	1388.665314	-0.009946	PGGPRGIVGGGMMR
11.4	1388.665314	-0.009946	PGGPRGIVGGGMMR
9.5	1388.643494	0.011874	PPPLHFSPSFCL
9.2	1388.667984	-0.012616	PLLLGNPQPMVM
8.3	1388.667114	-0.011746	PPPELTDTATSTK
7.1	1388.657227	-0.001859	PILGPGSFPSDDR
6.2	1388.650665	0.004703	TNRVLCSYDYR
5.5	1388.664597	-0.009229	KVTMNDFDYLK

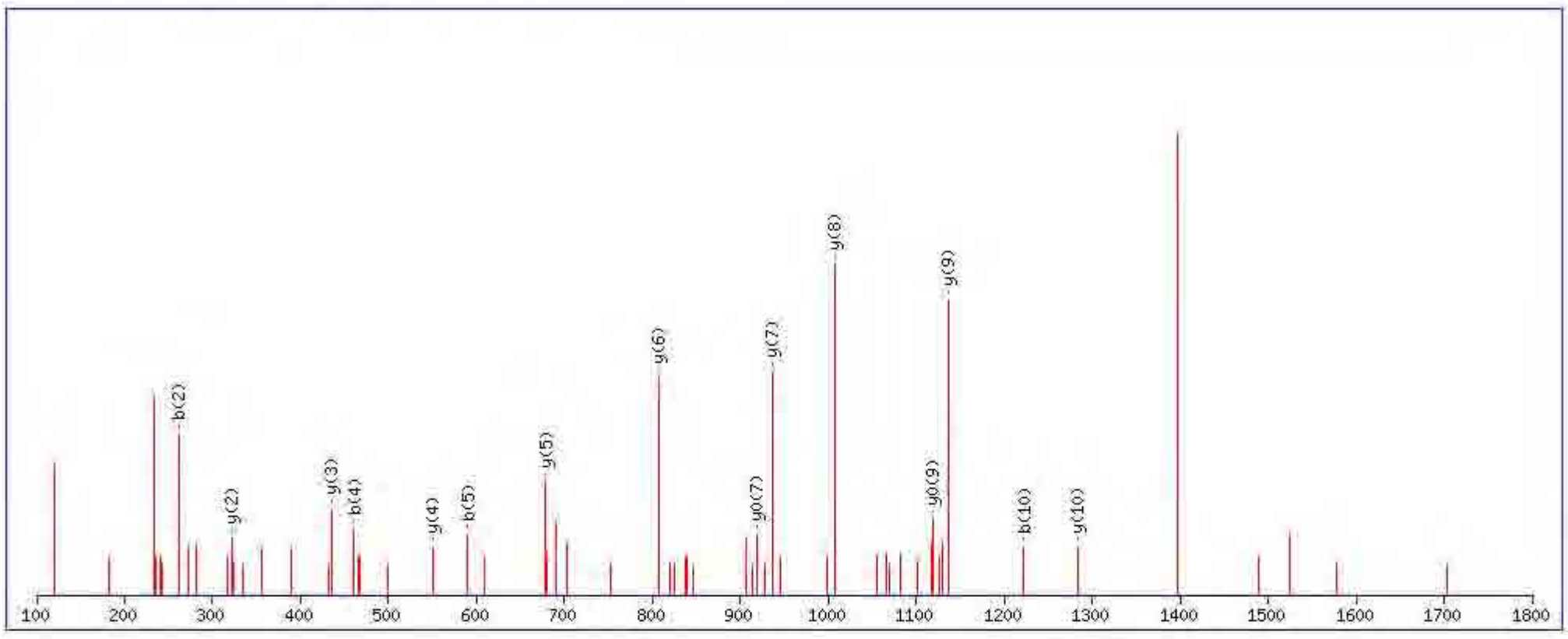
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFEAEEQDLFR**
Found in **EHD3_HUMAN**, EH domain-containing protein 3 OS=Homo sapiens GN=EHD3 PE=1 SV=2

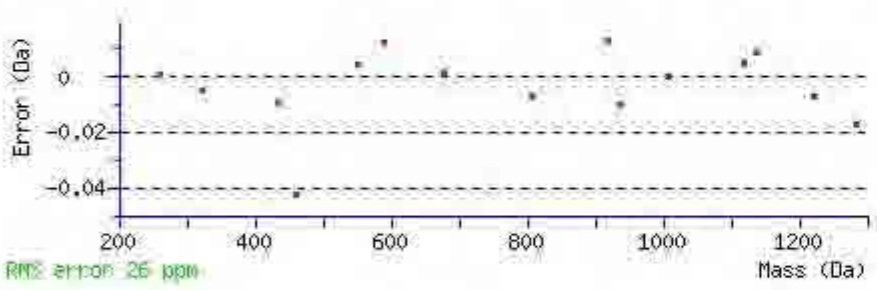
Match to Query 13868: 1395.653788 from(698.834170,2+) rtinseconds(2284) index(19474)
Title: Locus:1.1.1.2345.17
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

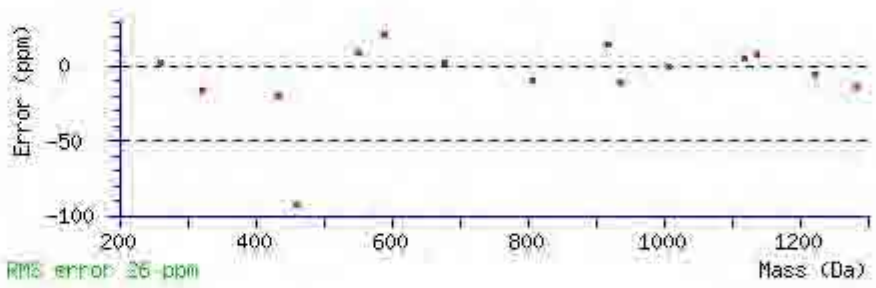
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1395.667023
Ions Score: 71 **Expect:** 1.4e-005
Matches : 15/98 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	**261.159754**	131.083515					F	*1283.590258*	642.298767	1266.563709	633.785493	1265.579693	633.293485	10
3	390.202347	195.604811			372.191782	186.599529	E	*1136.521844*	568.764560	1119.495295	560.251286	1118.511279	559.759278	9
4	**461.239461**	231.123368			443.228896	222.118086	A	*1007.479251*	504.243264	990.452702	495.729989	989.468686	495.237981	8
5	**590.282054**	295.644665			572.271489	286.639383	E	*936.442137*	468.724707	919.415588	460.211432	918.431572	459.719424	7
6	719.324647	360.165962			701.314082	351.160679	E	*807.399544*	404.203410	790.372995	395.690136	789.388979	395.198128	6
7	847.383225	424.195251	830.356676	415.681976	829.372660	415.189968	Q	*678.356951*	339.682114	661.330402	331.168839	660.346386	330.676831	5
8	962.410168	481.708722	945.383619	473.195448	944.399603	472.703440	D	*550.298373*	275.652825	533.271824	267.139550	532.287808	266.647542	4
9	1075.494232	538.250754	1058.467683	529.737480	1057.483667	529.245472	L	*435.271430*	218.139353	418.244881	209.626079			3
10	**1222.562646**	611.784961	1205.536097	603.271687	1204.552081	602.779679	F	*322.187366*	161.597321	305.160817	153.084047			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LFEAEEQDLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.3	1395.667023	-0.013235	LFEAEEQDLFR
18.5	1395.649277	0.004511	LEFSLAWDMPR
15.9	1395.649307	0.004481	FEPSLGPVCPFR
12.9	1395.643921	0.009867	LSMTGSTEDTILE
11.3	1395.659149	-0.005361	LMEALTEYPDAK
11.0	1395.662537	-0.008749	LMESITDSLQML
9.9	1395.649094	0.004694	SPHKPDEGSRDR
9.6	1395.664337	-0.010549	RPHRPFEEAAGN
9.6	1395.664337	-0.010549	RPHRPFEEAAGN
9.5	1395.667053	-0.013265	IFVAEFRPDSDT

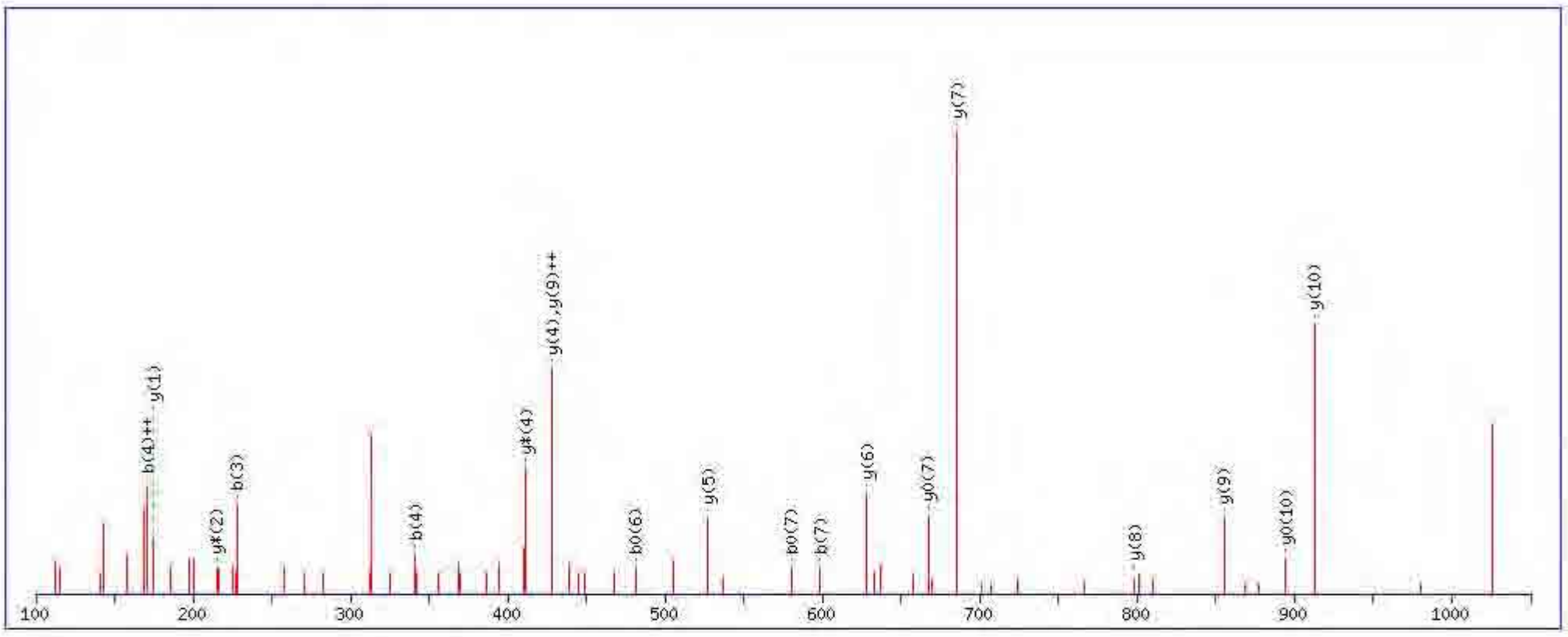
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

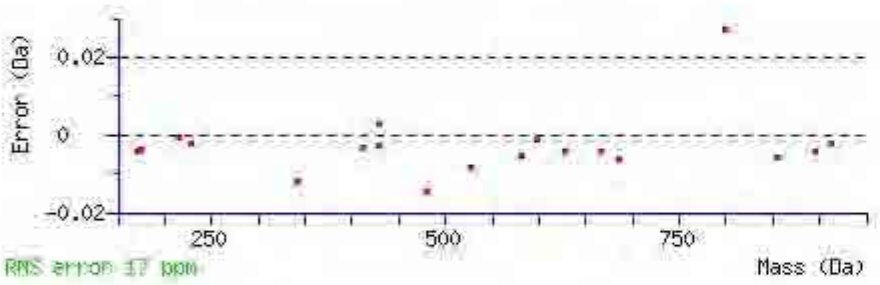
Match to Query 4203: 1024.596148 from(513.305350,2+) rtinseconds(1566) index(10113)
Title: Locus:1.1.1.1958.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

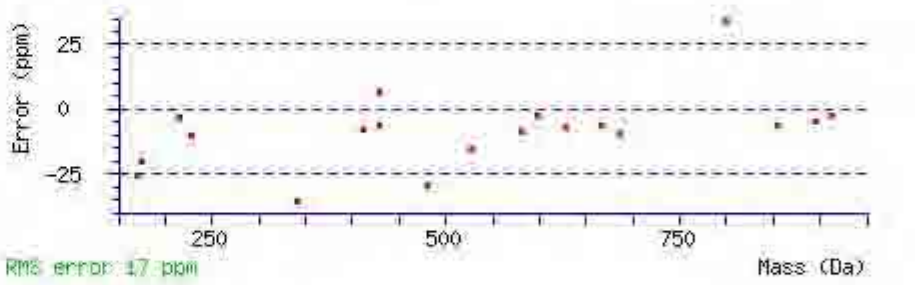
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 54 **Expect:** 0.00024
Matches : 20/80 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	*912.526143*	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	228.134268	114.570772			G	*855.504679*	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	341.218332	171.112804			I	*798.483215*	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	*685.399151*	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	*628.377687*	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	*527.330008*	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	*428.261594*	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	232.140416	116.573846	215.113867	108.060572			2
11					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.3	1024.602951	-0.006803	IGGIGTVPVGR
35.0	1024.591690	0.004458	LGGPSALPKGL
18.3	1024.602905	-0.006757	PGAVAAAAILR
16.2	1024.591690	0.004458	LGGINNILVP
15.0	1024.602905	-0.006757	ARLQPASVAL
11.1	1024.591721	0.004427	VQPSKVVGVP
10.7	1024.602890	-0.006742	ARALDAAKPL
9.3	1024.588989	0.007159	RSPSGLRPR
9.1	1024.591705	0.004443	VQLGGLGTAPL
8.8	1024.602936	-0.006788	LGKTVSHGVK

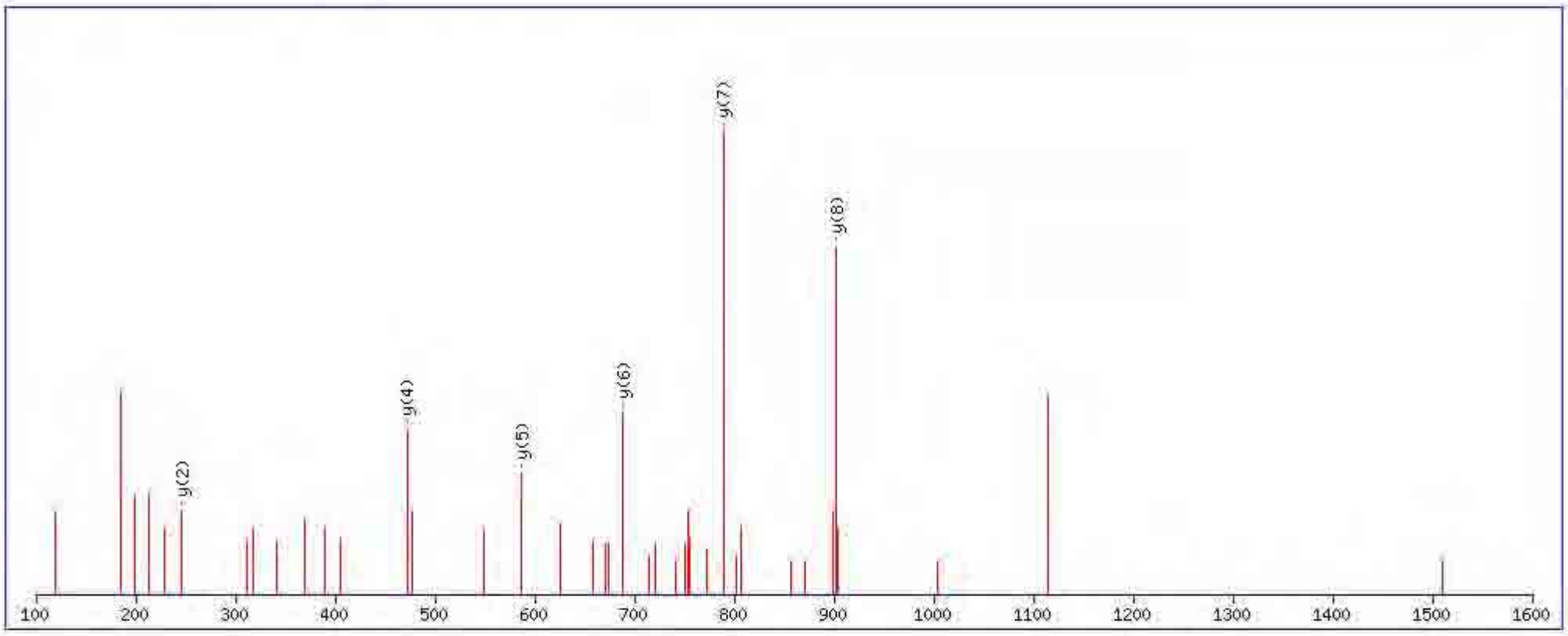
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLITTDLLAR**
Found in **IF4A1_HUMAN**, Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1

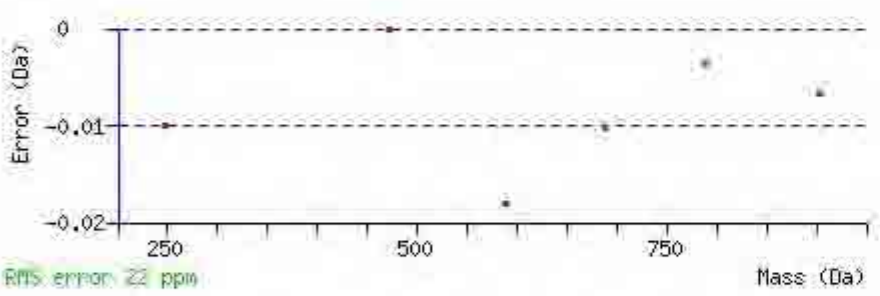
Match to Query 6494: 1113.668308 from(557.841430,2+) rtinseconds(2221) index(18643)
Title: Locus:1.1.1.2312.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

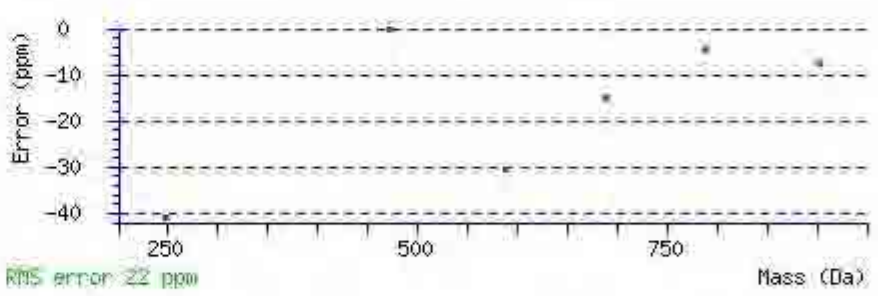
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1113.675751
Ions Score: 47 **Expect:** 0.00025
Matches : 6/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	213.159754	107.083515			L	1015.614623	508.310950	998.588074	499.797675	997.604058	499.305667	9
3	326.243818	163.625547			I	*902.530559*	451.768918	885.504010	443.255643	884.519994	442.763635	8
4	427.291497	214.149386	409.280932	205.144104	T	*789.446495*	395.226886	772.419946	386.713611	771.435930	386.221603	7
5	528.339176	264.673226	510.328611	255.667944	T	*688.398816*	344.703046	671.372267	336.189772	670.388251	335.697764	6
6	643.366119	322.186698	625.355554	313.181415	D	*587.351137*	294.179207	570.324588	285.665932	569.340572	285.173924	5
7	756.450183	378.728730	738.439618	369.723447	L	*472.324194*	236.665735	455.297645	228.152460			4
8	869.534247	435.270762	851.523682	426.265479	L	359.240130	180.123703	342.213581	171.610428			3
9	940.571361	470.789319	922.560796	461.784036	A	*246.156066*	123.581671	229.129517	115.068396			2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VLITTDLLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1113.675751	-0.007443	VLITTDLLAR
7.7	1113.657990	0.010318	LIVMIGLPAR
6.7	1113.675766	-0.007458	VPLISVTTLR
2.4	1113.657990	0.010318	VILRMLPISG
2.0	1113.675751	-0.007443	LVIGKGGETIK
0.7	1113.665863	0.002445	RPVPILPLHG

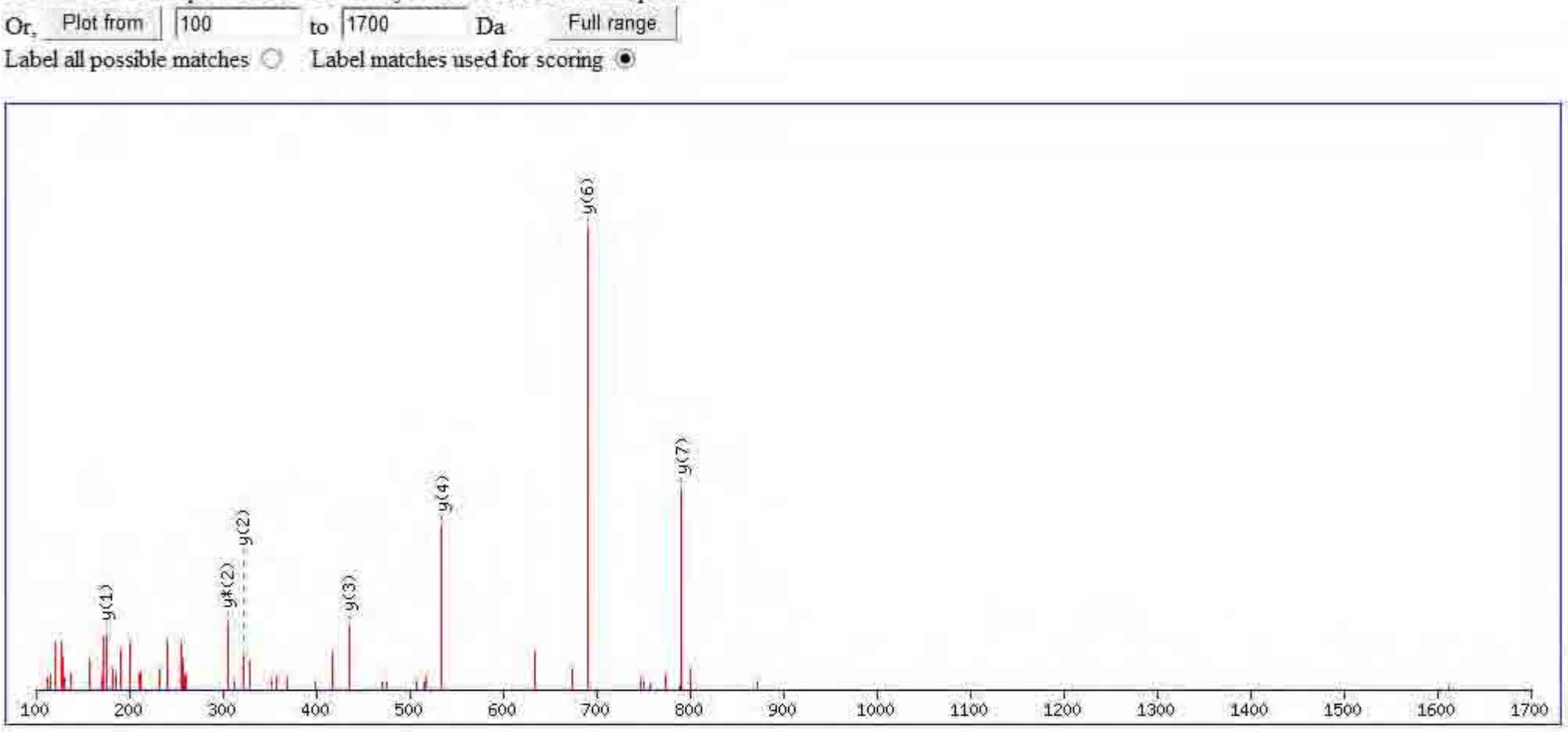
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTGVVLFR**
Found in **SODE_HUMAN**, Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2

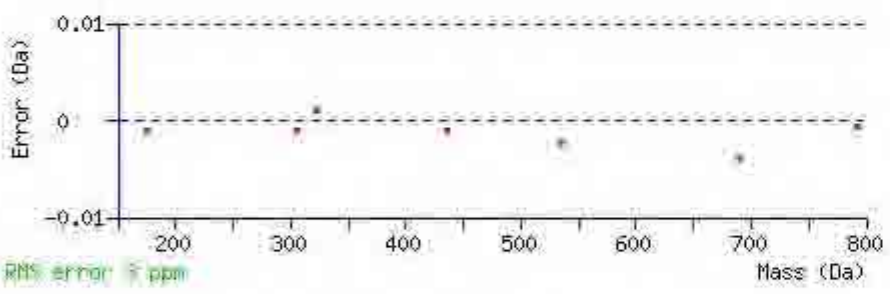
Match to Query 1726: 889.532368 from(445.773460,2+) rtinseconds(1953) index(15122)
Title: Locus:1.1.1.2169.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

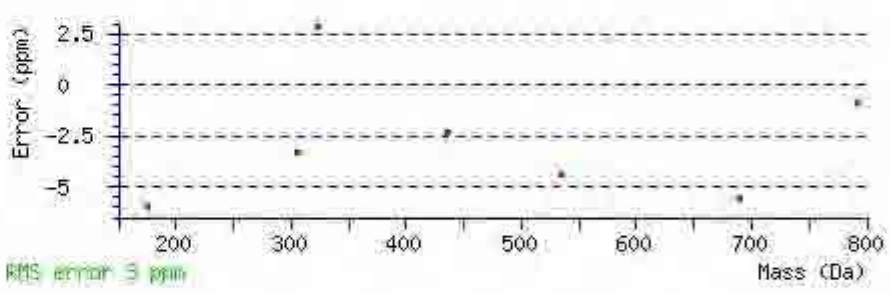
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 889.538559
Ions Score: 66 **Expect:** 1.6e-005
Matches : 7/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							8
2	201.123369	101.065322	183.112804	92.060040	T	*791.477401*	396.242339	774.450852	387.729064	773.466836	387.237056	7
3	258.144833	129.576055	240.134268	120.570772	G	*690.429722*	345.718499	673.403173	337.205225			6
4	357.213247	179.110262	339.202682	170.104979	V	633.408258	317.207767	616.381709	308.694493			5
5	456.281661	228.644469	438.271096	219.639186	V	*534.339844*	267.673560	517.313295	259.160286			4
6	569.365725	285.186501	551.355160	276.181218	L	*435.271430*	218.139353	418.244881	209.626079			3
7	716.434139	358.720708	698.423574	349.715425	F	*322.187366*	161.597321	305.160817	153.084047			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VTGVVLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	889.538559	-0.006191	VTGVVLFR
27.6	889.538528	-0.006160	VIKDIFR
19.9	889.538544	-0.006176	SLGVVFRL
14.1	889.538528	-0.006160	VIVEKFR
13.8	889.538528	-0.006160	TVIAAFIR
12.5	889.538528	-0.006160	VEKLFVR
12.5	889.538544	-0.006176	VSLGFLVR
12.0	889.538528	-0.006160	ITLKPFR
12.0	889.538513	-0.006145	LASAILFR
12.0	889.538528	-0.006160	LTVAAIFR

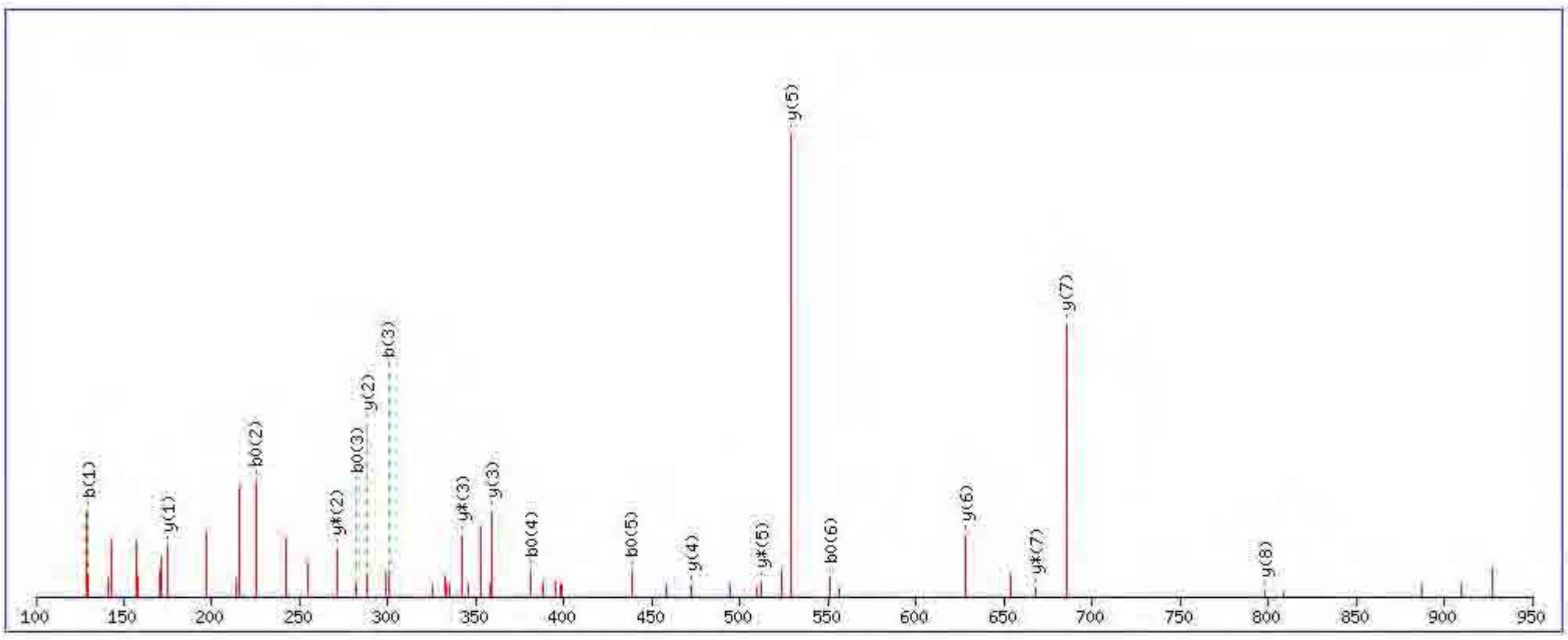
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGVGIALR**
Found in **FABP5_HUMAN**, Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3

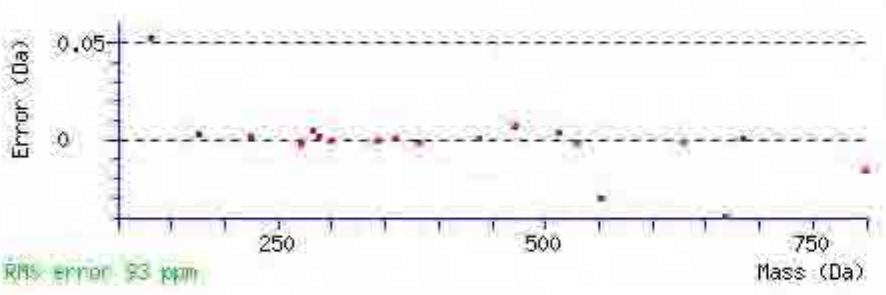
Match to Query 2357: 926.546628 from(464.280590,2+) rtinseconds(1918) index(14650)
Title: Locus:1.1.1.2150.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

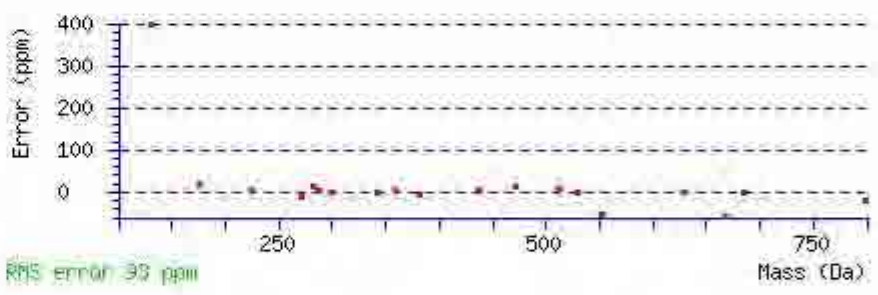
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 926.554901
Ions Score: 49 **Expect:** 0.0013
Matches : 19/64 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					9
2	243.133933	122.070605	225.123368	113.065322	L	*798.519600*	399.763438	781.493051	391.250163	8
3	300.155397	150.581336	282.144832	141.576054	G	*685.435536*	343.221406	668.408987	334.708131	7
4	399.223811	200.115544	381.213246	191.110261	V	*628.414072*	314.710674	611.387523	306.197400	6
5	456.245275	228.626275	438.234710	219.620993	G	*529.345658*	265.176467	512.319109	256.663192	5
6	569.329339	285.168308	551.318774	276.163025	I	*472.324194*	236.665735	455.297645	228.152460	4
7	640.366453	320.686865	622.355888	311.681582	A	*359.240130*	180.123703	342.213581	171.610428	3
8	753.450517	377.228897	735.439952	368.223614	L	*288.203016*	144.605146	271.176467	136.091871	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ELGVGIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	926.554901	-0.008273	ELGVGIALR
26.6	926.554901	-0.008273	ELRGLLQV
14.9	926.554901	-0.008273	ELVGRLGLA
12.4	926.554901	-0.008273	ELVARVLQ
11.8	926.554901	-0.008273	GPEVLKLR
11.4	926.554901	-0.008273	ELVQAVLR
9.8	926.554901	-0.008273	EGVLGALLR
9.4	926.540970	0.005658	QIGNRALR
8.8	926.554901	-0.008273	KLTPPALR
6.8	926.554901	-0.008273	TSLPLGALR

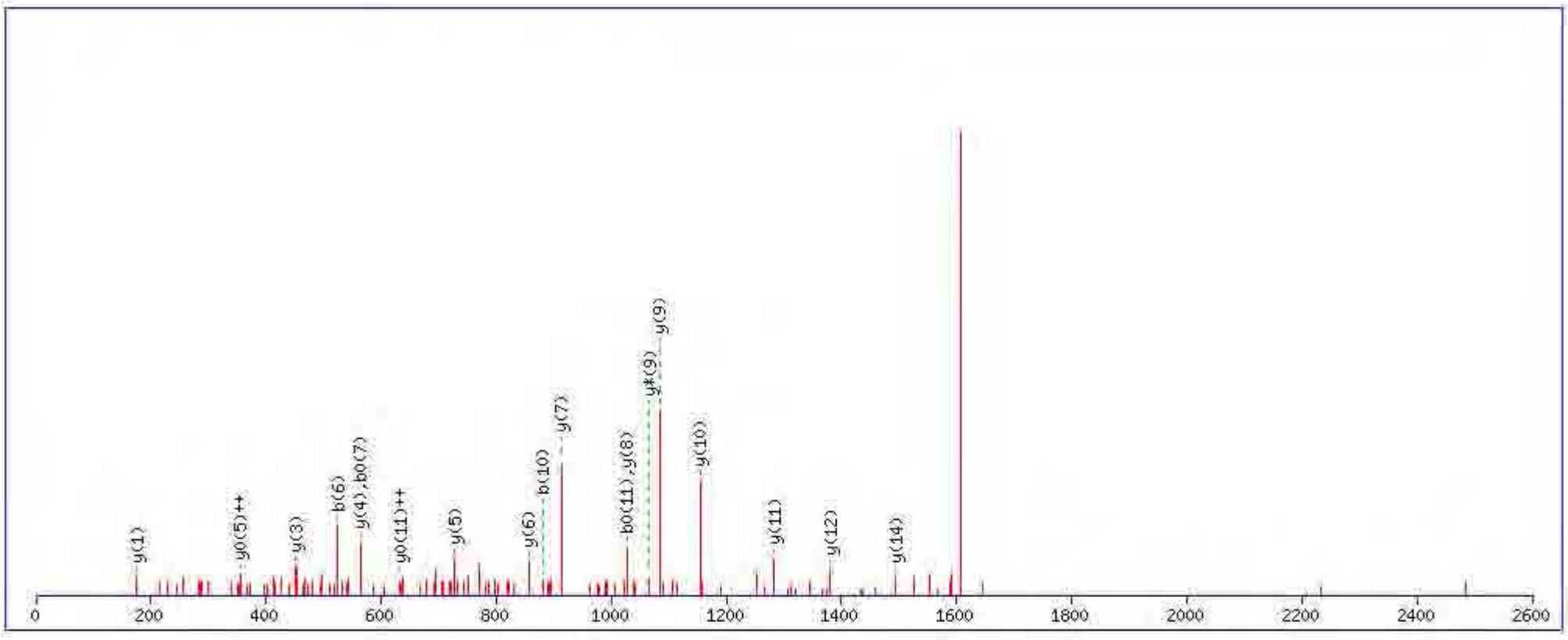
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGGPEAGLGEYLFER**
Found in **FRIL_HUMAN**, Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2

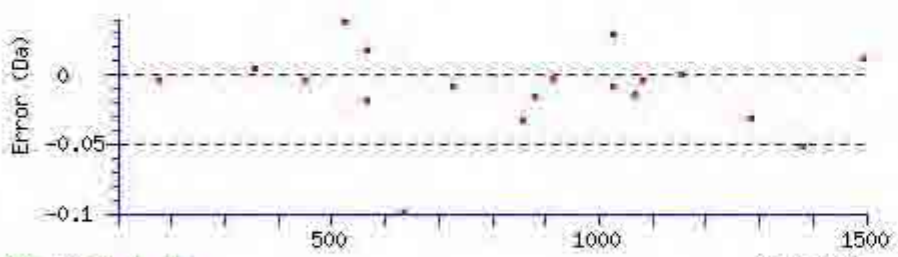
Match to Query 18203: 1606.784608 from(804.399580,2+) rtinseconds(2515) index(21490)
Title: Locus:1.1.1.2467.21
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

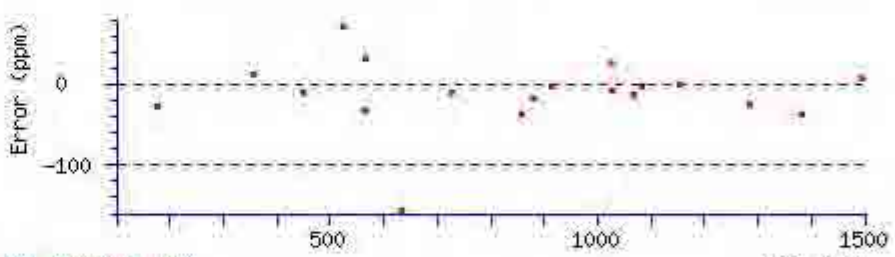
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1606.799103
Ions Score: 98 Expect: 1.2e-008
Matches : 19/130 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							15
2	171.112804	86.060040			G	*1494.722336*	747.864806	1477.695787	739.351532	1476.711771	738.859524	14
3	228.134268	114.570772			G	1437.700872	719.354074	1420.674323	710.840800	1419.690307	710.348792	13
4	325.187032	163.097154			P	*1380.679408*	690.843342	1363.652859	682.330068	1362.668843	681.838060	12
5	454.229625	227.618450	436.219060	218.613168	E	*1283.626644*	642.316960	1266.600095	633.803686	1265.616079	633.311678	11
6	525.266739	263.137008	507.256174	254.131725	A	*1154.584051*	577.795664	1137.557502	569.282389	1136.573486	568.790381	10
7	582.288203	291.647740	564.277638	282.642457	G	*1083.546937*	542.277107	1066.520388	533.763832	1065.536372	533.271824	9
8	695.372267	348.189772	677.361702	339.184489	L	*1026.525473*	513.766375	1009.498924	505.253100	1008.514908	504.761092	8
9	752.393731	376.700504	734.383166	367.695221	G	*913.441409*	457.224343	896.414860	448.711068	895.430844	448.219060	7
10	881.436324	441.221800	863.425759	432.216518	E	*856.419945*	428.713611	839.393396	420.200336	838.409380	419.708328	6
11	1044.499653	522.753465	1026.489088	513.748182	Y	*727.377352*	364.192314	710.350803	355.679040	709.366787	355.187032	5
12	1157.583717	579.295497	1139.573152	570.290214	L	*564.314023*	282.660650	547.287474	274.147375	546.303458	273.655367	4
13	1304.652131	652.829704	1286.641566	643.824421	F	*451.229959*	226.118618	434.203410	217.605343	433.219394	217.113335	3
14	1433.694724	717.351000	1415.684159	708.345718	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
15					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LGGPEAGLGEYLFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
98.2	1606.799103	-0.014495	LGGPEAGLGEYLFER
12.9	1606.795090	-0.010482	PNGLSPLSGYSSSLGR
12.6	1606.781372	0.003236	KPLGPPPPSYTCFR
11.0	1606.796432	-0.011824	WRGTSRPPEAVAAGH
10.5	1606.799164	-0.014556	GPPGSPGLQGFPGITPP
10.2	1606.799164	-0.014556	GPPGSPGLQGFPGITPP
10.1	1606.796432	-0.011824	WRGTSRPPEAVAAGH
8.9	1606.795105	-0.010497	EAGPGLPAGPSLPQPR
7.6	1606.781372	0.003236	KPLGPPPPSYTCFR
6.8	1606.780716	0.003892	GLGGCDQSVMDLIKR

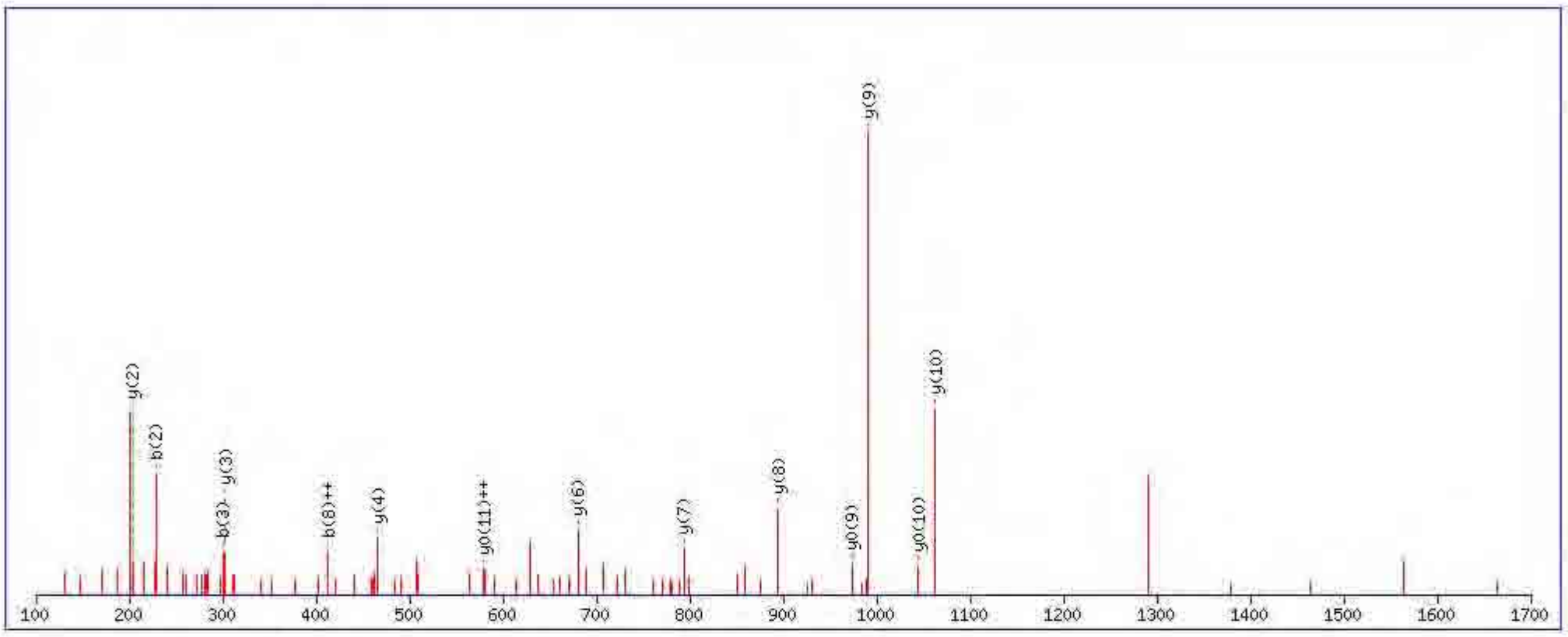
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIAPTLTLYVGK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

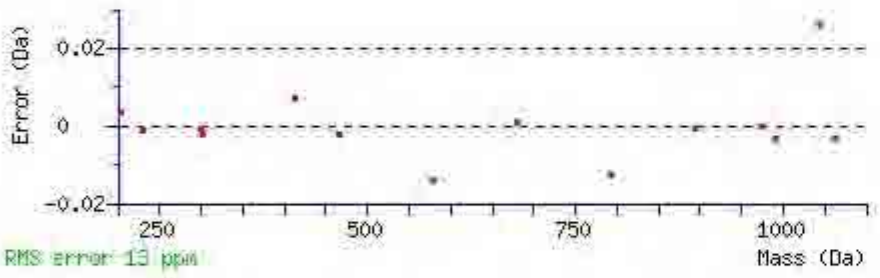
Match to Query 11344: 1289.714468 from(645.864510,2+) rtinseconds(2259) index(19146)
Title: Locus:1.1.1.2332.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

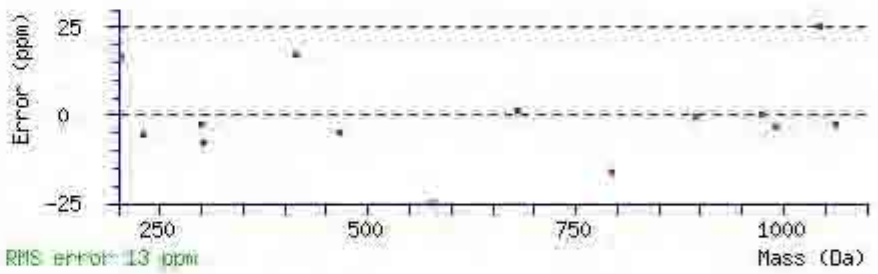
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1289.723099
Ions Score: 60 Expect: 0.0001
Matches : 15/100 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							12
2	229.118283	115.062779	211.107718	106.057497	I	1175.703439	588.355358	1158.676890	579.842083	1157.692874	579.350075	11
3	300.155397	150.581336	282.144832	141.576054	A	*1062.619375*	531.813326	1045.592826	523.300051	1044.608810	522.808043	10
4	397.208161	199.107718	379.197596	190.102436	P	*991.582261*	496.294769	974.555712	487.781494	973.571696	487.289486	9
5	498.255840	249.631558	480.245275	240.626275	T	*894.529497*	447.768387	877.502948	439.255112	876.518932	438.763104	8
6	611.339904	306.173590	593.329339	297.168308	L	*793.481818*	397.244547	776.455269	388.731273	775.471253	388.239265	7
7	712.387583	356.697430	694.377018	347.692147	T	*680.397754*	340.702515	663.371205	332.189241	662.387189	331.697233	6
8	825.471647	413.239462	807.461082	404.234179	L	*579.350075*	290.178676	562.323526	281.665401			5
9	988.534976	494.771126	970.524411	485.765844	Y	*466.266011*	233.636644	449.239462	225.123369			4
10	1087.603390	544.305333	1069.592825	535.300051	V	*303.202682*	152.104979	286.176133	143.591704			3
11	1144.624854	572.816065	1126.614289	563.810783	G	*204.134268*	102.570772	187.107719	94.057497			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DIAPTLTLYVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.7	1289.723099	-0.008631	DIAPTLTLYVGK
18.5	1289.709183	0.005285	RPGGPQSLTPLPA
15.9	1289.709198	0.005270	SLVPGTHTPPIR
14.9	1289.709198	0.005270	SLVPGTHTPPIR
14.9	1289.709198	0.005270	SPVPTTLPGLRH
11.9	1289.707840	0.006628	VTVLEEKLVSSS
11.5	1289.709167	0.005301	NKGLPRPDSPIP
10.1	1289.726471	-0.012003	TVVLTMKASVIE
9.8	1289.720413	-0.005945	LSVPQPRPPGAR
9.8	1289.709198	0.005270	SLVPGTHTPPIR

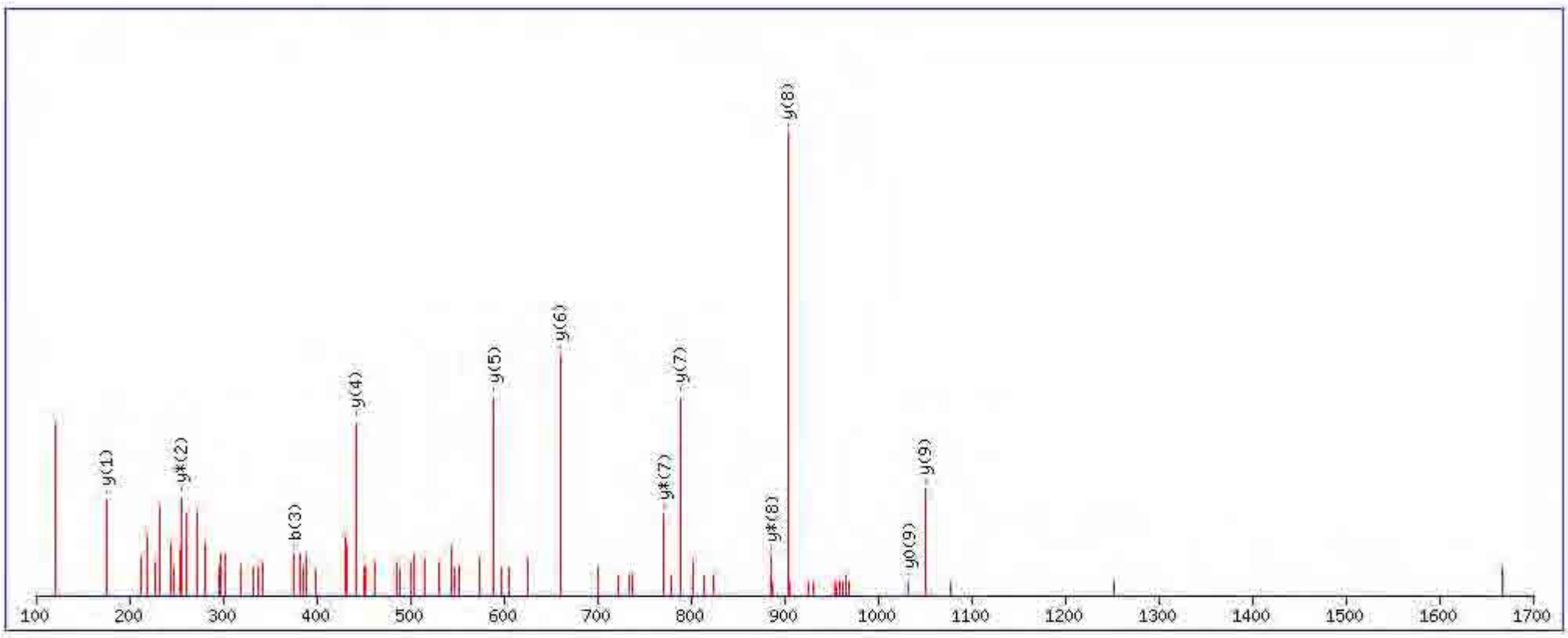
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFDQAFGLPR**
Found in **HSPB1_HUMAN**, Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2

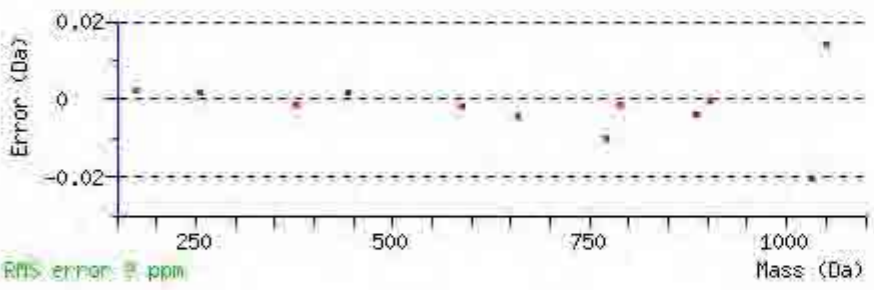
Match to Query 7779: 1162.609468 from(582.312010,2+) rtinseconds(2291) index(19562)
Title: Locus:1.1.1.2349.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

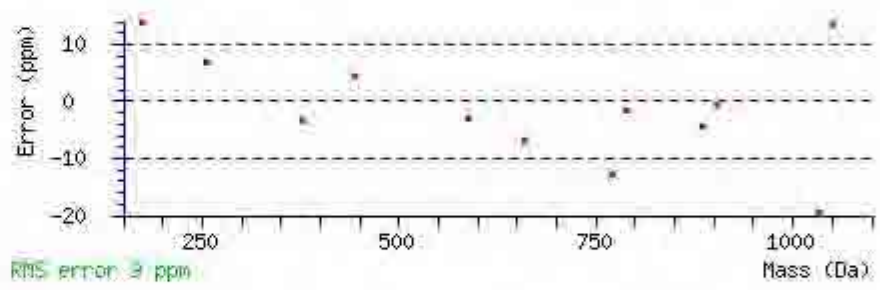
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1162.613495
Ions Score: 47 **Expect:** 0.0019
Matches : 12/84 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							10
2	261.159754	131.083515					F	*1050.536707*	525.771992	1033.510158	517.258717	1032.526142	516.766709	9
3	376.186697	188.596986			358.176132	179.591704	D	*903.468293*	452.237785	886.441744	443.724510	885.457728	443.232502	8
4	504.245275	252.626275	487.218726	244.113001	486.234710	243.620993	Q	*788.441350*	394.724313	771.414801	386.211039			7
5	575.282389	288.144833	558.255840	279.631558	557.271824	279.139550	A	*660.382772*	330.695024	643.356223	322.181750			6
6	722.350803	361.679040	705.324254	353.165765	704.340238	352.673757	F	*589.345658*	295.176467	572.319109	286.663193			5
7	779.372267	390.189772	762.345718	381.676497	761.361702	381.184489	G	*442.277244*	221.642260	425.250695	213.128986			4
8	892.456331	446.731804	875.429782	438.218529	874.445766	437.726521	L	385.255780	193.131528	368.229231	184.618253			3
9	989.509095	495.258186	972.482546	486.744911	971.498530	486.252903	P	272.171716	136.589496	255.145167	128.076221			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LFDQAFGLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.3	1162.613495	-0.004027	LFDQAFGLPR
17.1	1162.598236	0.011232	PGVTFSAKDNK
11.5	1162.613480	-0.004012	LFDIYHLSR
11.2	1162.613480	-0.004012	LFNHKQYLT
9.8	1162.616852	-0.007384	LMQDLKPFR
9.4	1162.601608	0.007860	LMTTLRNTTP
8.9	1162.598251	0.011217	LPLPGPDPGPR
8.9	1162.616852	-0.007384	IDMQKFPLR
8.5	1162.598251	0.011217	LPLPGPDPGPR
8.0	1162.605621	0.003847	IMAVIKEWGT

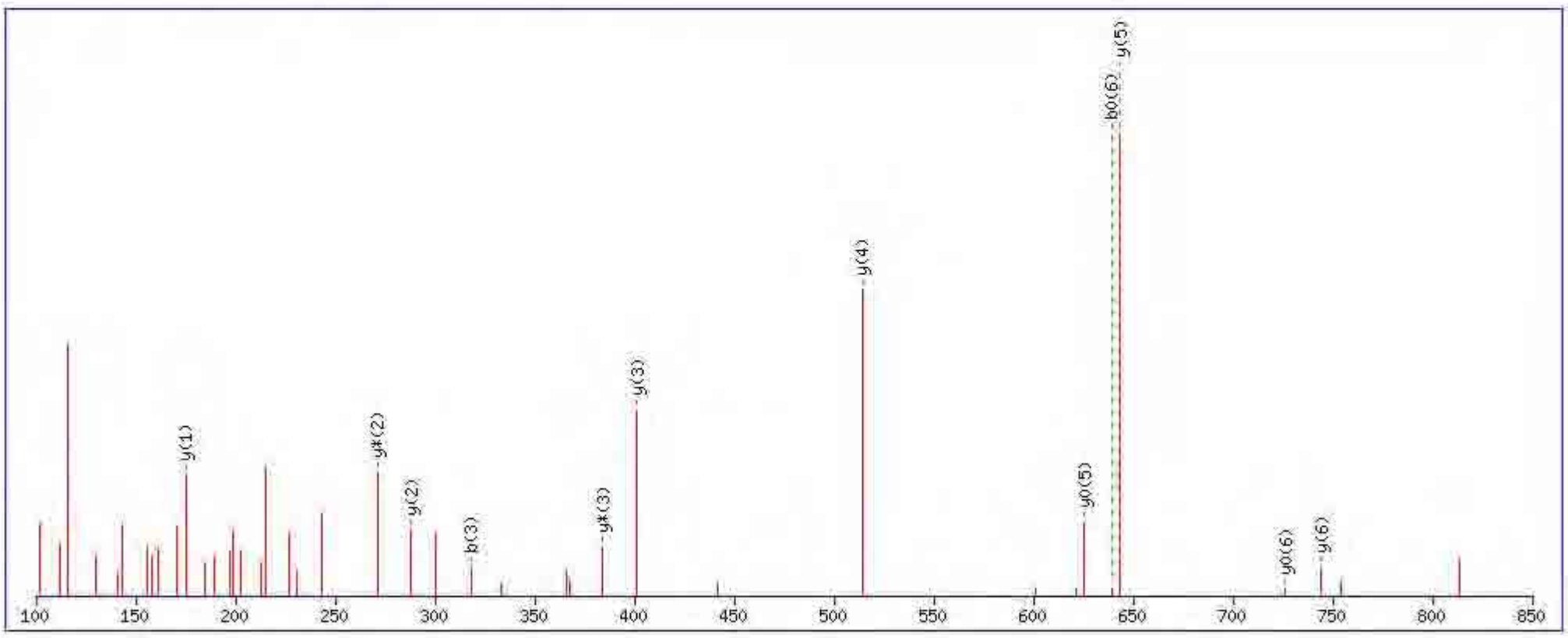
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELLIR**
Found in **H31T_HUMAN**, Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3

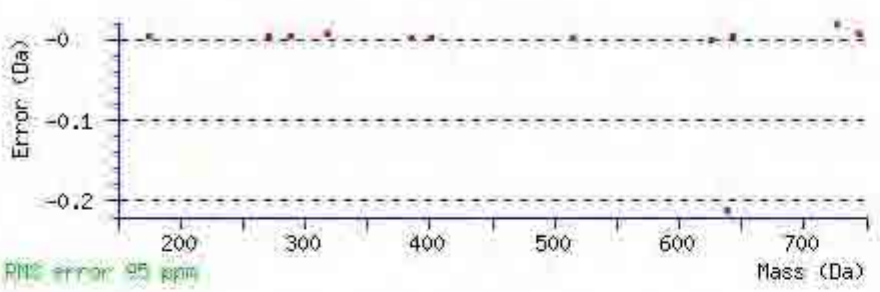
Match to Query 890: 830.484708 from(416.249630,2+) rtinseconds(1545) index(9833)
Title: Locus:1.1.1.1947.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

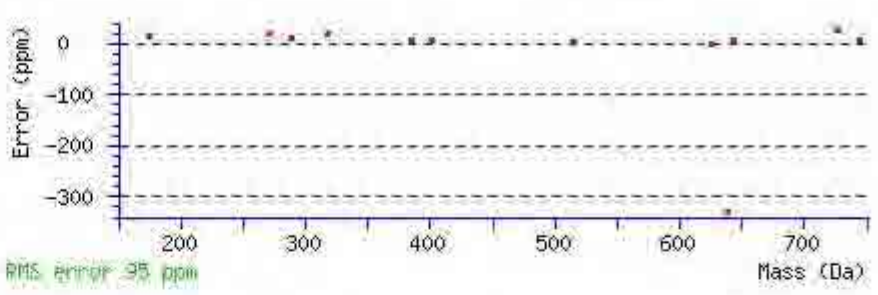
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 830.486145
Ions Score: 39 **Expect:** 0.011
Matches : 12/52 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	189.086983	95.047129	171.076418	86.041847	T	*744.461416*	372.734346	727.434867	364.221072	726.450851	363.729064	6
3	318.129576	159.568426	300.119011	150.563144	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
4	431.213640	216.110458	413.203075	207.105176	L	*514.371144*	257.689210	497.344595	249.175936			4
5	544.297704	272.652490	526.287139	263.647208	L	*401.287080*	201.147178	384.260531	192.633904			3
6	657.381768	329.194522	639.371203	320.189240	I	*288.203016*	144.605146	271.176467	136.091872			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of STELLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	830.486145	-0.001437	STELLIR
27.8	830.486145	-0.001437	TESLLLR
18.6	830.486160	-0.001452	TTDIILR
13.3	830.490189	-0.005481	LTWLVSL
13.1	830.486145	-0.001437	SSLLLNGK
12.5	830.486145	-0.001437	TELSLLR
12.5	830.486145	-0.001437	ESTLLIR
12.1	830.486145	-0.001437	ETISIIR
12.1	830.486145	-0.001437	SLTEIIR
11.5	830.486145	-0.001437	TLESILR

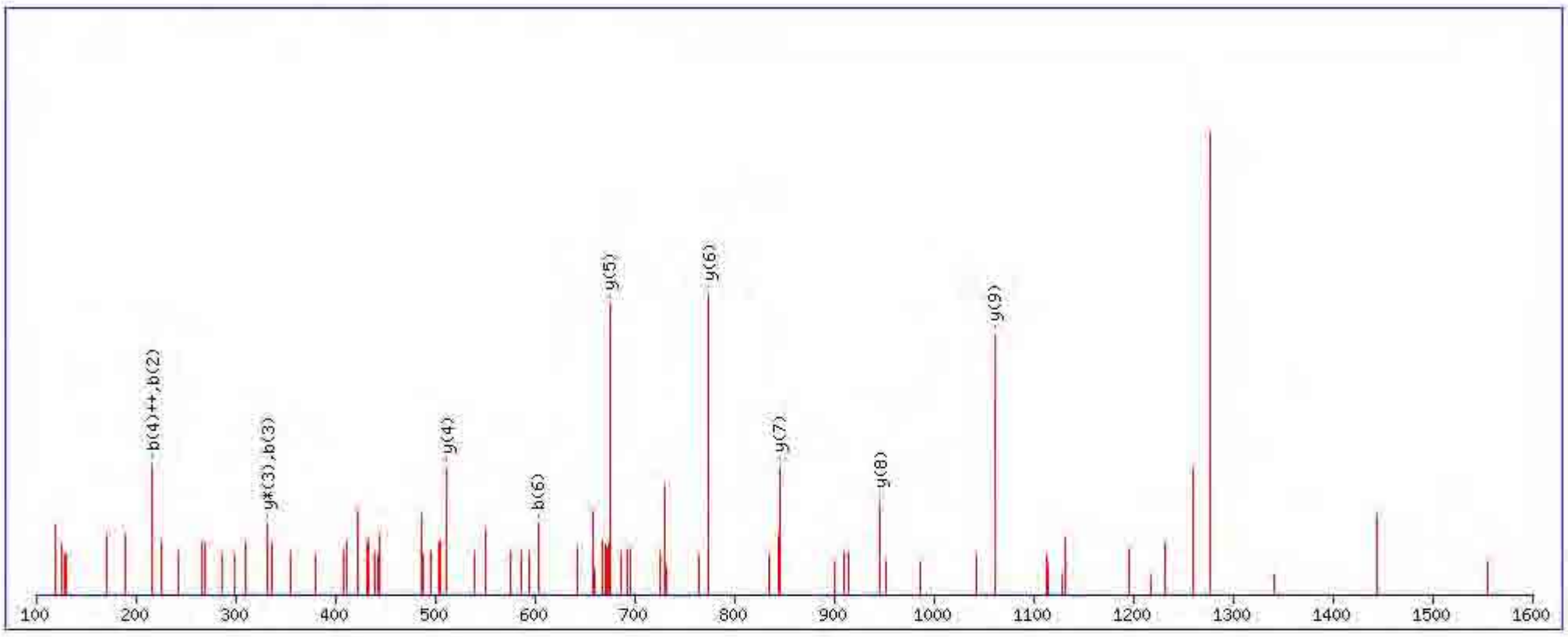
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEDTAVYYCAR**
Found in **HV102_HUMAN**, Ig heavy chain V-I region HG3 OS=Homo sapiens PE=4 SV=1

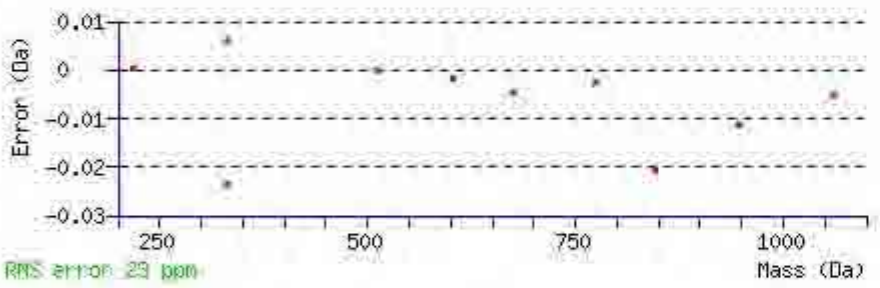
Match to Query 10882: 1276.550868 from(639.282710,2+) rtinseconds(1438) index(8454)
Title: Locus:1.1.1.1885.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

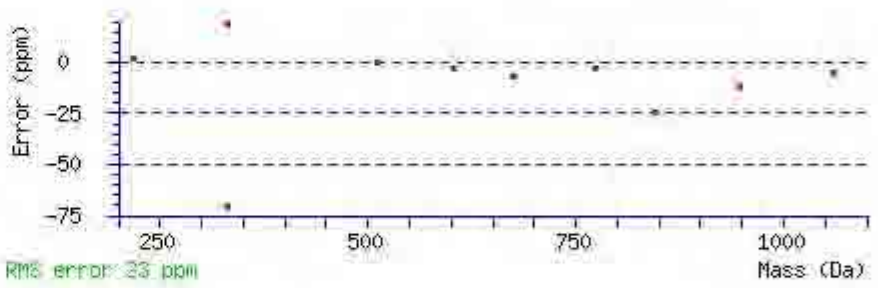
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1276.539383
Ions Score: 50 **Expect:** 8.5e-005
Matches : 11/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	217.081897	109.044586	199.071332	100.039304	E	1190.514652	595.760964	1173.488103	587.247689	1172.504087	586.755681	10
3	332.108840	166.558058	314.098275	157.552776	D	*1061.472059*	531.239668	1044.445510	522.726393	1043.461494	522.234385	9
4	433.156519	217.081898	415.145954	208.076615	T	*946.445116*	473.726196	929.418567	465.212921	928.434551	464.720913	8
5	504.193633	252.600455	486.183068	243.595172	A	*845.397437*	423.202356	828.370888	414.689082			7
6	603.262047	302.134662	585.251482	293.129379	V	*774.360323*	387.683799	757.333774	379.170525			6
7	766.325376	383.666326	748.314811	374.661044	Y	*675.291909*	338.149592	658.265360	329.636318			5
8	929.388705	465.197991	911.378140	456.192708	Y	*512.228580*	256.617928	495.202031	248.104653			4
9	1032.397890	516.702583	1014.387325	507.697300	C	349.165251	175.086263	332.138702	166.572989			3
10	1103.435004	552.221140	1085.424439	543.215857	A	246.156066	123.581671	229.129517	115.068396			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SEDTAVYYCAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	1276.539383	0.011485	SEDTAVYYCAR
6.1	1276.557159	-0.006291	ESTDDHAIVQY
6.0	1276.542770	0.008098	CPSEAGAMTQPAV
3.1	1276.543655	0.007213	MCGLVMGMFTR
2.8	1276.554016	-0.003148	MTAPGAAGRCPPT
2.6	1276.541870	0.008998	ESESPENQTEK
2.6	1276.539413	0.011455	FASQQGMTAYGT
1.9	1276.541901	0.008967	PEGEGETETQGK
0.8	1276.542770	0.008098	ICERTDPECPV
0.8	1276.542770	0.008098	ICERTDPECPV

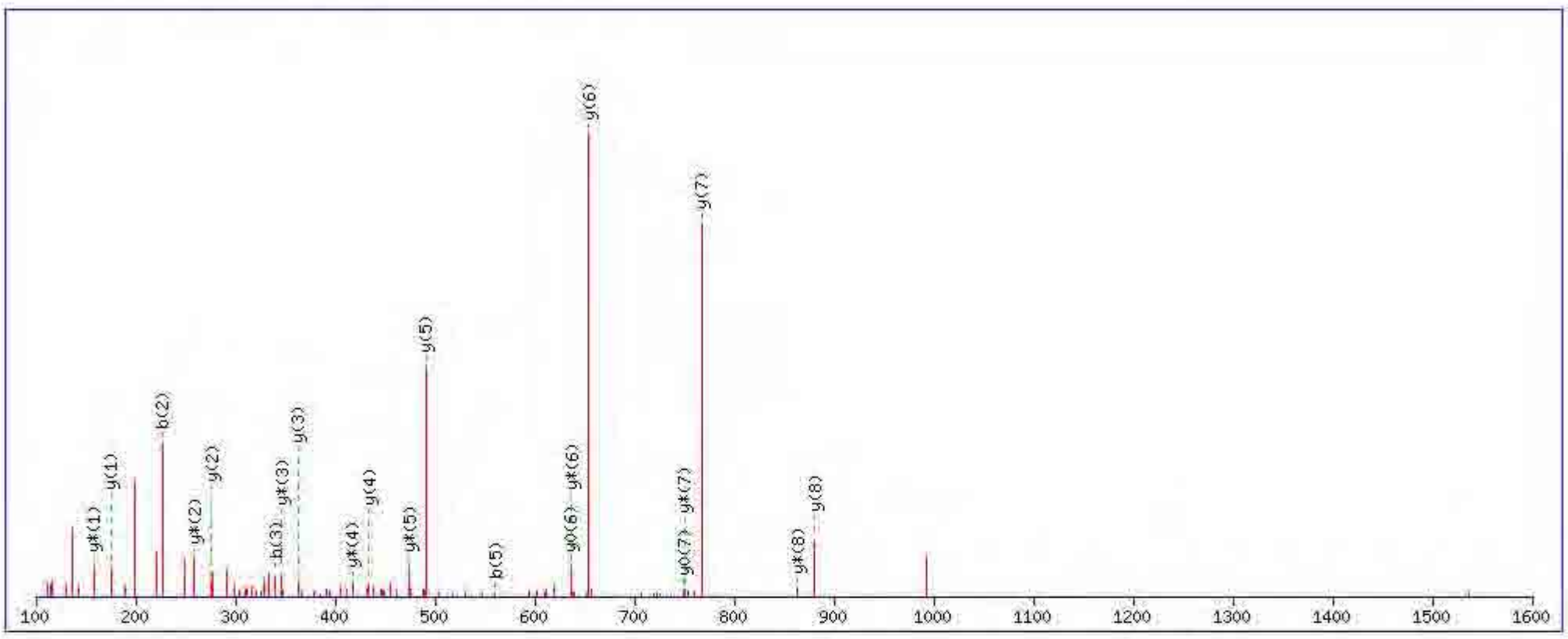
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

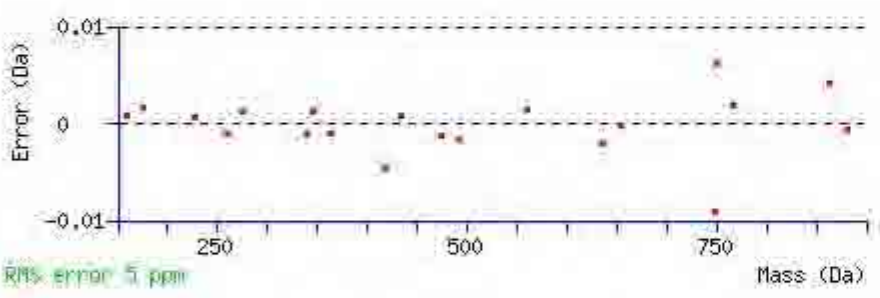
Match to Query 3586: 992.559668 from(497.287110,2+) rtinseconds(1639) index(10985)
Title: Locus:1.1.1.2000.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

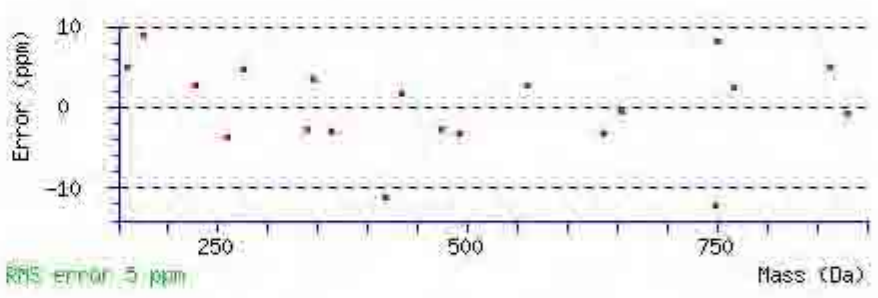
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 49 **Expect:** 0.0013
Matches : 21/66 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	*363.198659*	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	992.565460	-0.005792	LLIYGASTR
43.9	992.565460	-0.005792	LLIYGATSR
18.2	992.554245	0.005423	ILPPLSPPQ
16.4	992.565475	-0.005807	PLLGPPDIR
15.8	992.551544	0.008124	IPLRDHAR
15.7	992.554230	0.005438	LLLKSSEGF
15.6	992.554245	0.005423	ILPPLSPPQ
15.6	992.565475	-0.005807	ILPSVSHKP
15.6	992.565475	-0.005807	LLPHVSSPK
14.0	992.565491	-0.005823	PLPPPVAVR

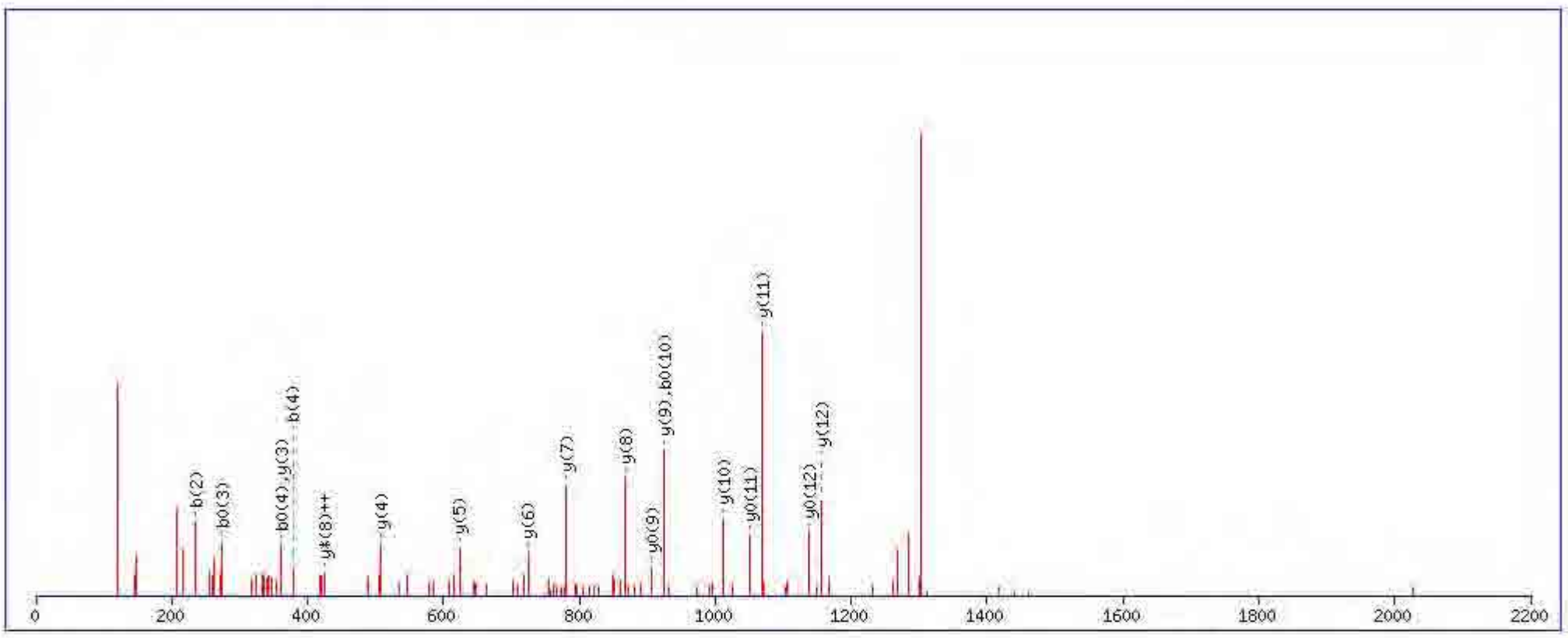
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSGSGTDFTLK**
Found in **KV201_HUMAN**, Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1

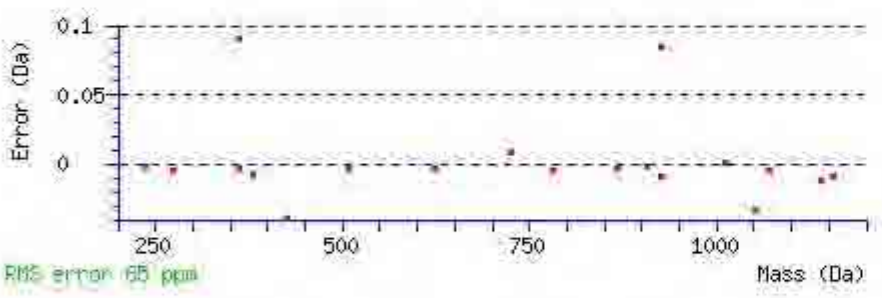
Match to Query 11692: 1302.608388 from(652.311470,2+) rtinseconds(1634) index(10921)
Title: Locus:1.1.1.1997.15
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

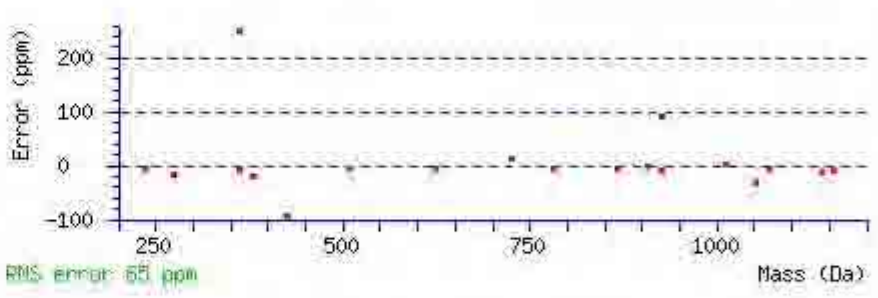
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1302.609222
Ions Score: 93 Expect: 4.7e-008
Matches : 19/114 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	235.107718	118.057497	217.097153	109.052214	S	*1156.548059*	578.777667	1139.521510	570.264393	1138.537494	569.772385	12
3	292.129182	146.568229	274.118617	137.562946	G	*1069.516031*	535.261653	1052.489482	526.748379	1051.505466	526.256371	11
4	379.161210	190.084243	361.150645	181.078960	S	*1012.494567*	506.750921	995.468018	498.237647	994.484002	497.745639	10
5	436.182674	218.594975	418.172109	209.589692	G	*925.462539*	463.234907	908.435990	454.721633	907.451974	454.229625	9
6	523.214702	262.110989	505.204137	253.105707	S	*868.441075*	434.724176	851.414526	426.210901	850.430510	425.718893	8
7	580.236166	290.621721	562.225601	281.616439	G	*781.409047*	391.208161	764.382498	382.694887	763.398482	382.202879	7
8	681.283845	341.145561	663.273280	332.140278	T	*724.387583*	362.697429	707.361034	354.184155	706.377018	353.692147	6
9	796.310788	398.659032	778.300223	389.653750	D	*623.339904*	312.173590	606.313355	303.660315	605.329339	303.168307	5
10	943.379202	472.193239	925.368637	463.187956	F	*508.312961*	254.660118	491.286412	246.146844	490.302396	245.654836	4
11	1044.426881	522.717078	1026.416316	513.711796	T	*361.244547*	181.125911	344.217998	172.612637	343.233982	172.120629	3
12	1157.510945	579.259110	1139.500380	570.253828	L	260.196868	130.602072	243.170319	122.088797			2
13					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSGSGSGTDFTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.2	1302.609222	-0.000834	FSGSGSGTDFTLK
93.2	1302.609222	-0.000834	FSGSGSGTBFTLK
14.1	1302.612534	-0.004146	YKESTATSAMSK
12.2	1302.597961	0.010427	QYSTEDTILSF
12.2	1302.599503	0.008885	HILRCMGNSGIC
9.6	1302.597977	0.010411	FTAESYTVLGDT
9.5	1302.609192	-0.000804	FSPSPPKSADASP
9.5	1302.609192	-0.000804	FSPSPPKSADASP
9.2	1302.602676	0.005712	HPKWGSICATST
9.0	1302.610550	-0.002162	HPTPHQAAGQPF

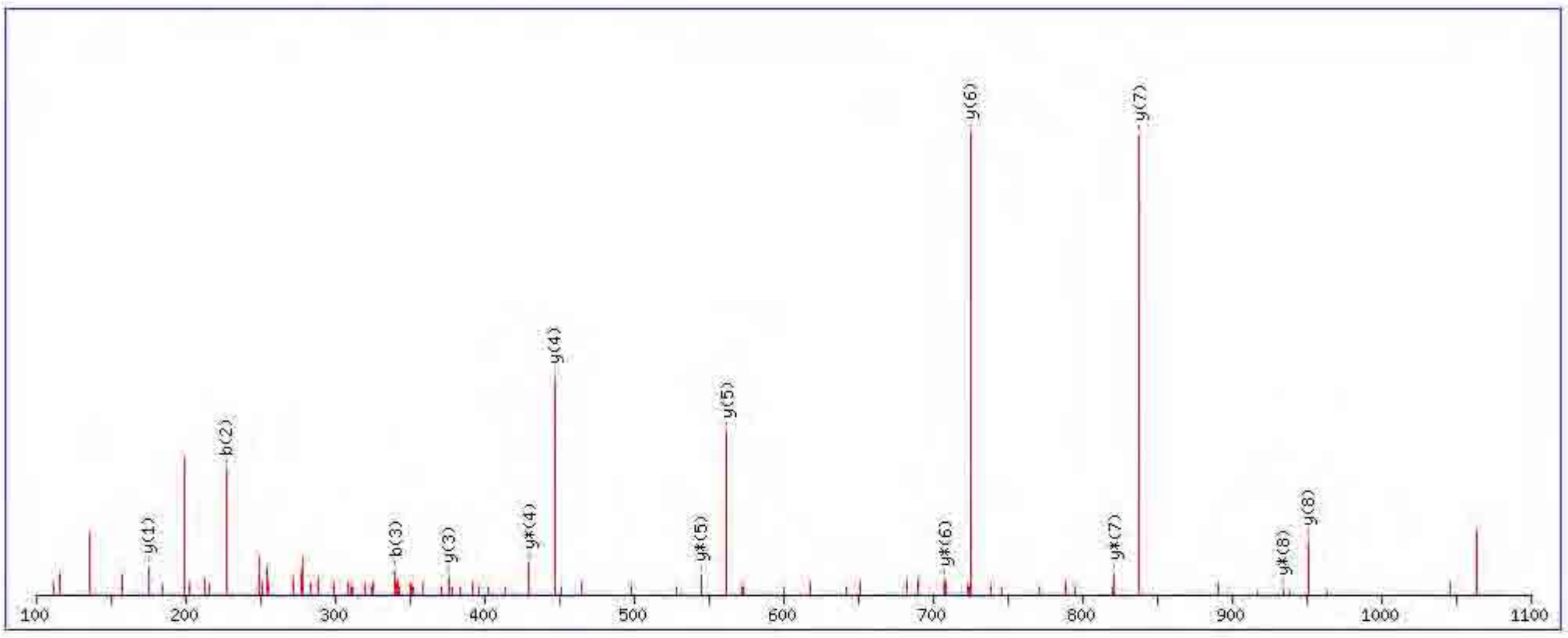
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

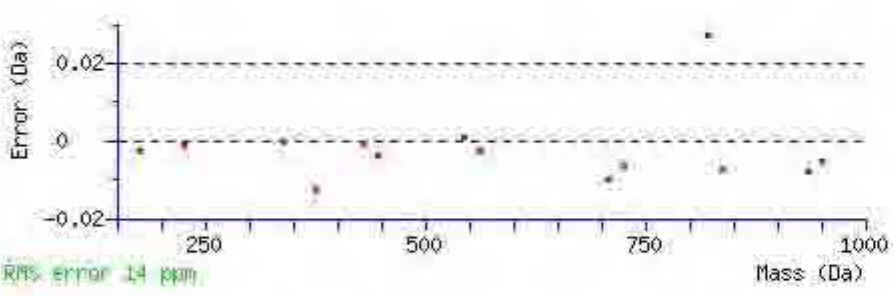
Match to Query 5140: 1063.558268 from(532.786410,2+) rtinseconds(1649) index(11113)
Title: Locus:1.1.1.2005.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

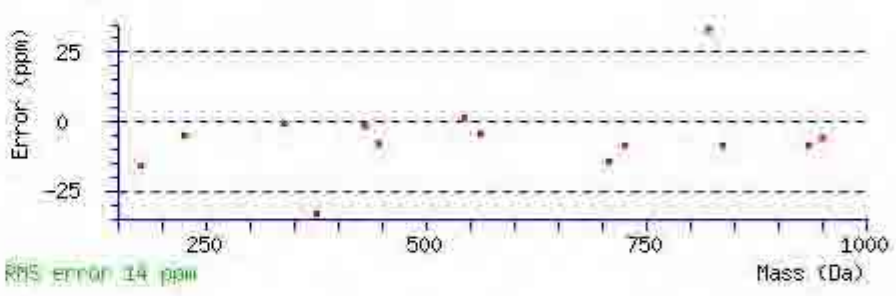
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 47 **Expect:** 0.0039
Matches : 14/70 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	951.489421	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	838.405357	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	725.321293	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	562.257964	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	447.231021	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1063.566177	-0.007909	LLIYDASNR
28.0	1063.548431	0.009837	LLPYCRGNI
24.9	1063.566208	-0.007940	LPLAQVSAHP
19.0	1063.559677	-0.001409	PLRHPGMPK
18.3	1063.566208	-0.007940	LLLQHGADPT
16.8	1063.554947	0.003321	IIIADYDNK
15.9	1063.558334	-0.000066	ILLTAGSDMK
15.9	1063.566208	-0.007940	ILPPDQRPP
15.9	1063.566208	-0.007940	ILPPDQRPP
15.9	1063.566208	-0.007940	ILPPDQRPP

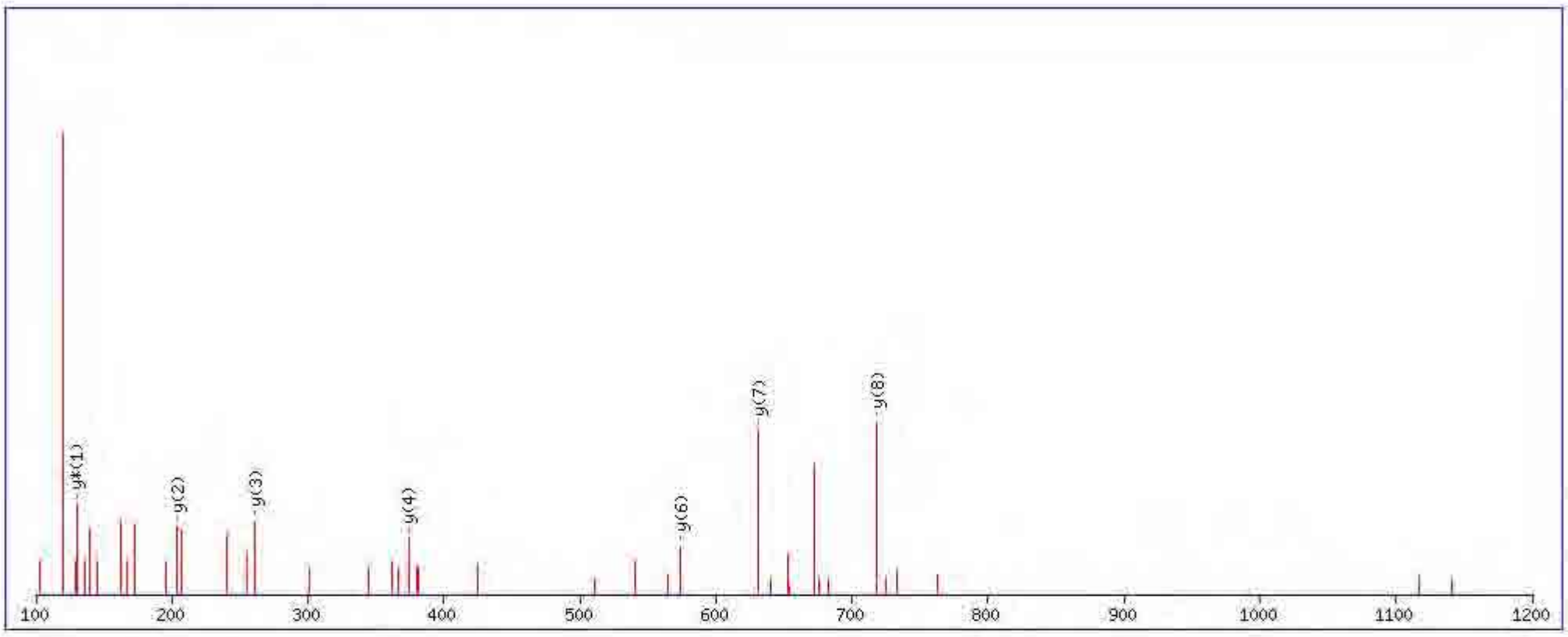
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSLLGGK**
Found in **LV001_HUMAN**, Ig lambda chain V region 4A OS=Homo sapiens PE=4 SV=1

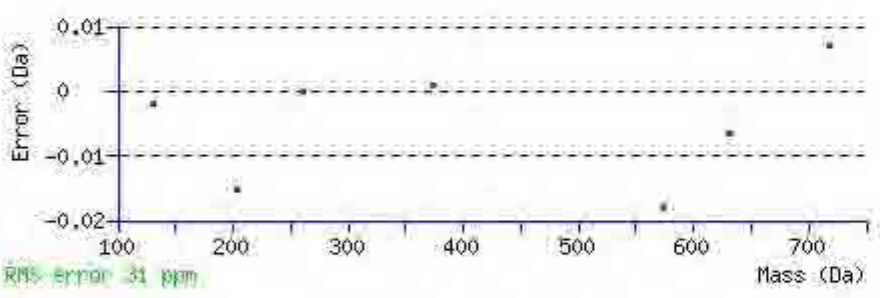
Match to Query 1332: 864.478848 from(433.246700,2+) rtinseconds(1575) index(10235)
Title: Locus:1.1.1.1963.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

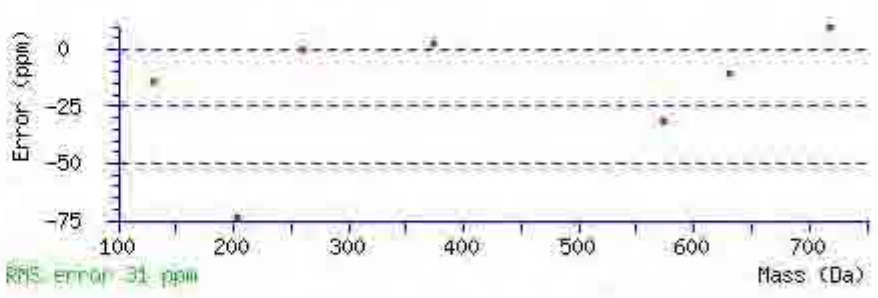
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 864.470520
Ions Score: 45 **Expect:** 0.0034
Matches : 7/68 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							9
2	235.107718	118.057497	217.097153	109.052214	S	*718.409380*	359.708328	701.382831	351.195054	700.398815	350.703046	8
3	292.129182	146.568229	274.118617	137.562946	G	*631.377352*	316.192314	614.350803	307.679040	613.366787	307.187032	7
4	379.161210	190.084243	361.150645	181.078960	S	*574.355888*	287.681582	557.329339	279.168308	556.345323	278.676300	6
5	492.245274	246.626275	474.234709	237.620992	L	487.323860	244.165568	470.297311	235.652294			5
6	605.329338	303.168307	587.318773	294.163025	L	*374.239796*	187.623536	357.213247	179.110262			4
7	662.350802	331.679039	644.340237	322.673757	G	*261.155732*	131.081504	244.129183	122.568230			3
8	719.372266	360.189771	701.361701	351.184489	G	*204.134268*	102.570772	187.107719	94.057498			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSGSLLGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	864.470520	0.008328	FSGSLLGGK
17.2	864.481766	-0.002918	PHVVATGGK
14.9	864.477921	0.000927	FLLCLVGT
14.1	864.470490	0.008358	FSEKNLK
13.0	864.470474	0.008374	AYEKINK
12.8	864.481735	-0.002887	FGSISRAK
11.2	864.470505	0.008343	IIFRTSE
11.1	864.470474	0.008374	KYAELNK
9.6	864.477905	0.000943	LIFLSGLC
8.7	864.481735	-0.002887	FSIRNTK

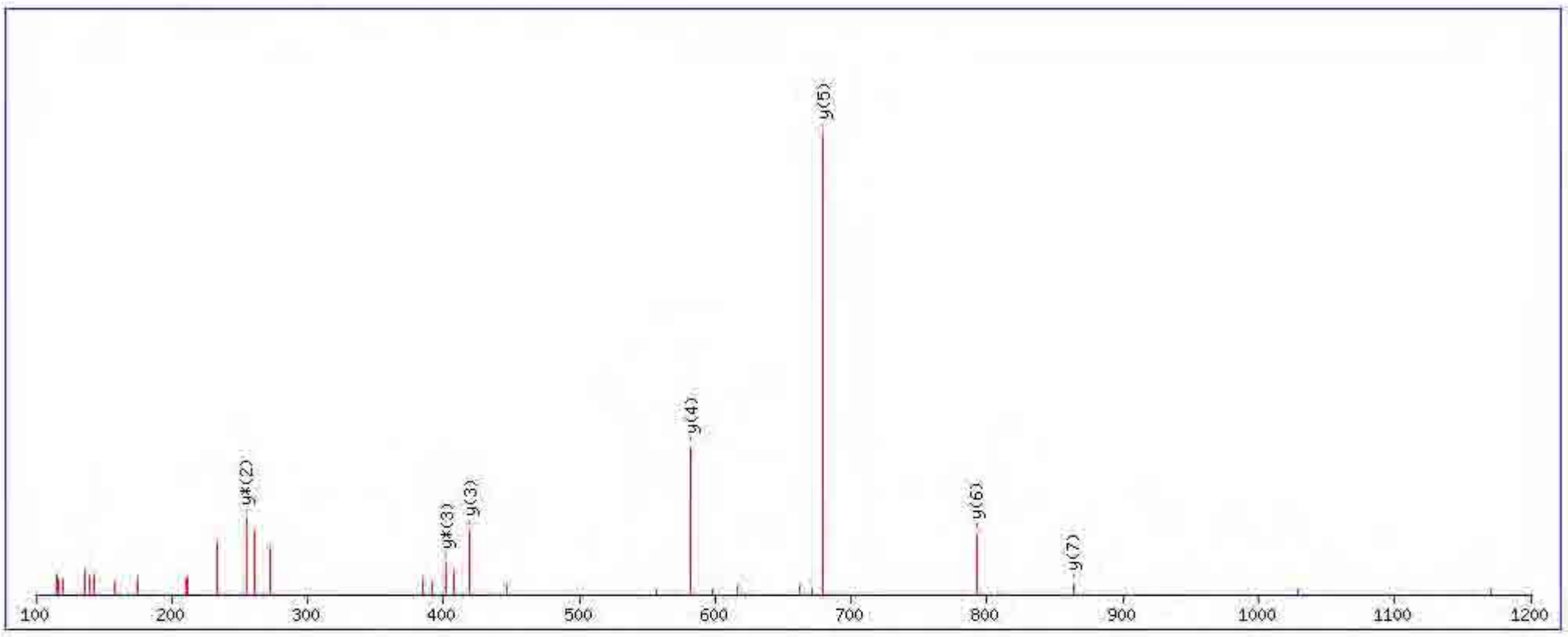
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALPYFPR**
Found in **OLFL3_HUMAN**, Olfactomedin-like protein 3 OS=Homo sapiens GN=OLFML3 PE=2 SV=1

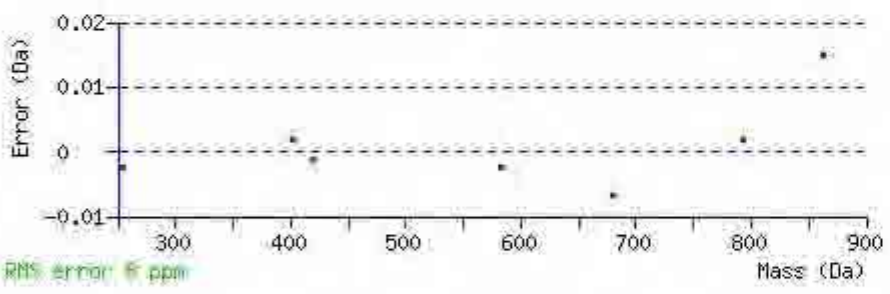
Match to Query 2474: 933.499868 from(467.757210,2+) rtinseconds(1981) index(15497)
Title: Locus:1.1.1.2185.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

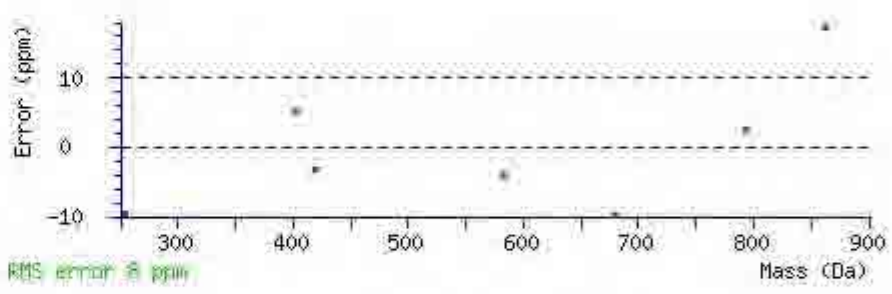
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 933.507217
Ions Score: 48 **Expect:** 0.0031
Matches : 7/42 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833	A					8
2	143.081504	72.044390	A	*863.477401*	432.242339	846.450852	423.729064	7
3	256.165568	128.586422	L	*792.440287*	396.723782	775.413738	388.210507	6
4	353.218332	177.112804	P	*679.356223*	340.181750	662.329674	331.668475	5
5	516.281661	258.644469	Y	*582.303459*	291.655368	565.276910	283.142093	4
6	663.350075	332.178676	F	*419.240130*	210.123703	402.213581	201.610429	3
7	760.402839	380.705058	P	272.171716	136.589496	255.145167	128.076222	2
8			R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of AALPYFPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	933.507217	-0.007349	AALPYFPR
20.0	933.503189	-0.003321	APAPAAPAPR
15.7	933.507233	-0.007365	AAFPLFPR
13.0	933.491959	0.007909	AALERYVP
13.0	933.495316	0.004552	AALMSKNSL
12.3	933.503189	-0.003321	AAPAAPPPAR
10.1	933.503189	-0.003321	AARDIFNK
7.2	933.503189	-0.003321	APAPAAPAPR
6.7	933.493317	0.006551	LAHGHFPR
5.1	933.491959	0.007909	VRPAYSLE

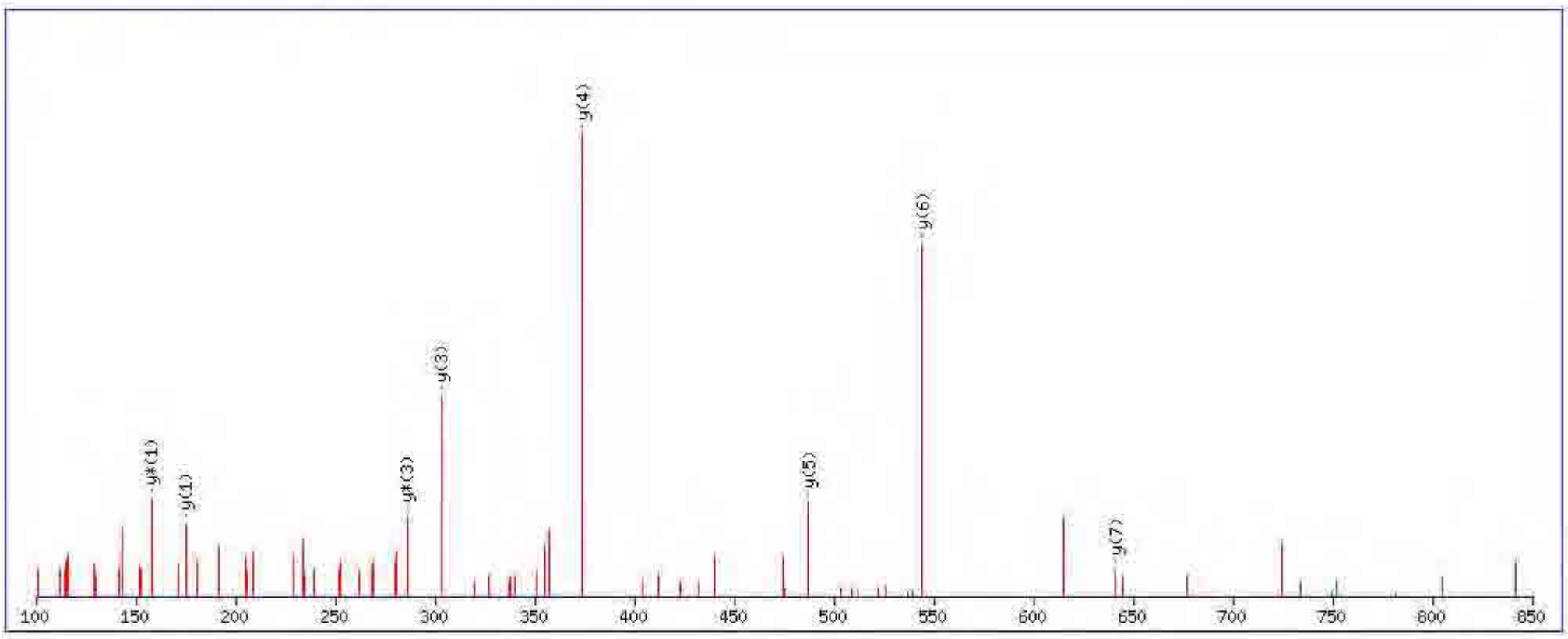
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PSPGPAAGR**
Found in **OTU7A_HUMAN**, OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=1 SV=1

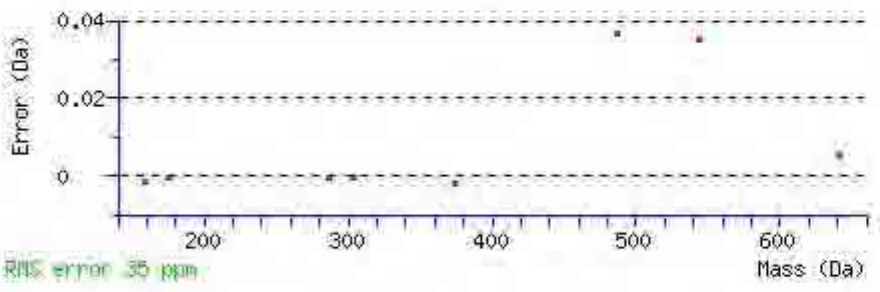
Match to Query 1015: 840.409848 from(421.212200,2+) rtinseconds(580) index(470)
Title: Locus:1.1.1.1419.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

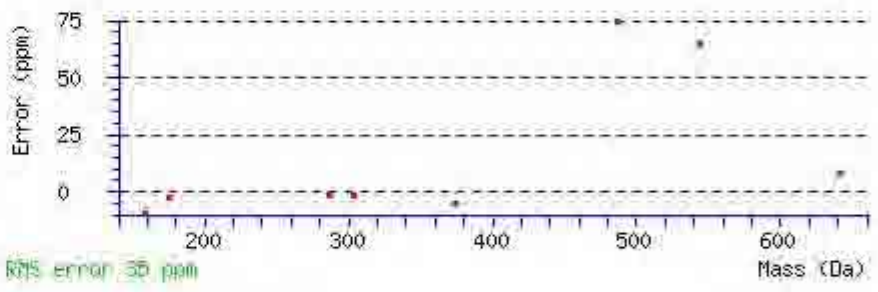
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 840.408981
Variable modifications:
P1 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 42 Expect: 0.0086
Matches : 8/64 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116			P							9
2	201.086983	101.047129	183.076418	92.041847	S	728.368579	364.687928	711.342030	356.174653	710.358014	355.682645	8
3	298.139747	149.573512	280.129182	140.568229	P	*641.336551*	321.171914	624.310002	312.658639			7
4	355.161211	178.084243	337.150646	169.078961	G	*544.283787*	272.645532	527.257238	264.132257			6
5	468.208890	234.608083	450.198325	225.602800	P	*487.262323*	244.134799	470.235774	235.621525			5
6	539.246004	270.126640	521.235439	261.121357	A	*374.214644*	187.610960	357.188095	179.097685			4
7	610.283118	305.645197	592.272553	296.639914	A	*303.177530*	152.092403	286.150981	143.579128			3
8	667.304582	334.155929	649.294017	325.150646	G	232.140416	116.573846	215.113867	108.060571			2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PSPGPAAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	840.408981	0.000867	PSPGPAAGR
30.8	840.408981	0.000867	PPAPGAQR
30.3	840.408981	0.000867	PPAGSPAGR
29.5	840.408966	0.000882	EPAGAPQR
29.4	840.408981	0.000867	PSPGPAAGR
28.2	840.408981	0.000867	PSGPPAGAR
21.5	840.408966	0.000882	PEASPGQR
18.2	840.408981	0.000867	PGAPPAQR
17.4	840.408966	0.000882	EAPQPQR
17.4	840.408981	0.000867	SPPPQQR

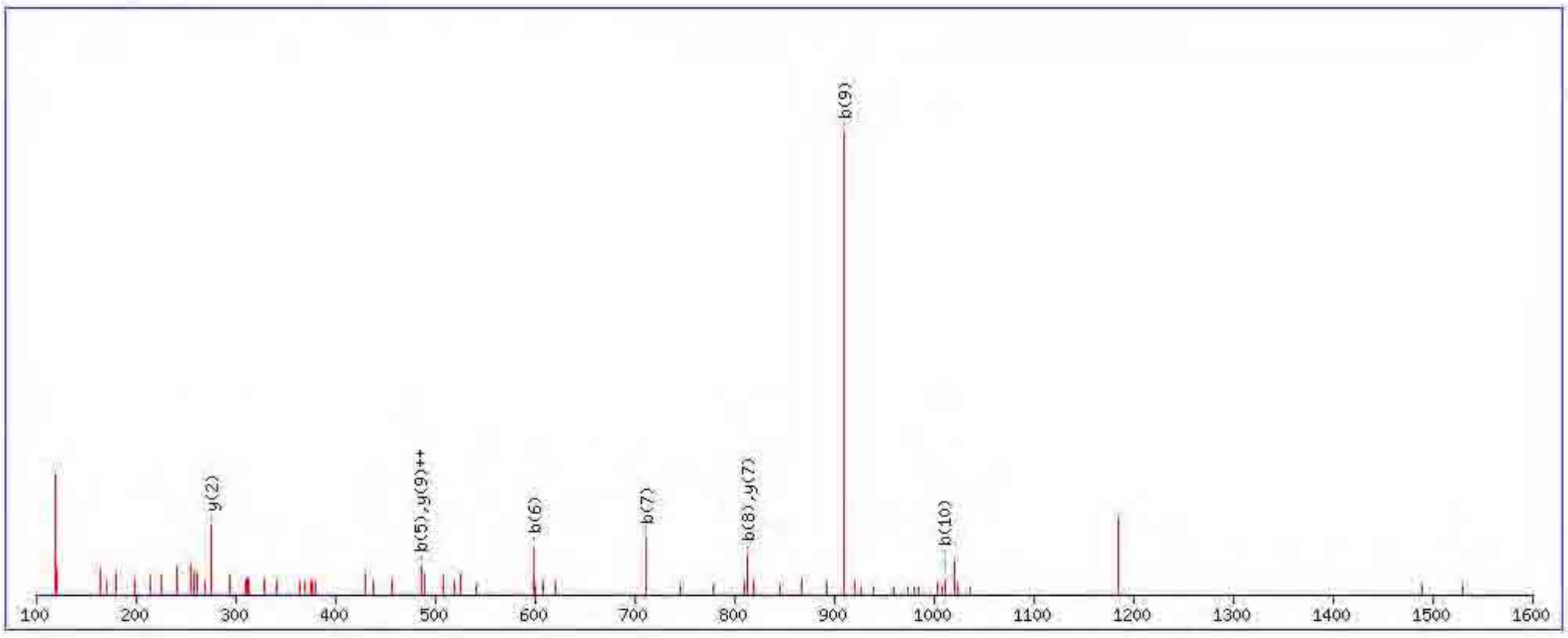
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPSALILTPTR**
Found in **DDX59_HUMAN**, Probable ATP-dependent RNA helicase DDX59 OS=Homo sapiens GN=DDX59 PE=1 SV=1

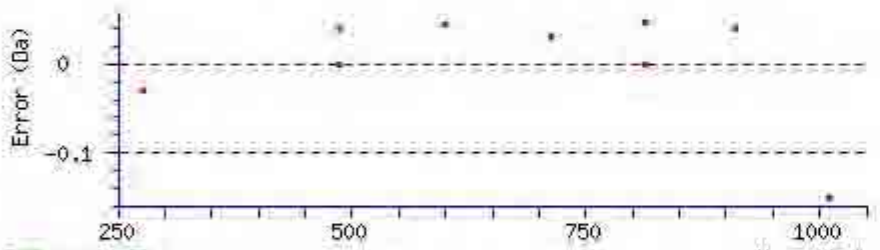
Match to Query 8456: 1184.685028 from(593.349790,2+) rtinseconds(2316) index(19809)
Title: Locus:1.1.1.2363.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

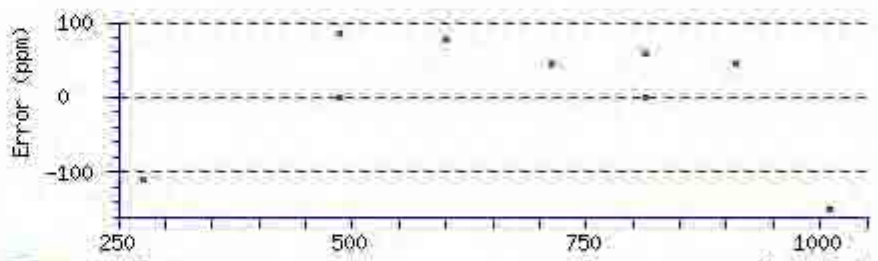
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676483
Variable modifications:
P2 : Oxidation (P)
Ions Score: 48 Expect: 0.0015
Matches : 9/98 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							11
2	215.102634	108.054955	197.092069	99.049672	P	1084.636087	542.821682	1067.609538	534.308407	1066.625522	533.816399	10
3	302.134662	151.570969	284.124097	142.565687	S	971.588408	486.297842	954.561859	477.784568	953.577843	477.292560	9
4	373.171776	187.089526	355.161211	178.084243	A	884.556380	442.781828	867.529831	434.268554	866.545815	433.776546	8
5	*486.255840*	243.631558	468.245275	234.626275	L	813.519266	407.263271	796.492717	398.749997	795.508701	398.257989	7
6	*599.339904*	300.173590	581.329339	291.168308	I	700.435202	350.721239	683.408653	342.207965	682.424637	341.715957	6
7	*712.423968*	356.715622	694.413403	347.710340	L	587.351138	294.179207	570.324589	285.665933	569.340573	285.173925	5
8	*813.471647*	407.239462	795.461082	398.234179	T	474.267074	237.637175	457.240525	229.123900	456.256509	228.631892	4
9	*910.524411*	455.765844	892.513846	446.760561	P	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
10	*1011.572090*	506.289683	993.561525	497.284401	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TPSALILTPTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	1184.676483	0.008545	TPSALILTPTR
40.2	1184.691742	-0.006714	FQPTLLTLPR
15.9	1184.677811	0.007217	FKPPRQLGAR
14.1	1184.695099	-0.010071	ICSAVLPLLTR
13.0	1184.676483	0.008545	DPSGLLISVIR
12.0	1184.676468	0.008560	LDLGSIIAEVR
12.0	1184.676453	0.008575	VKEEIIDAIR
11.6	1184.676498	0.008530	LPTTLGPVSLR
10.8	1184.676468	0.008560	KEDLTTLLPR
9.3	1184.676483	0.008545	LTLTRLDPGSL

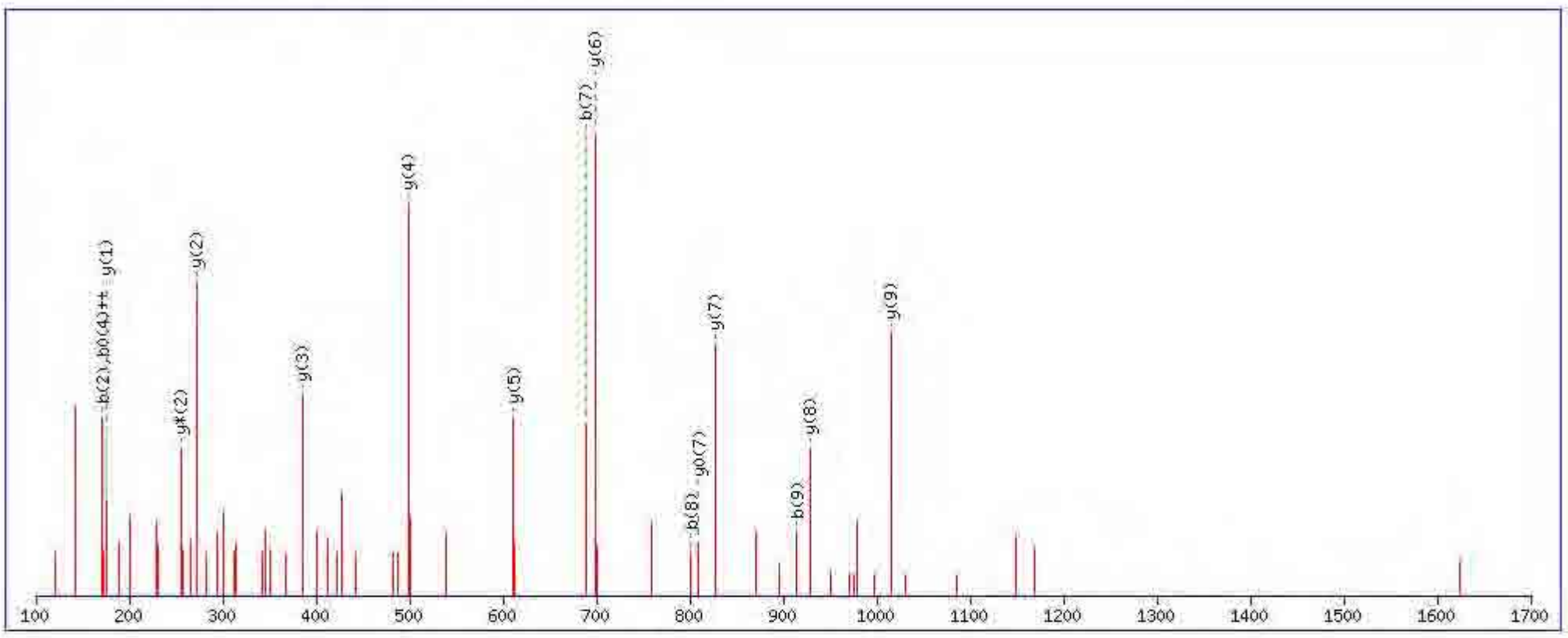
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

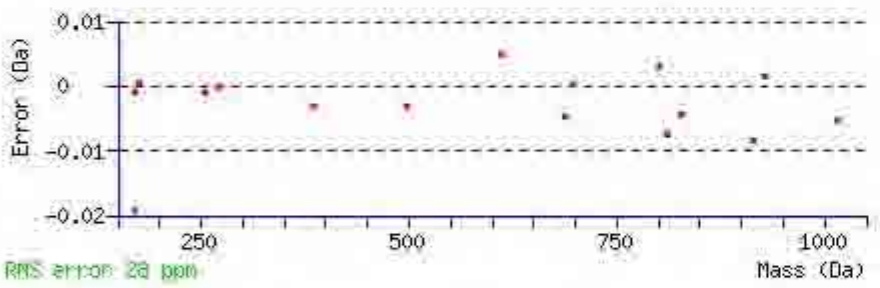
Match to Query 8452: 1184.673028 from(593.343790,2+) rtinseconds(2078) index(16765)
Title: Locus:1.1.1.2236.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

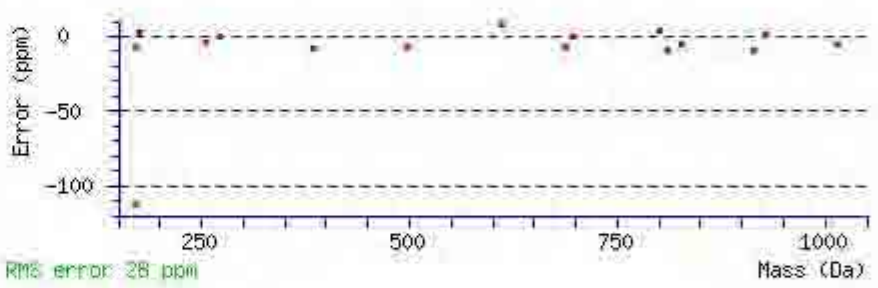
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 66 Expect: 2.4e-005
Matches : 16/86 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	**171.112804**	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	***1015.578236***	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	***928.546208***	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	***827.498529***	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	***698.455936***	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	**688.351196**	344.679236	670.340631	335.673954	I	***611.423908***	306.215592	594.397359	297.702318			5
8	**801.435260**	401.221268	783.424695	392.215986	L	***498.339844***	249.673560	481.313295	241.160285			4
9	**914.519324**	457.763300	896.508759	448.758018	I	***385.255780***	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	***272.171716***	136.589496	255.145167	128.076221			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.4	1184.676468	-0.003440	GLSTESILIPR
25.0	1184.676468	-0.003440	KEDLTTLLPR
18.1	1184.677795	-0.004767	PRHPEALLPR
16.7	1184.665237	0.007791	SSPIIIQLLSD
12.2	1184.676483	-0.003455	GPVVEISLISR
12.1	1184.662552	0.010476	RGQTSASILPR
11.9	1184.680527	-0.007499	GLTLPPVPFTK
11.4	1184.670609	0.002419	WPAGLFLLPR
10.4	1184.676498	-0.003470	TITVTDLGIPR
10.1	1184.665222	0.007806	LLEAAITPETK

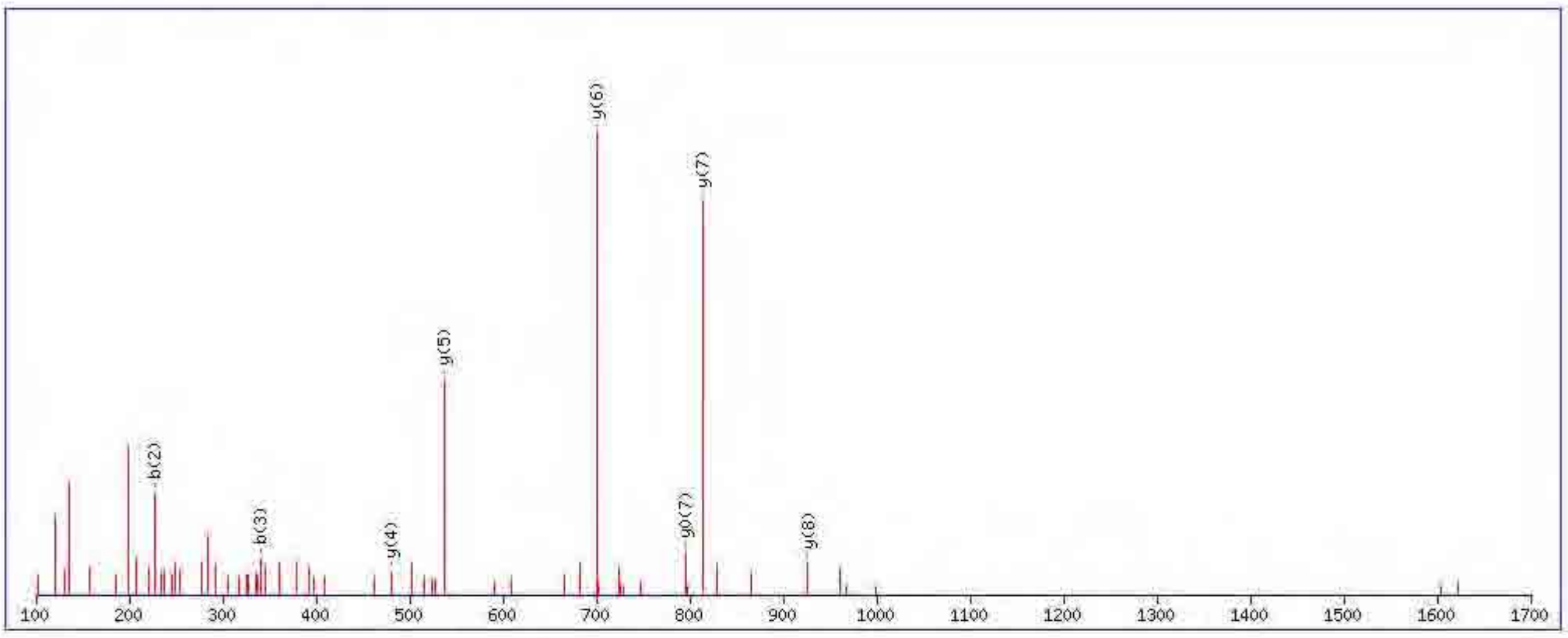
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIYGNISF**
Found in **RMI1_HUMAN**, RecQ-mediated genome instability protein 1 OS=Homo sapiens GN=RMI1 PE=1 SV=3

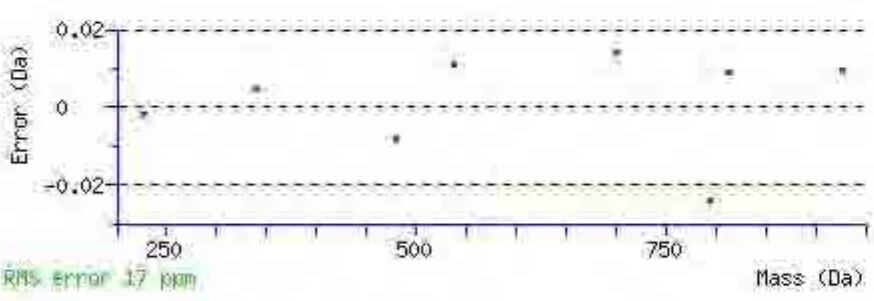
Match to Query 4558: 1038.578088 from(520.296320,2+) rtinseconds(2603) index(22004)
Title: Locus:1.1.1.2514.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

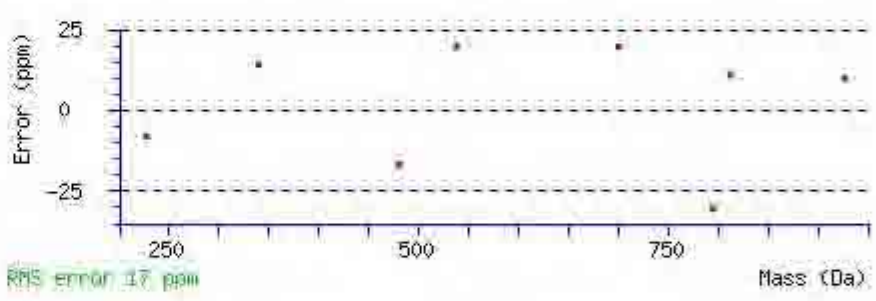
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1038.574966
Ions Score: 45 **Expect:** 0.0032
Matches : 8/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							9
2	227.175404	114.091340					L	*926.498195*	463.752736	909.471646	455.239461	908.487630	454.747453	8
3	340.259468	170.633372					I	*813.414131*	407.210704	796.387582	398.697429	795.403566	398.205421	7
4	503.322797	252.165036					Y	*700.330067*	350.668672	683.303518	342.155397	682.319502	341.663389	6
5	560.344261	280.675769					G	*537.266738*	269.137007	520.240189	260.623733	519.256173	260.131725	5
6	674.387188	337.697232	657.360639	329.183958			N	*480.245274*	240.626275	463.218725	232.113000	462.234709	231.620992	4
7	787.471252	394.239264	770.444703	385.725990			I	366.202347	183.604811			348.191782	174.599529	3
8	874.503280	437.755278	857.476731	429.242004	856.492715	428.749996	S	253.118283	127.062779			235.107718	118.057497	2
9							F	166.086255	83.546765					1





NCBI **BLAST** search of ILIYGNISF
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	1038.574966	0.003122	ILIYGNISF
21.7	1038.582184	-0.004096	IPLQNGRLP
20.9	1038.578339	-0.000251	LLLGTYMTK
19.8	1038.570969	0.007119	PIPGTAQPVK
19.8	1038.570938	0.007150	IPLERPLGE
17.5	1038.582184	-0.004096	PLPGATPAKR
17.2	1038.582184	-0.004096	PPLPTRQAK
17.0	1038.570953	0.007135	LIPPDAIPR
17.0	1038.570938	0.007150	LLLEPAPDR
17.0	1038.570938	0.007150	LLLEPAPDR

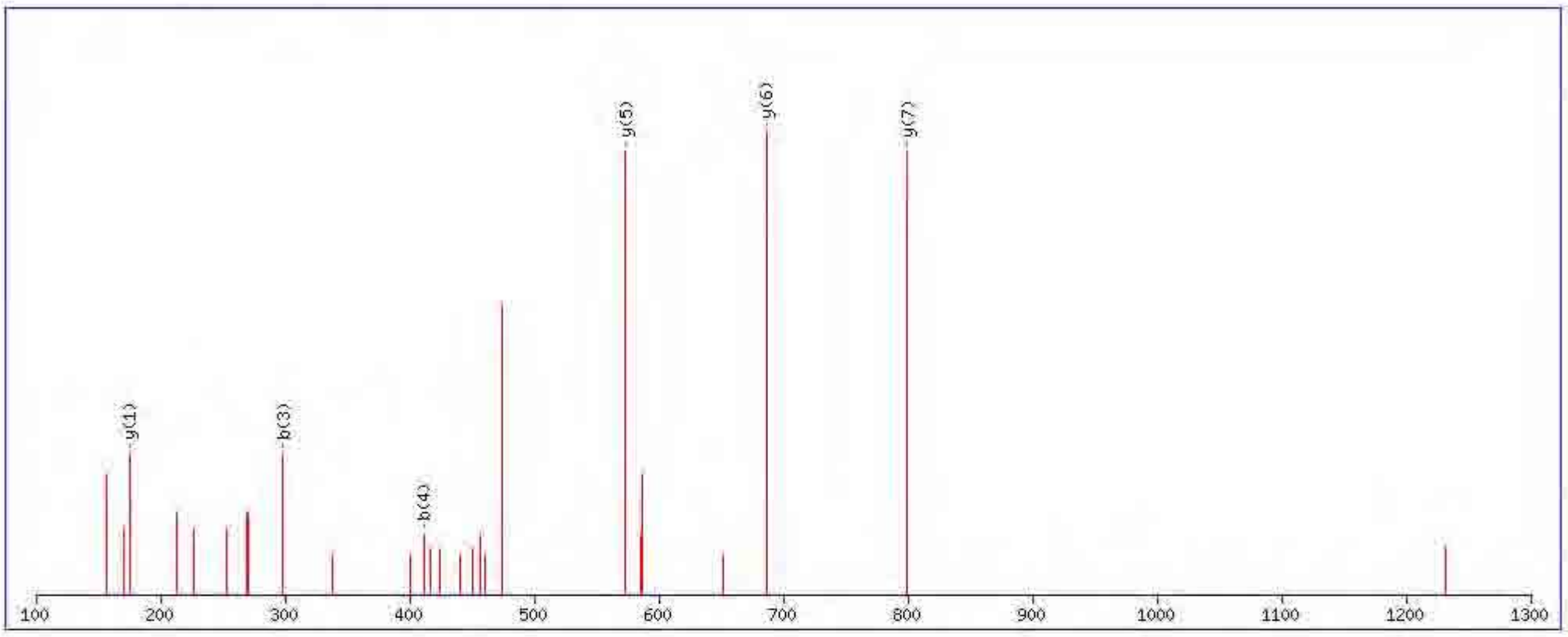
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LALIEAVVR**
Found in **RNF26_HUMAN**, RING finger protein 26 OS=Homo sapiens GN=RNF26 PE=2 SV=1

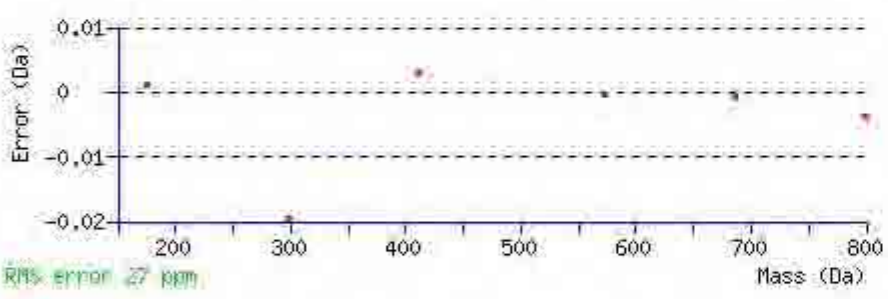
Match to Query 3419: 982.612388 from(492.313470,2+) rtinseconds(2963) index(23630)
Title: Locus:1.1.1.2701.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

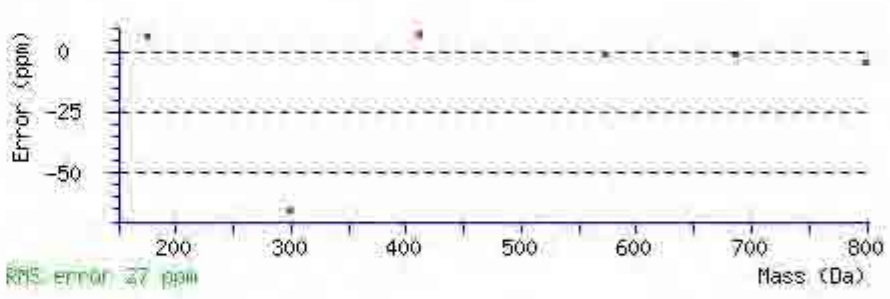
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 982.617493
Ions Score: 40 **Expect:** 0.0038
Matches : 6/64 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	185.128454	93.067865			A	870.540729	435.774002	853.514180	427.260728	852.530164	426.768720	8
3	298.212518	149.609897			L	*799.503615*	400.255446	782.477066	391.742171	781.493050	391.250163	7
4	411.296582	206.151929			I	*686.419551*	343.713414	669.393002	335.200139	668.408986	334.708131	6
5	540.339175	270.673226	522.328610	261.667943	E	*573.335487*	287.171382	556.308938	278.658107	555.324922	278.166099	5
6	611.376289	306.191783	593.365724	297.186500	A	444.292894	222.650085	427.266345	214.136810			4
7	710.444703	355.725990	692.434138	346.720707	V	373.255780	187.131528	356.229231	178.618253			3
8	809.513117	405.260197	791.502552	396.254914	V	274.187366	137.597321	257.160817	129.084046			2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LALIEAVVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	982.617493	-0.005105	ALILVGLER
39.9	982.617493	-0.005105	LALIEAVVR
23.9	982.606262	0.006126	APLLPSLLK
23.9	982.606277	0.006111	PALLTPVLK
23.9	982.606262	0.006126	PAPLSLLIK
20.2	982.617493	-0.005105	APIIQKVAK
20.2	982.617477	-0.005089	LAILQNALK
20.2	982.621506	-0.009118	LALLWALAL
20.0	982.617508	-0.005120	ALIPVTTIR
20.0	982.617493	-0.005105	IALALEVVR

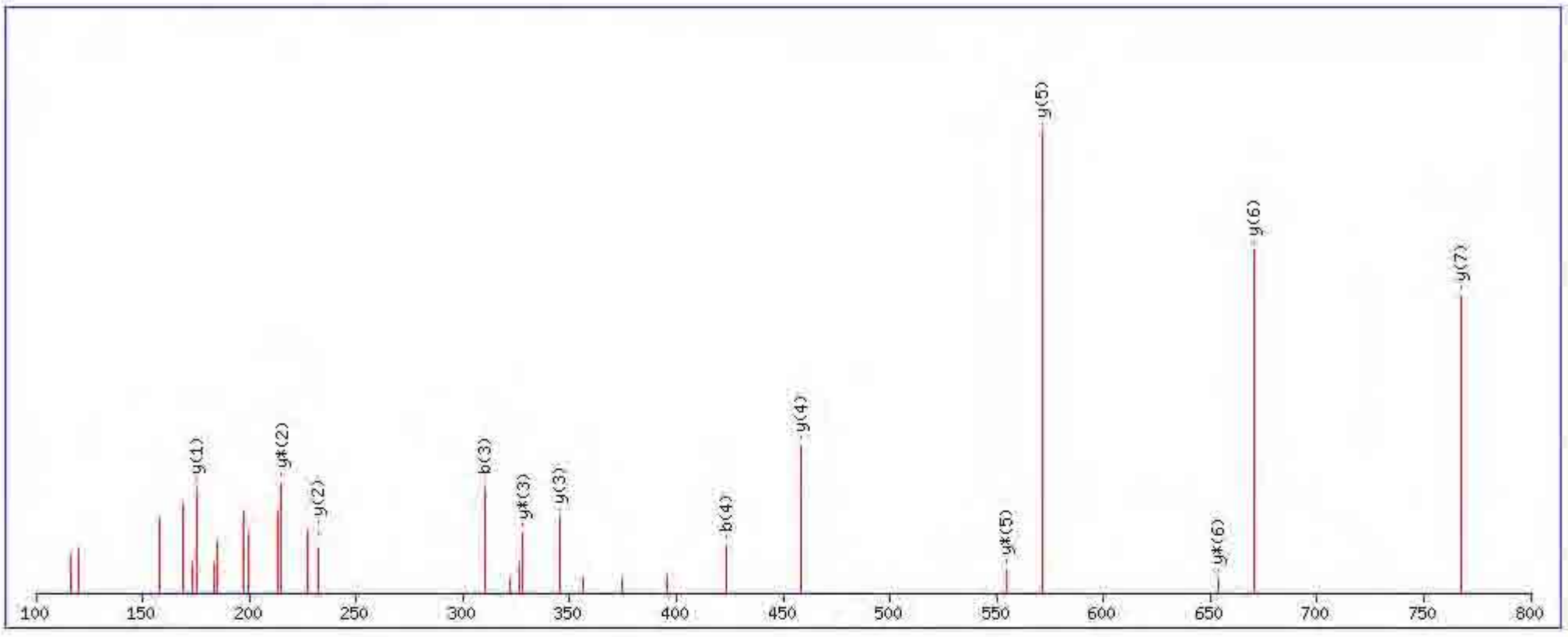
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVLLLGR**
Found in **HTRA1_HUMAN**, Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1

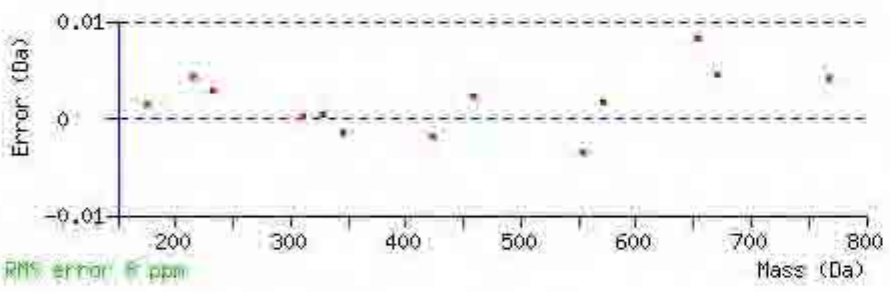
Match to Query 1532: 879.586968 from(440.800760,2+) rtinseconds(2324) index(19893)
Title: Locus:1.1.1.2367.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

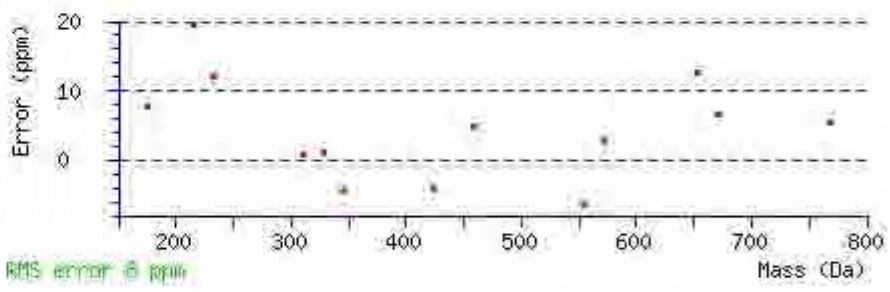
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 879.590561
Ions Score: 72 **Expect:** 3.5e-007
Matches : 13/42 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308	L					8
2	211.144104	106.075690	P	*767.513786*	384.260531	750.487237	375.747257	7
3	**310.212518**	155.609897	V	*670.461022*	335.734149	653.434473	327.220875	6
4	**423.296582**	212.151929	L	*571.392608*	286.199942	554.366059	277.686668	5
5	536.380646	268.693961	L	*458.308544*	229.657910	441.281995	221.144635	4
6	649.464710	325.235993	L	*345.224480*	173.115878	328.197931	164.602603	3
7	706.486174	353.746725	G	*232.140416*	116.573846	215.113867	108.060571	2
8			R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of LPVLLLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	879.590561	-0.003593	LPVLLLGR
39.8	879.590561	-0.003593	LVPILVAR
38.7	879.590561	-0.003593	ILVPLIGR
33.7	879.590561	-0.003593	IPLVLAVR
32.0	879.579330	0.007638	IPVIPITK
18.2	879.579346	0.007622	PPVVVILK
17.5	879.579346	0.007622	LPVVIGGLL
16.3	879.579330	0.007638	VIPLLVNI
14.7	879.590561	-0.003593	LVLPLGRL
13.4	879.590561	-0.003593	VLLPLGLR

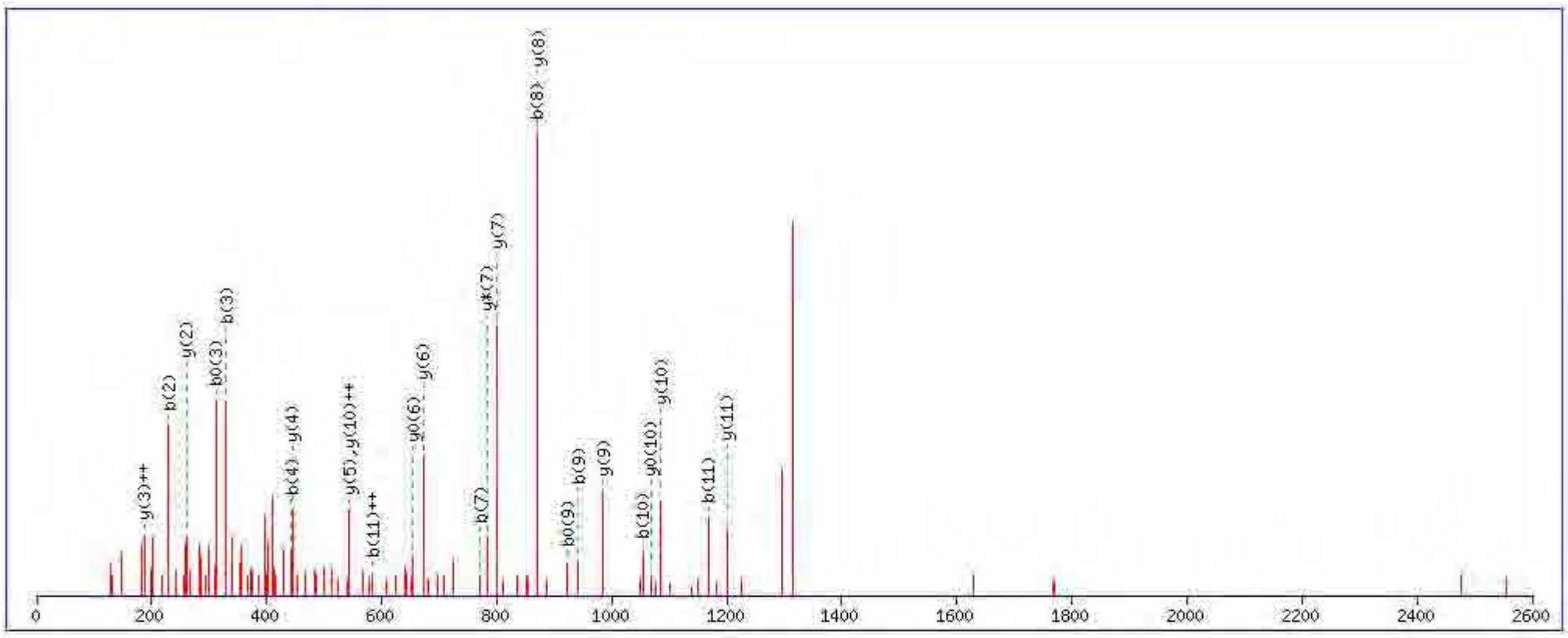
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

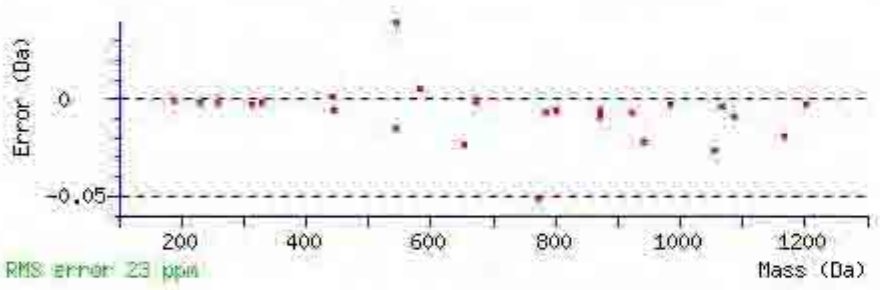
Match to Query 11990: 1312.748988 from(657.381770,2+) rtinseconds(2500) index(21373)
Title: Locus:1.1.1.2459.13
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

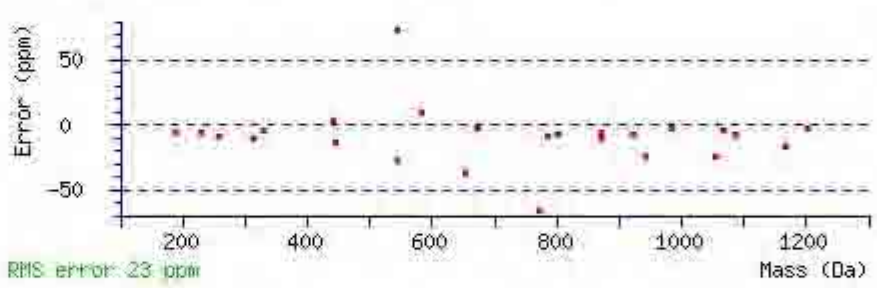
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1312.760193
Ions Score: 81 **Expect:** 5.9e-007
Matches : 25/110 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	*229.118283*	115.062779			211.107718	106.057497	D	*1200.683431*	600.845353	1183.656882	592.332079	1182.672866	591.840071	11
3	*330.165962*	165.586619			312.155397	156.581336	T	*1085.656488*	543.331882	1068.629939	534.818607	1067.645923	534.326599	10
4	*443.250026*	222.128651			425.239461	213.123369	L	*984.608809*	492.808042	967.582260	484.294768	966.598244	483.802760	9
5	514.287140	257.647208			496.276575	248.641926	A	*871.524745*	436.266010	854.498196	427.752736	853.514180	427.260728	8
6	642.345718	321.676497	625.319169	313.163223	624.335153	312.671215	Q	*800.487631*	400.747453	783.461082	392.234179	782.477066	391.742171	7
7	*771.388311*	386.197794	754.361762	377.684519	753.377746	377.192511	E	*672.429053*	336.718164	655.402504	328.204890	654.418488	327.712882	6
8	*870.456725*	435.732001	853.430176	427.218726	852.446160	426.726718	V	*543.386460*	272.196868	526.359911	263.683593			5
9	*941.493839*	471.250558	924.467290	462.737283	923.483274	462.245275	A	*444.318046*	222.662661	427.291497	214.149386			4
10	*1054.577903*	527.792589	1037.551354	519.279315	1036.567338	518.787307	L	373.280932	187.144104	356.254383	178.630829			3
11	*1167.661967*	584.334621	1150.635418	575.821347	1149.651402	575.329339	L	*260.196868*	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDTLAQEVALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.4	1312.760193	-0.011205	LDTLAQEVALLK
26.1	1312.750305	-0.001317	SVSLVWKAPQAK
24.2	1312.739075	0.009913	LDTSQWPLLLK
19.6	1312.760193	-0.011205	ITSAAPLISSPLK
19.3	1312.742462	0.006526	LKSVPMVPPGIK
17.6	1312.760193	-0.011205	ITSAAPLISSPLK
16.6	1312.761520	-0.012532	ESLRPAFPRLK
16.6	1312.760193	-0.011205	KALEVTESPLVK
16.2	1312.739090	0.009898	LPTVGFNVEPLK
15.6	1312.742447	0.006541	GSLDVPMAVAILK

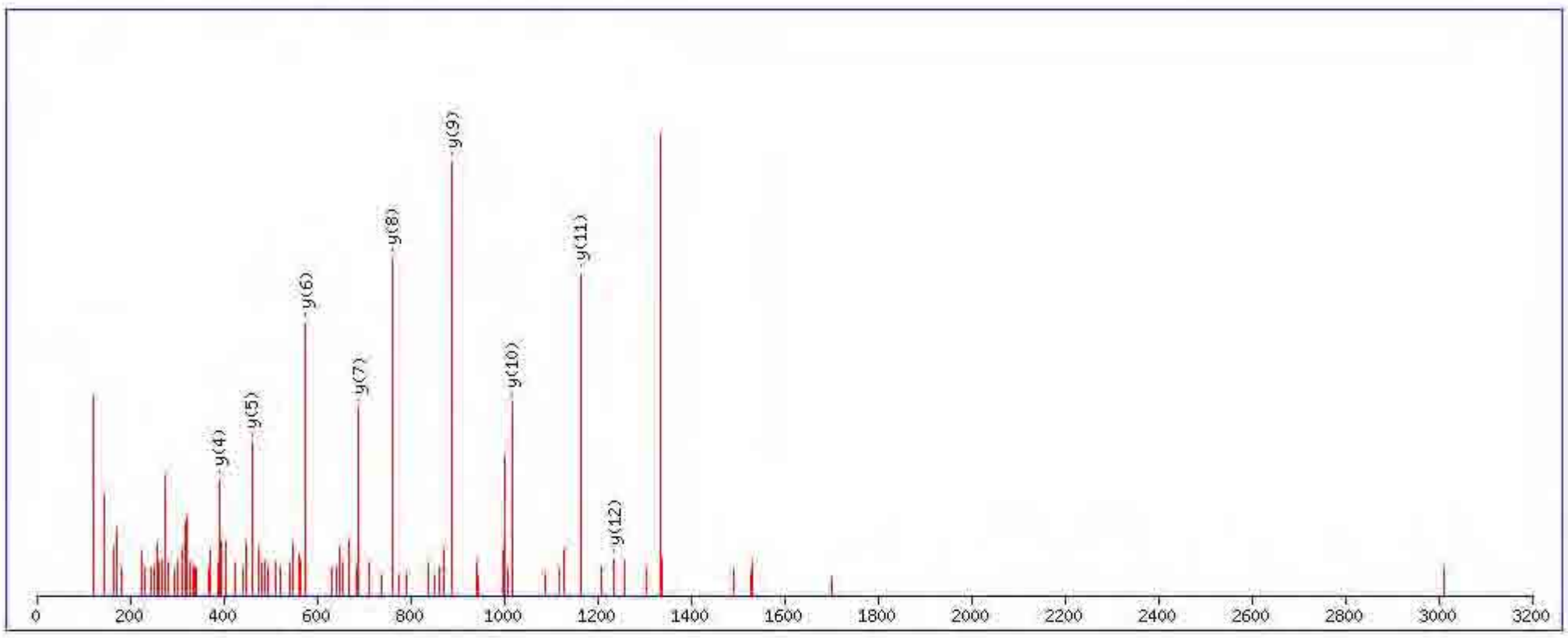
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

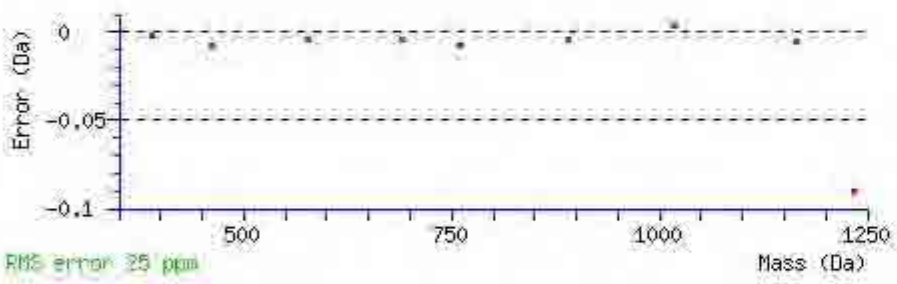
Match to Query 12681: 1335.630448 from(668.822500,2+) rtinseconds(1897) index(14367)
Title: Locus:1.1.1.2138.19
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120608_ETP_StromaControl_2.mgf

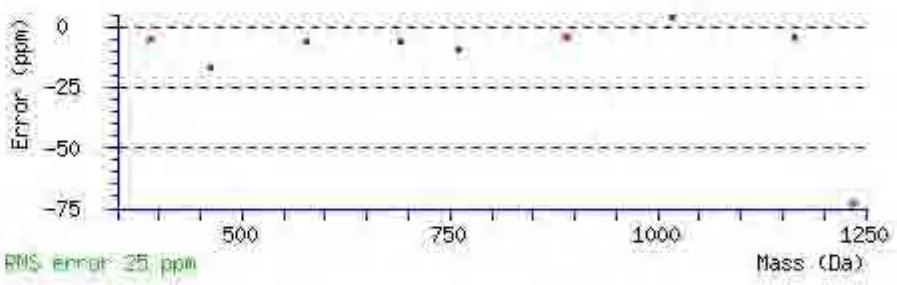
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 82 **Expect:** 3.6e-007
Matches : 9/136 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	*1235.590259*	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	319.161211	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.2	1335.630646	-0.000198	TAFQEALDAAGDK
12.7	1335.638031	-0.007583	FIDISPAEMANL
10.5	1335.626633	0.003815	TASSSTEPSVSRQ
8.6	1335.630661	-0.000213	TVTAWDSQTAEK
3.6	1335.640564	-0.010116	TSIDSIDSGVELT
2.9	1335.634033	-0.003585	TQTANMLSGPIST
2.8	1335.634689	-0.004241	KFASVPEPEFPG
2.2	1335.620773	0.009675	GDFNPSAGWLTR
1.3	1335.634003	-0.003555	QMIADGKEAETK
1.1	1335.635376	-0.004928	MGDKPPGFRGSR

Control – technical replicate # 3

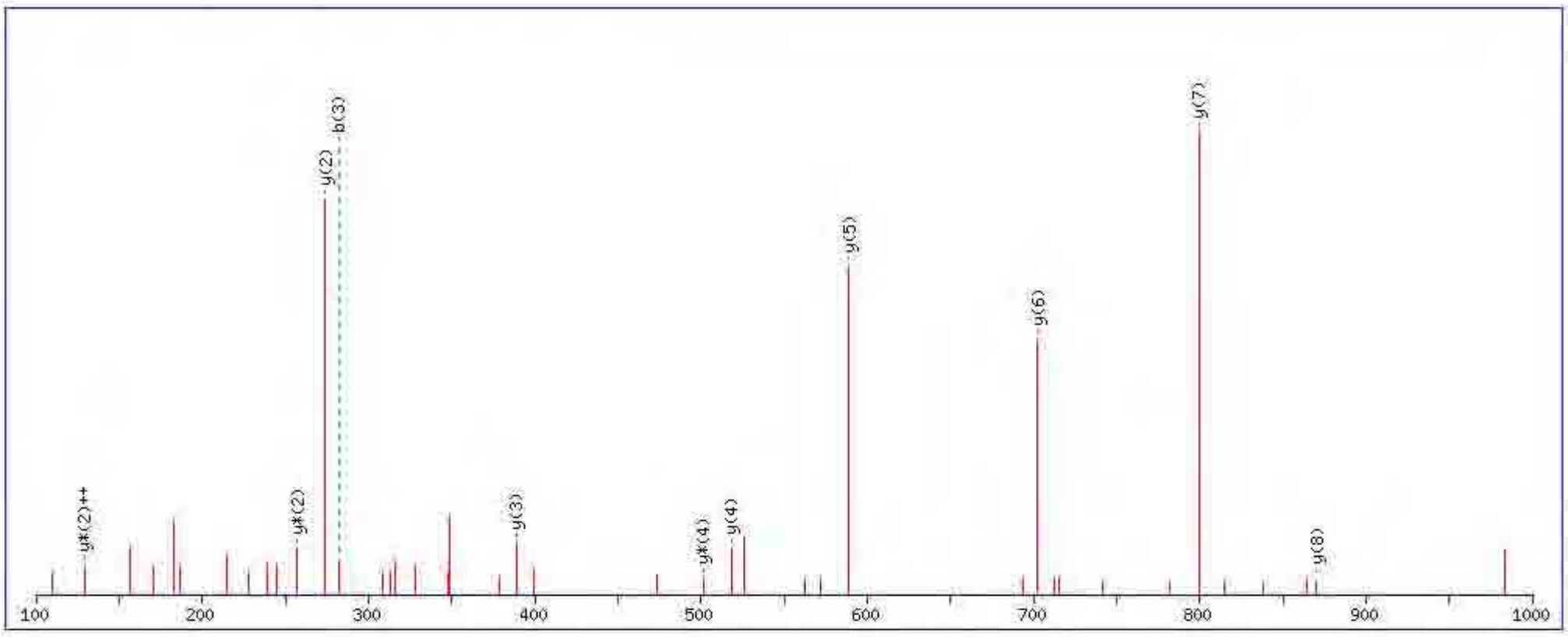
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAPLAEDVR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

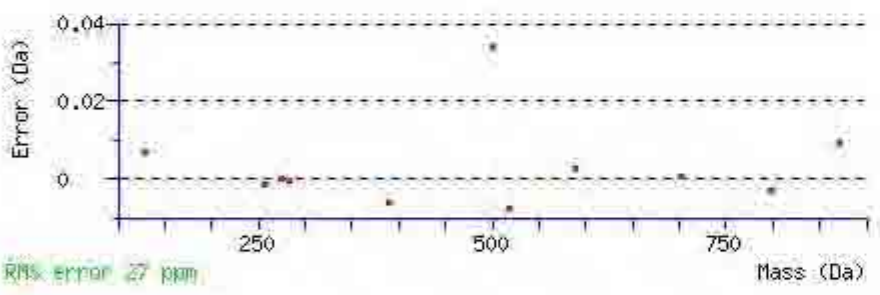
Match to Query 2818: 982.546888 from(492.280720,2+) rtinseconds(1142) index(9468)
Title: Locus:1.1.1.691.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

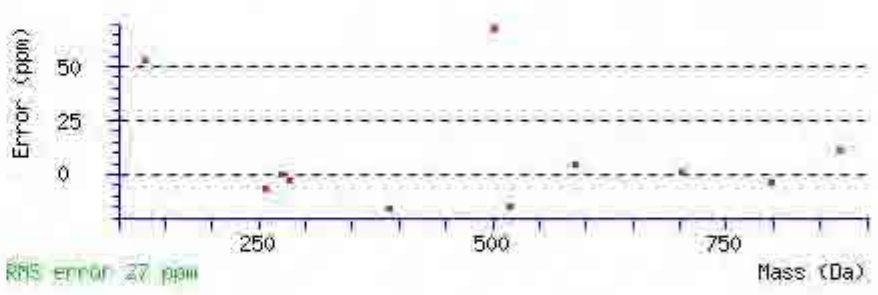
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 982.544724
Ions Score: 40 **Expect:** 0.0035
Matches : 11/66 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	185.128454	93.067865			A	*870.467958*	435.737617	853.441409	427.224343	852.457393	426.732335	8
3	282.181218	141.594247			P	*799.430844*	400.219060	782.404295	391.705786	781.420279	391.213778	7
4	395.265282	198.136279			L	*702.378080*	351.692678	685.351531	343.179404	684.367515	342.687396	6
5	466.302396	233.654836			A	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	595.344989	298.176133	577.334424	289.170850	E	*518.256902*	259.632089	501.230353	251.118815	500.246337	250.626807	4
7	710.371932	355.689604	692.361367	346.684322	D	*389.214309*	195.110792	372.187760	186.597518	371.203744	186.105510	3
8	809.440346	405.223811	791.429781	396.218528	V	*274.187366*	137.597321	257.160817	129.084047			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LAPLAEDVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	982.544724	0.002164	LAPLAEDVR
12.8	982.544724	0.002164	ALPIIQSNQ
8.4	982.555984	-0.009096	PAGQPVKVR
8.4	982.544754	0.002134	PASPLVPVR
7.6	982.544739	0.002149	AISVSHSGLL
5.6	982.552109	-0.005221	LPALAASPML
3.9	982.555954	-0.009066	ALSPPASRGK
2.5	982.544739	0.002149	SPLPLSPTR
2.1	982.544724	0.002164	AIPPESLTR
2.1	982.544739	0.002149	APPSPLLTR

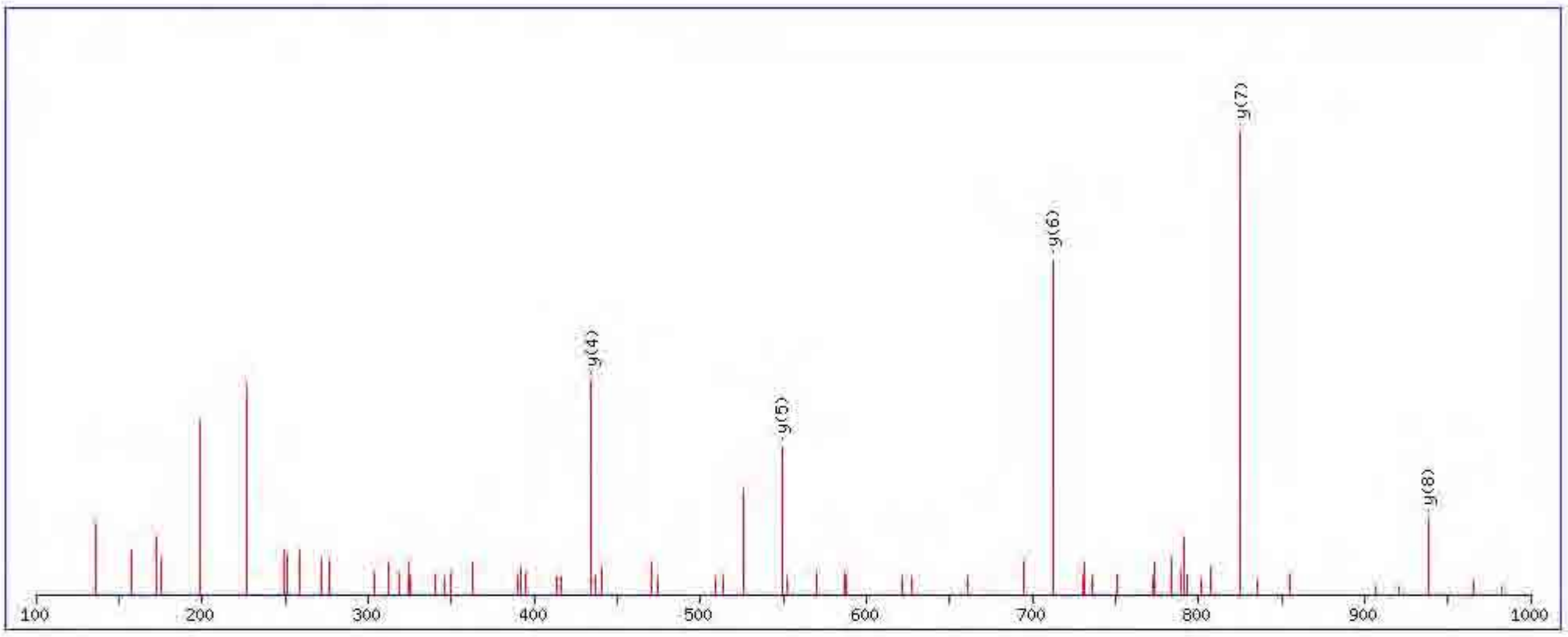
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIIYDSTAR**
Found in **BMP10_HUMAN**, Bone morphogenetic protein 10 OS=Homo sapiens GN=BMP10 PE=2 SV=1

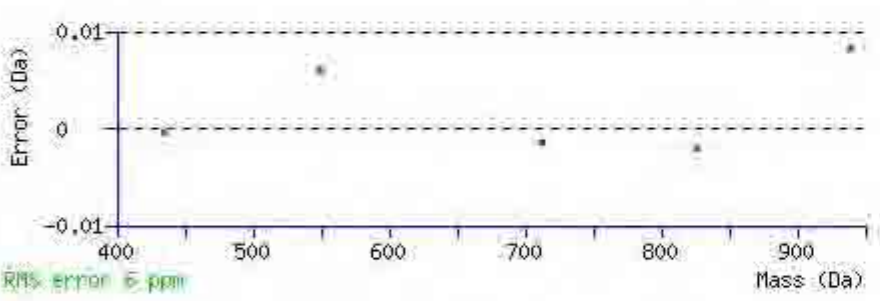
Match to Query 3949: 1051.527548 from(526.771050,2+) rtinseconds(1344) index(12080)
Title: Locus:1.1.1.804.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

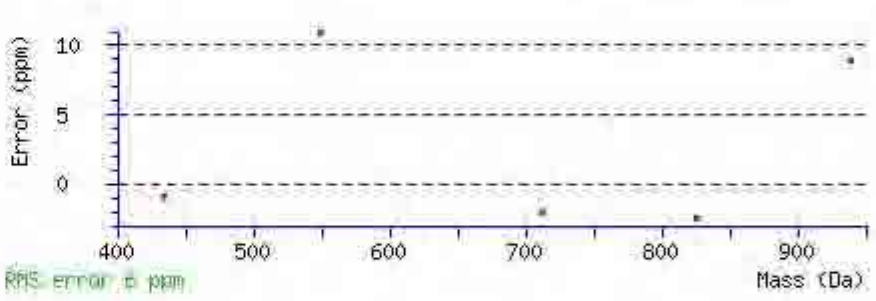
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1051.529800
Ions Score: 33 **Expect:** 0.011
Matches : 5/84 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							9
2	228.134267	114.570771	211.107718	106.057497			I	*938.494173*	469.750725	921.467624	461.237450	920.483608	460.745442	8
3	341.218331	171.112803	324.191782	162.599529			I	*825.410109*	413.208693	808.383560	404.695418	807.399544	404.203410	7
4	504.281660	252.644468	487.255111	244.131193			Y	*712.326045*	356.666661	695.299496	348.153386	694.315480	347.661378	6
5	619.308603	310.157940	602.282054	301.644665	601.298038	301.152657	D	*549.262716*	275.134996	532.236167	266.621721	531.252151	266.129713	5
6	706.340631	353.673954	689.314082	345.160679	688.330066	344.668671	S	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	807.388310	404.197793	790.361761	395.684519	789.377745	395.192511	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
8	878.425424	439.716350	861.398875	431.203076	860.414859	430.711068	A	246.156066	123.581671	229.129517	115.068396			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NIIYDSTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.4	1051.529800	-0.002252	NIIYDSTAR
11.8	1051.529800	-0.002252	NPLAPNPADK
9.8	1051.529831	-0.002283	NPPTIVHDK
9.7	1051.529800	-0.002252	ARLYSLQSD
9.7	1051.518555	0.008993	INIYSNSLE
9.5	1051.518585	0.008963	VKLDAFSSAD
9.5	1051.537231	-0.009683	VQLSVSGFLC
9.4	1051.518570	0.008978	PEAPGPLEDK
9.4	1051.529800	-0.002252	NIIDTYSAR
9.4	1051.537201	-0.009653	NIIFCDLKS

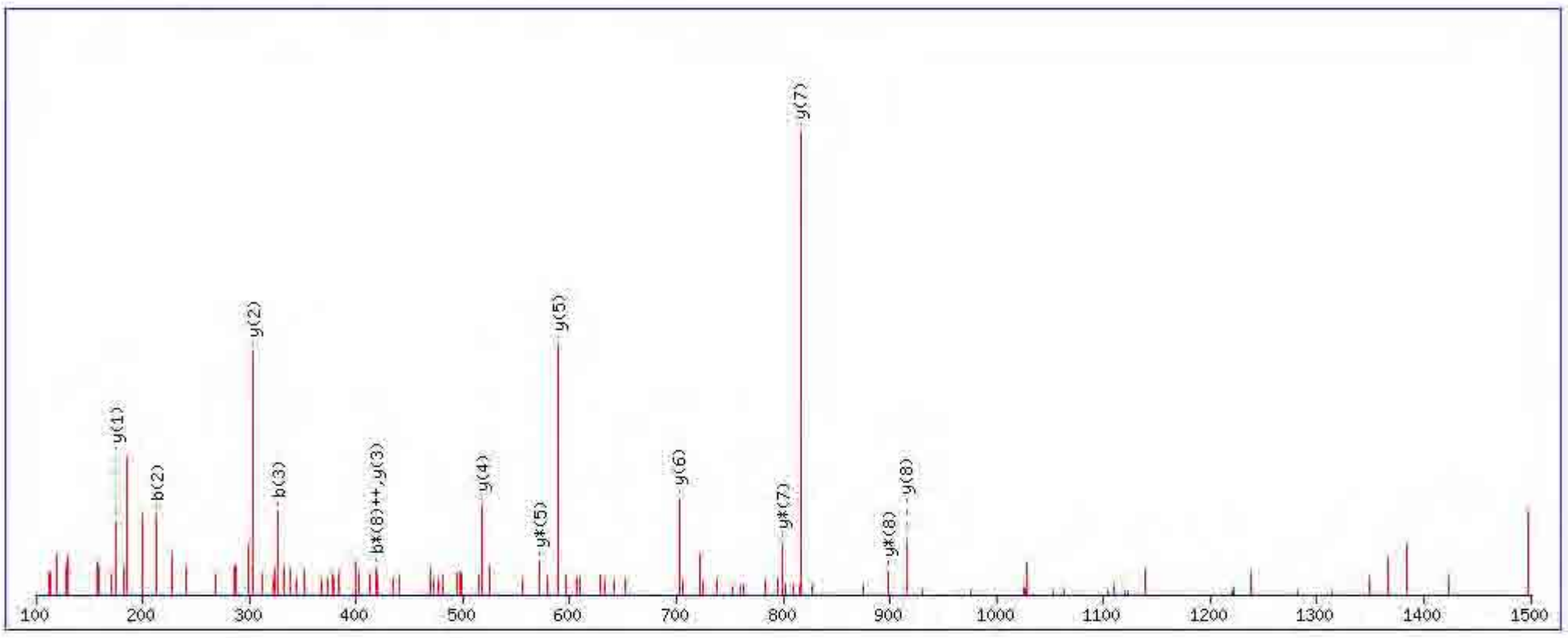
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVNIAVDER**
Found in **CRAC1_HUMAN**, Cartilage acidic protein 1 OS=Homo sapiens GN=CRTAC1 PE=1 SV=2

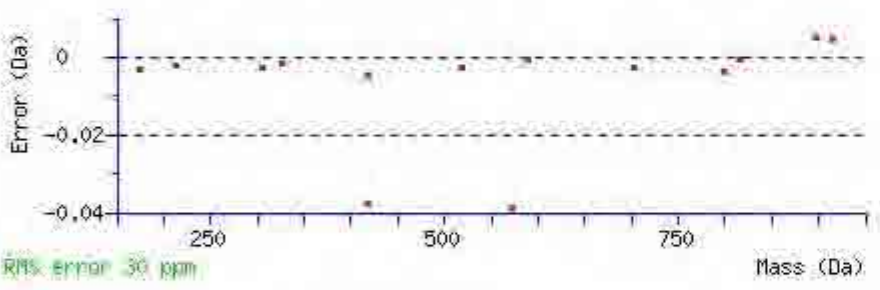
Match to Query 3548: 1027.570308 from(514.792430,2+) rtinseconds(1187) index(10015)
Title: Locus:1.1.1.716.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

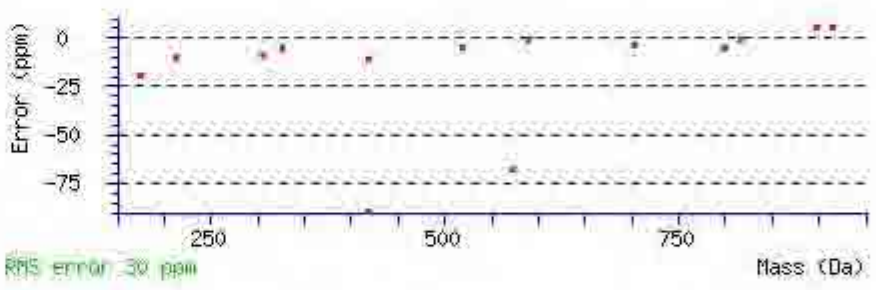
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1027.566193
Ions Score: 54 **Expect:** 0.0001
Matches : 14/78 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	213.159754	107.083515					V	*915.489421*	458.248349	898.462872	449.735074	897.478856	449.243066	8
3	327.202681	164.104978	310.176132	155.591704			N	*816.421007*	408.714142	799.394458	400.200867	798.410442	399.708859	7
4	440.286745	220.647010	423.260196	212.133736			I	*702.378080*	351.692678	685.351531	343.179404	684.367515	342.687396	6
5	511.323859	256.165568	494.297310	247.652293			A	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	610.392273	305.699775	593.365724	297.186500			V	*518.256902*	259.632089	501.230353	251.118815	500.246337	250.626807	4
7	725.419216	363.213246	708.392667	354.699972	707.408651	354.207964	D	*419.188488*	210.097882	402.161939	201.584608	401.177923	201.092600	3
8	854.461809	427.734543	837.435260	419.221268	836.451244	418.729260	E	*304.161545*	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LVNIAVDER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	1027.566193	0.004115	LVNIAVDER
10.5	1027.573593	-0.003285	VINLMVPKD
10.5	1027.577423	-0.007115	IVNKNTPAR
10.3	1027.566193	0.004115	PVKPASLER
9.9	1027.570251	0.000057	IVVQVPSTW
7.8	1027.566193	0.004115	INVLPAETR
6.1	1027.566162	0.004146	AASPIAKENK
5.8	1027.566193	0.004115	IGRIIEGSPA
5.8	1027.566208	0.004100	LGRTPAEVVS
5.7	1027.577423	-0.007115	LVDELRQR

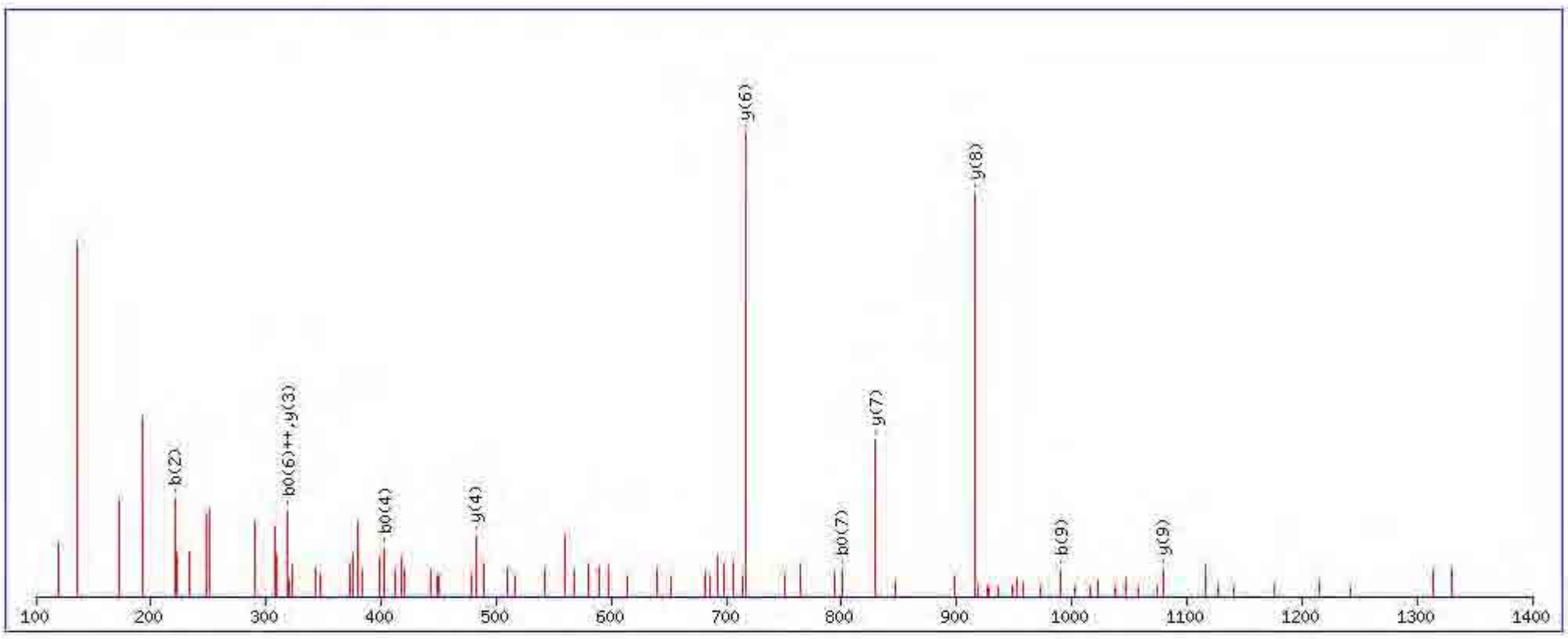
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYSIFSYATK**
Found in **CRP_HUMAN**, C-reactive protein OS=Homo sapiens GN=CRP PE=1 SV=1

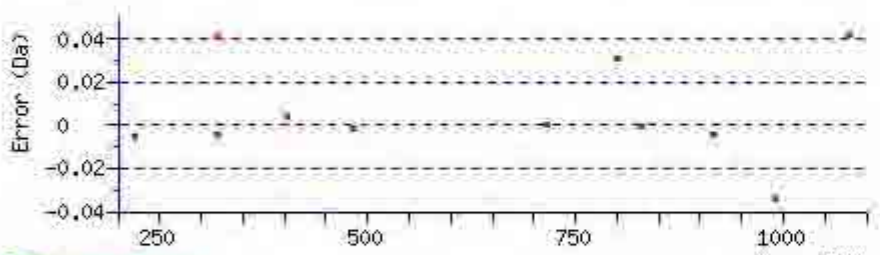
Match to Query 5604: 1135.554348 from(568.784450,2+) rtinseconds(1696) index(16711)
Title: Locus:1.1.1.999.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

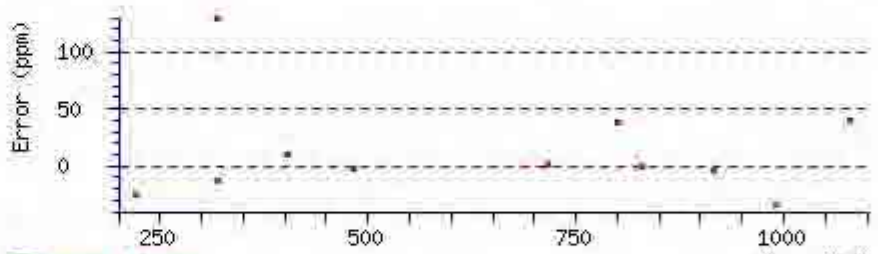
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1135.554962
Ions Score: 34 **Expect:** 0.0032
Matches : 11/84 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							10
2	**221.092069**	111.049673			Y	***1079.540789***	540.274033	1062.514240	531.760758	1061.530224	531.268750	9
3	308.124097	154.565687	290.113532	145.560404	S	***916.477460***	458.742368	899.450911	450.229094	898.466895	449.737086	8
4	421.208161	211.107719	403.197596	202.102436	I	***829.445432***	415.226354	812.418883	406.713079	811.434867	406.221071	7
5	568.276575	284.641926	550.266010	275.636643	F	***716.361368***	358.684322	699.334819	350.171048	698.350803	349.679040	6
6	655.308603	328.157940	637.298038	319.152657	S	569.292954	285.150115	552.266405	276.636841	551.282389	276.144833	5
7	818.371932	409.689604	800.361367	400.684322	Y	***482.260926***	241.634101	465.234377	233.120826	464.250361	232.628818	4
8	889.409046	445.208161	871.398481	436.202879	A	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	3
9	**990.456725**	495.732001	972.446160	486.726718	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GYSIFSYATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1135.554962	-0.000614	GYSIFSYATK
7.4	1135.565521	-0.011173	RSLEEMSLR
6.4	1135.543106	0.011242	LQMDLDVTTT
5.6	1135.548431	0.005917	GYLRPEICW
3.6	1135.550949	0.003399	GYSILPNPQK
1.1	1135.558350	-0.004002	YGIEPTMVVQ
0.4	1135.543091	0.011257	SAPVMLTLSDS
0.4	1135.543091	0.011257	SAPVMLTLSDS
0.0	1135.565521	-0.011173	RSLMELSER

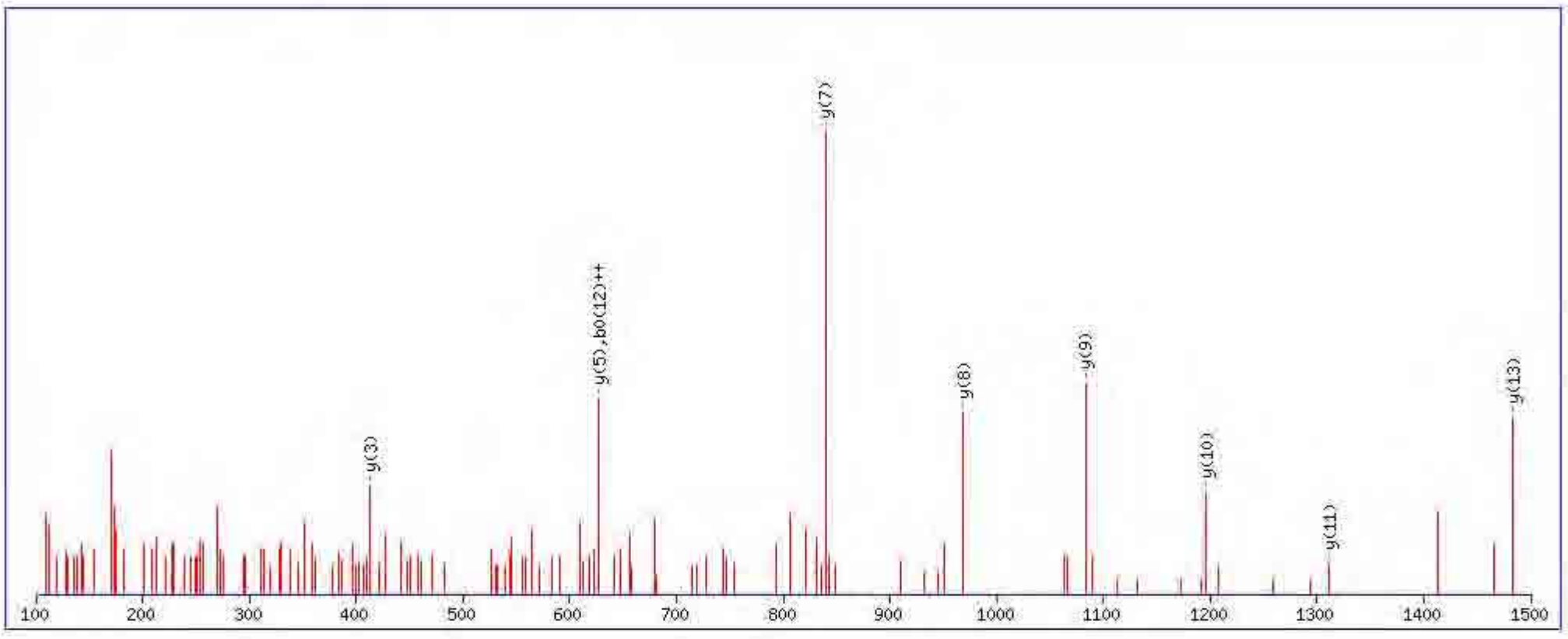
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTATDLDEPDTLHTR**
Found in **DSC1_HUMAN**, Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2

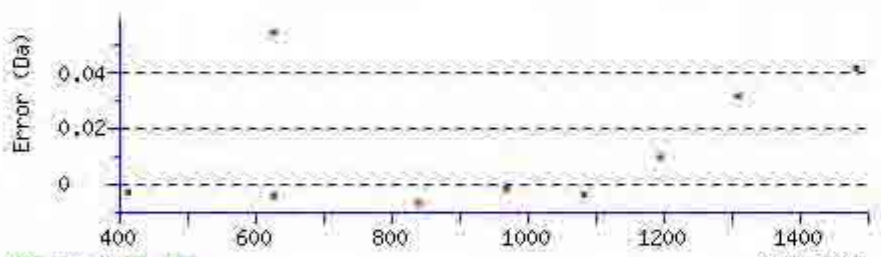
Match to Query 18857: 1682.803452 from(561.941760,3+) rtinseconds(1133) index(9347)
Title: Locus:1.1.1.686.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

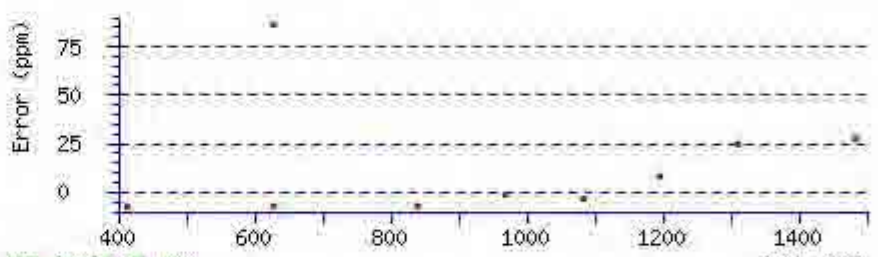
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1682.811157
Ions Score: 53 Expect: 8.7e-005
Matches : 9/136 fragment ions using 14 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483			V							15
2	201.123369	101.065322	183.112804	92.060040	T	1584.750008	792.878642	1567.723459	784.365368	1566.739443	783.873359	14
3	272.160483	136.583879	254.149918	127.578597	A	*1483.702329*	742.354803	1466.675780	733.841528	1465.691764	733.349520	13
4	373.208162	187.107719	355.197597	178.102437	T	1412.665215	706.836246	1395.638666	698.322971	1394.654650	697.830963	12
5	488.235105	244.621191	470.224540	235.615908	D	*1311.617536*	656.312406	1294.590987	647.799132	1293.606971	647.307123	11
6	601.319169	301.163223	583.308604	292.157940	L	*1196.590593*	598.798935	1179.564044	590.285660	1178.580028	589.793652	10
7	716.346112	358.676694	698.335547	349.671412	D	*1083.506529*	542.256903	1066.479980	533.743628	1065.495964	533.251620	9
8	845.388705	423.197991	827.378140	414.192708	E	*968.479586*	484.743431	951.453037	476.230157	950.469021	475.738149	8
9	942.441469	471.724373	924.430904	462.719090	P	*839.436993*	420.222135	822.410444	411.708860	821.426428	411.216852	7
10	1057.468412	529.237844	1039.457847	520.232562	D	742.384229	371.695753	725.357680	363.182478	724.373664	362.690470	6
11	1158.516091	579.761684	1140.505526	570.756401	T	*627.357286*	314.182281	610.330737	305.669006	609.346721	305.176998	5
12	1271.600155	636.303716	1253.589590	627.298433	L	526.309607	263.658441	509.283058	255.145167	508.299042	254.653159	4
13	1408.659067	704.833172	1390.648502	695.827889	H	*413.225543*	207.116409	396.198994	198.603135	395.214978	198.111127	3
14	1509.706746	755.357011	1491.696181	746.351729	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
15					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VTATDLDEPDTLHTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	1682.811157	-0.007705	VTATDLDEPDTLHTR
8.8	1682.793396	0.010056	GITTLDDPLGHMPER
8.0	1682.789520	0.013932	LNAVTKEMEPYMPL
4.6	1682.804626	-0.001174	SPTGSPPRASPMTPPR
2.4	1682.811172	-0.007720	PSATPTAATPTPGPTPR
2.4	1682.793396	0.010056	SSPGIDGDPKPPCLPR
1.2	1682.811172	-0.007720	PSATPTAATPTPGPTPR
0.4	1682.797394	0.006058	DCIRSYTEDWAIVI
0.3	1682.811157	-0.007705	RPNTATPSPIPSPTPA
0.3	1682.811157	-0.007705	RPNTATPSPIPSPTPA

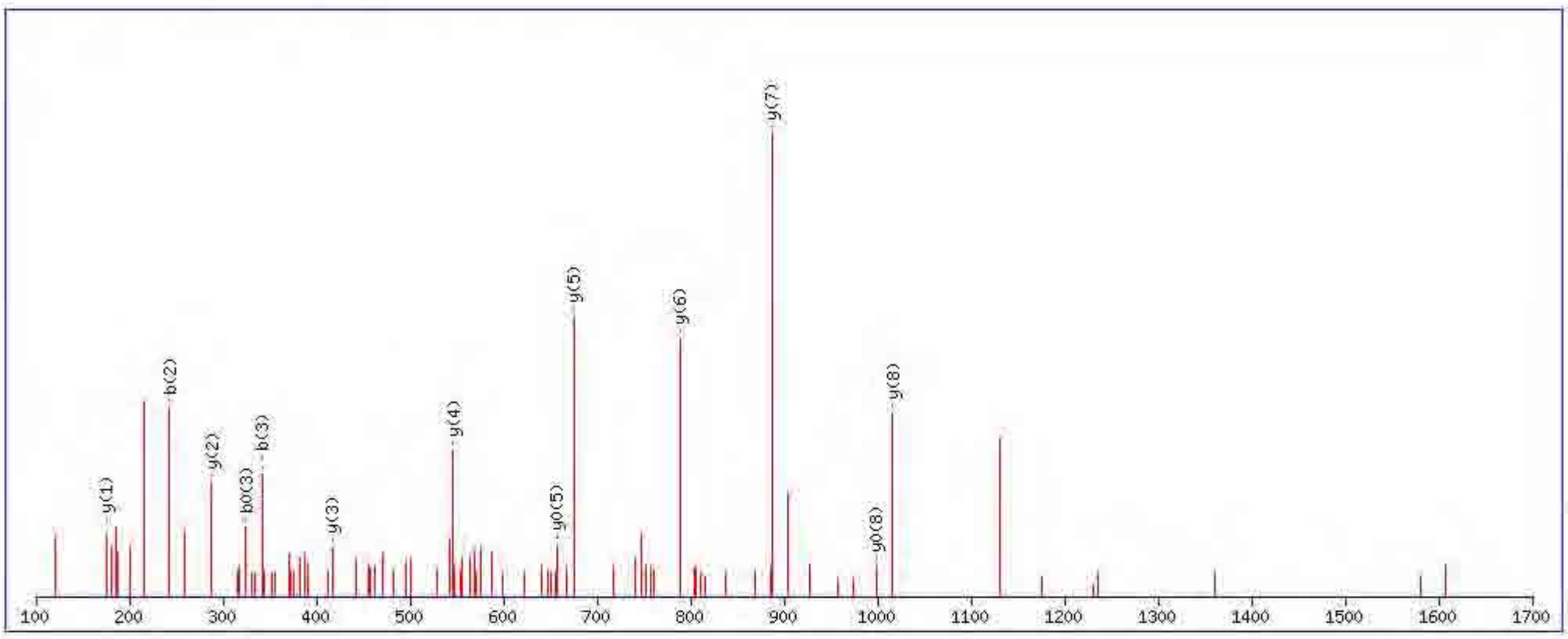
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEVLEEELR**
Found in **DESP_HUMAN**, Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3

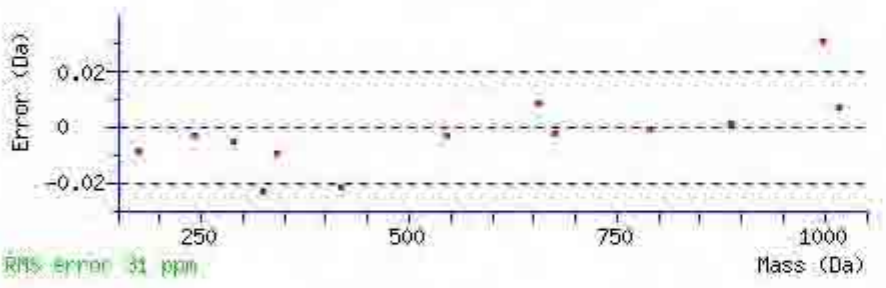
Match to Query 5504: 1128.595808 from(565.305180,2+) rtinseconds(1555) index(14930)
Title: Locus:1.1.1.921.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

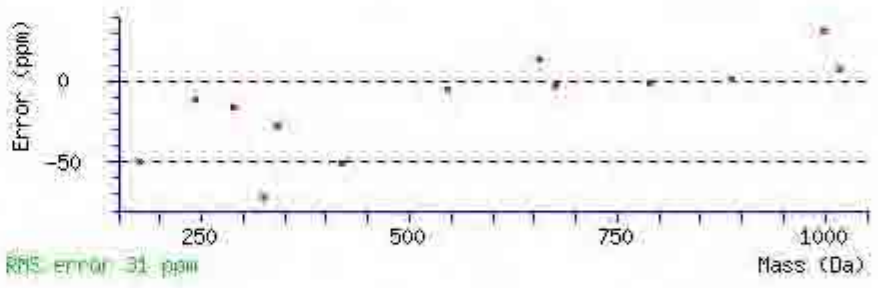
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1128.602615
Ions Score: 52 **Expect:** 0.0037
Matches : 13/74 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	**243.133933**	122.070605	225.123368	113.065322	E	*1016.525866*	508.766571	999.499317	500.253297	998.515301	499.761289	8
3	**342.202347**	171.604812	324.191782	162.599529	V	*887.483273*	444.245275	870.456724	435.732000	869.472708	435.239992	7
4	455.286411	228.146844	437.275846	219.141561	L	*788.414859*	394.711068	771.388310	386.197793	770.404294	385.705785	6
5	584.329004	292.668140	566.318439	283.662858	E	*675.330795*	338.169036	658.304246	329.655761	657.320230	329.163753	5
6	713.371597	357.189437	695.361032	348.184154	E	*546.288202*	273.647739	529.261653	265.134465	528.277637	264.642457	4
7	842.414190	421.710733	824.403625	412.705451	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
8	955.498254	478.252765	937.487689	469.247483	L	*288.203016*	144.605146	271.176467	136.091872			2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IEVLEEELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.5	1128.602615	-0.006807	IEVLEEELR
28.1	1128.602646	-0.006838	LEVISVLQND
25.1	1128.602631	-0.006823	PEVPISEKAK
24.7	1128.596115	-0.000307	QNVNKLMAVP
21.1	1128.602661	-0.006853	LIDPVSVQDK
20.6	1128.596115	-0.000307	LNSTMKLVSH
20.0	1128.596115	-0.000307	AGGRETCLPLI
18.9	1128.588699	0.007109	QRGLEEELR
17.8	1128.588715	0.007093	LDIPERSQR
17.8	1128.602631	-0.006823	LVELEPKSNT

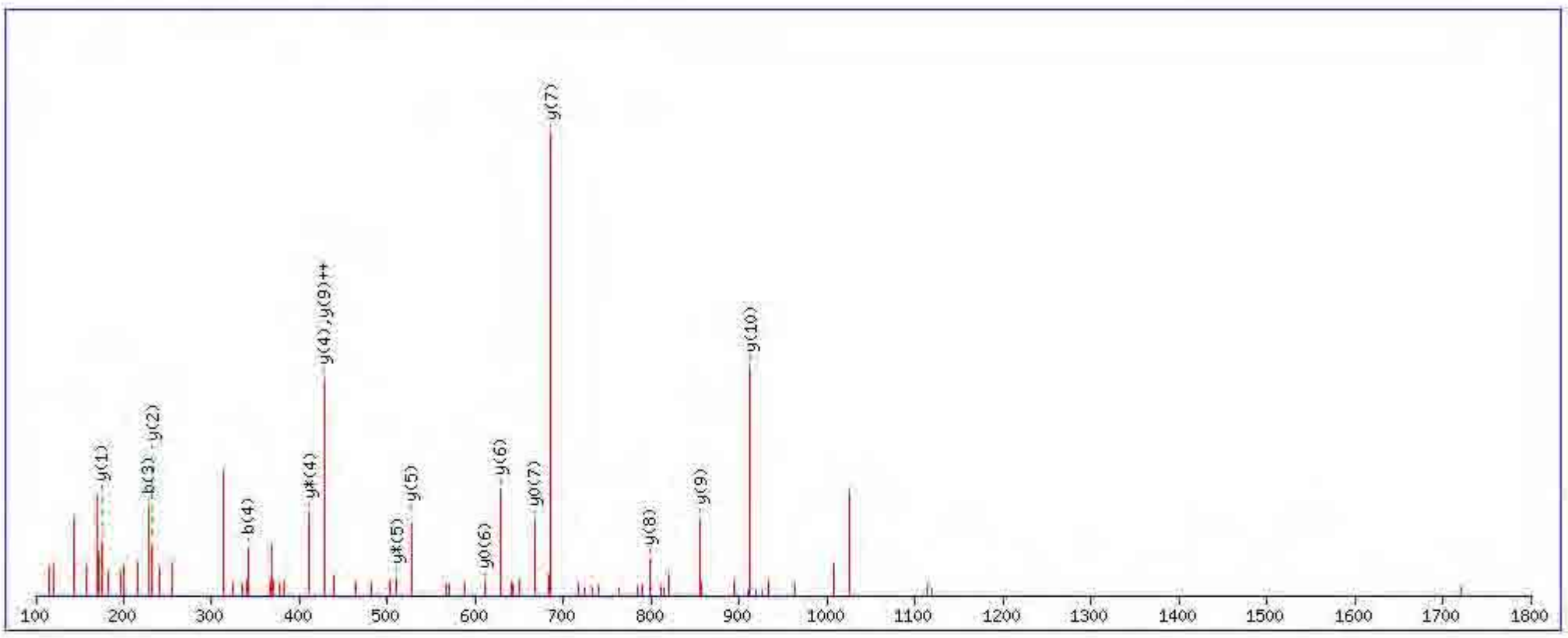
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

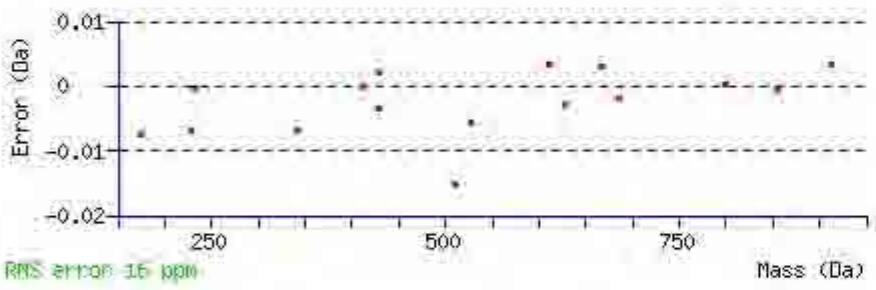
Match to Query 3501: 1024.603388 from(513.308970,2+) rtinseconds(1237) index(10670)
Title: Locus:1.1.1.744.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

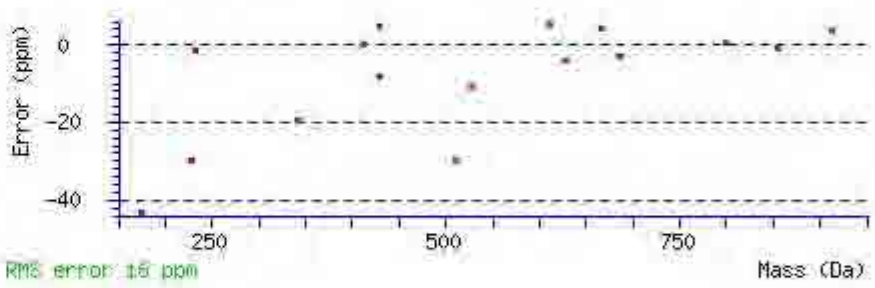
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 71 Expect: 3e-006
Matches : 16/80 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	*912.526143*	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	**228.134268**	114.570772			G	*855.504679*	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	**341.218332**	171.112804			I	*798.483215*	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	*685.399151*	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	*628.377687*	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	*527.330008*	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	*428.261594*	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	*232.140416*	116.573846	215.113867	108.060572			2
11					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.0	1024.602951	0.000437	IGGIGTVPVGR
19.4	1024.602905	0.000483	LNLPEGKVR
11.9	1024.602905	0.000483	INLKRPPTA
11.9	1024.602905	0.000483	INLKRPPTA
11.2	1024.602905	0.000483	LNLKPRSTP
10.2	1024.602890	0.000498	INQNKAPLK
8.3	1024.602905	0.000483	PGAVAAAAILR
8.2	1024.602951	0.000437	IGVQGTPVVR
6.6	1024.602921	0.000467	LGLPGLKGDR
5.8	1024.602936	0.000452	IKVIGGPPGR

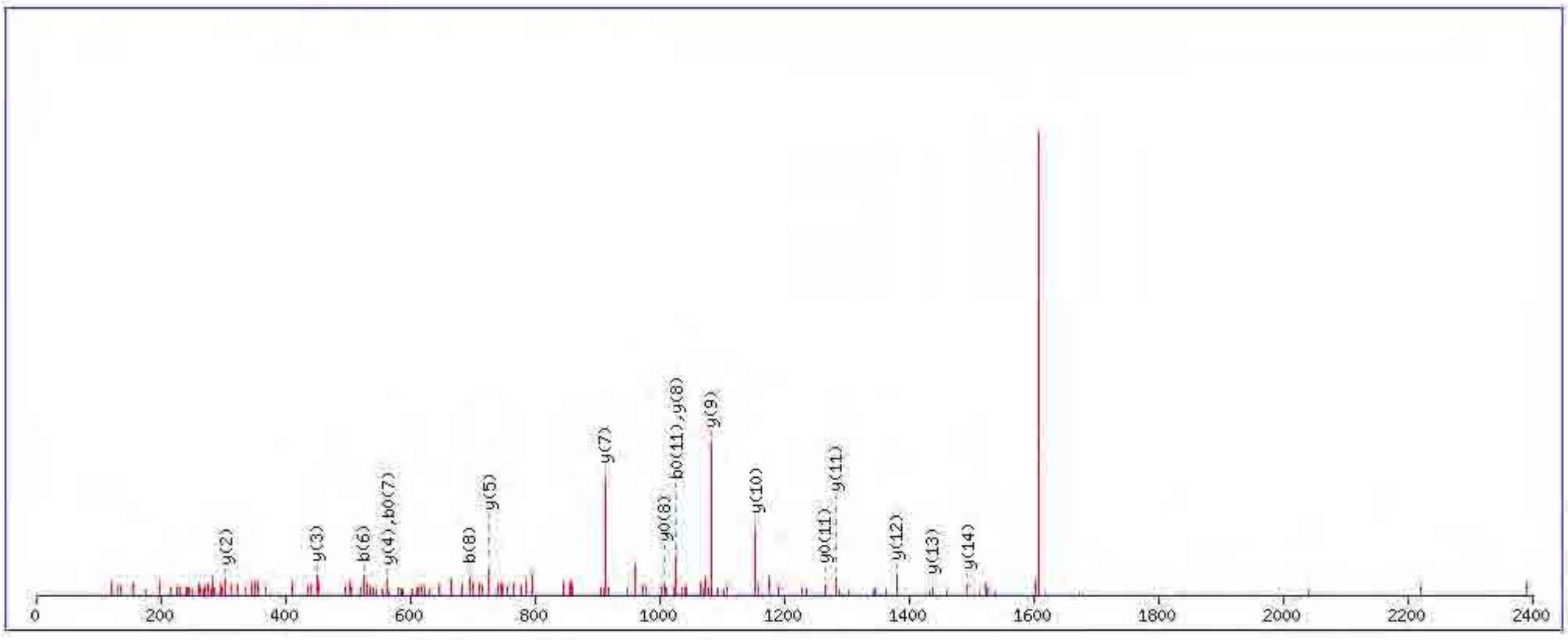
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGGPEAGLGEYLFER**
Found in **FRIL_HUMAN**, Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2

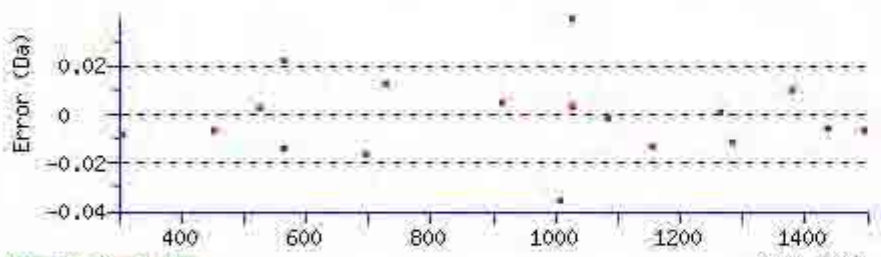
Match to Query 17376: 1606.803048 from(804.408800,2+) rtinseconds(2108) index(22161)
Title: Locus:1.1.1.1223.15
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

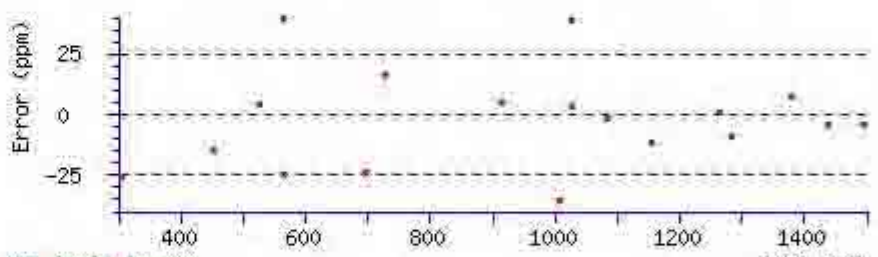
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1606.799103
Ions Score: 92 **Expect:** 4.1e-008
Matches : 18/130 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							15
2	171.112804	86.060040			G	*1494.722336*	747.864806	1477.695787	739.351532	1476.711771	738.859524	14
3	228.134268	114.570772			G	*1437.700872*	719.354074	1420.674323	710.840800	1419.690307	710.348792	13
4	325.187032	163.097154			P	*1380.679408*	690.843342	1363.652859	682.330068	1362.668843	681.838060	12
5	454.229625	227.618450	436.219060	218.613168	E	*1283.626644*	642.316960	1266.600095	633.803686	1265.616079	633.311678	11
6	525.266739	263.137008	507.256174	254.131725	A	*1154.584051*	577.795664	1137.557502	569.282389	1136.573486	568.790381	10
7	582.288203	291.647740	564.277638	282.642457	G	*1083.546937*	542.277107	1066.520388	533.763832	1065.536372	533.271824	9
8	695.372267	348.189772	677.361702	339.184489	L	*1026.525473*	513.766375	1009.498924	505.253100	1008.514908	504.761092	8
9	752.393731	376.700504	734.383166	367.695221	G	*913.441409*	457.224343	896.414860	448.711068	895.430844	448.219060	7
10	881.436324	441.221800	863.425759	432.216518	E	856.419945	428.713611	839.393396	420.200336	838.409380	419.708328	6
11	1044.499653	522.753465	1026.489088	513.748182	Y	*727.377352*	364.192314	710.350803	355.679040	709.366787	355.187032	5
12	1157.583717	579.295497	1139.573152	570.290214	L	*564.314023*	282.660650	547.287474	274.147375	546.303458	273.655367	4
13	1304.652131	652.829704	1286.641566	643.824421	F	*451.229959*	226.118618	434.203410	217.605343	433.219394	217.113335	3
14	1433.694724	717.351000	1415.684159	708.345718	E	*304.161545*	152.584411	287.134996	144.071136	286.150980	143.579128	2
15					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LGGPEAGLGEYLFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.0	1606.799103	0.003945	LGGPEAGLGEYLFER
12.4	1606.799164	0.003884	GPPGSPGLQGFPGITPP
10.2	1606.806503	-0.003455	IMTYVAQFLQYSK
9.0	1606.810364	-0.007316	GPGPSLPEPHGVYLR
9.0	1606.810364	-0.007316	GPGPSLPEPHGVYLR
8.2	1606.799164	0.003884	GPPGSPGLQGFPGITPP
7.9	1606.810349	-0.007301	INLPAPNPDHVGGYK
7.0	1606.806351	-0.003303	PPPGSGLGNLGAGQTPR
7.0	1606.799164	0.003884	GPPGSPGLQGFPGITPP
6.5	1606.810379	-0.007331	LGPPGPQGPIGYPGPR

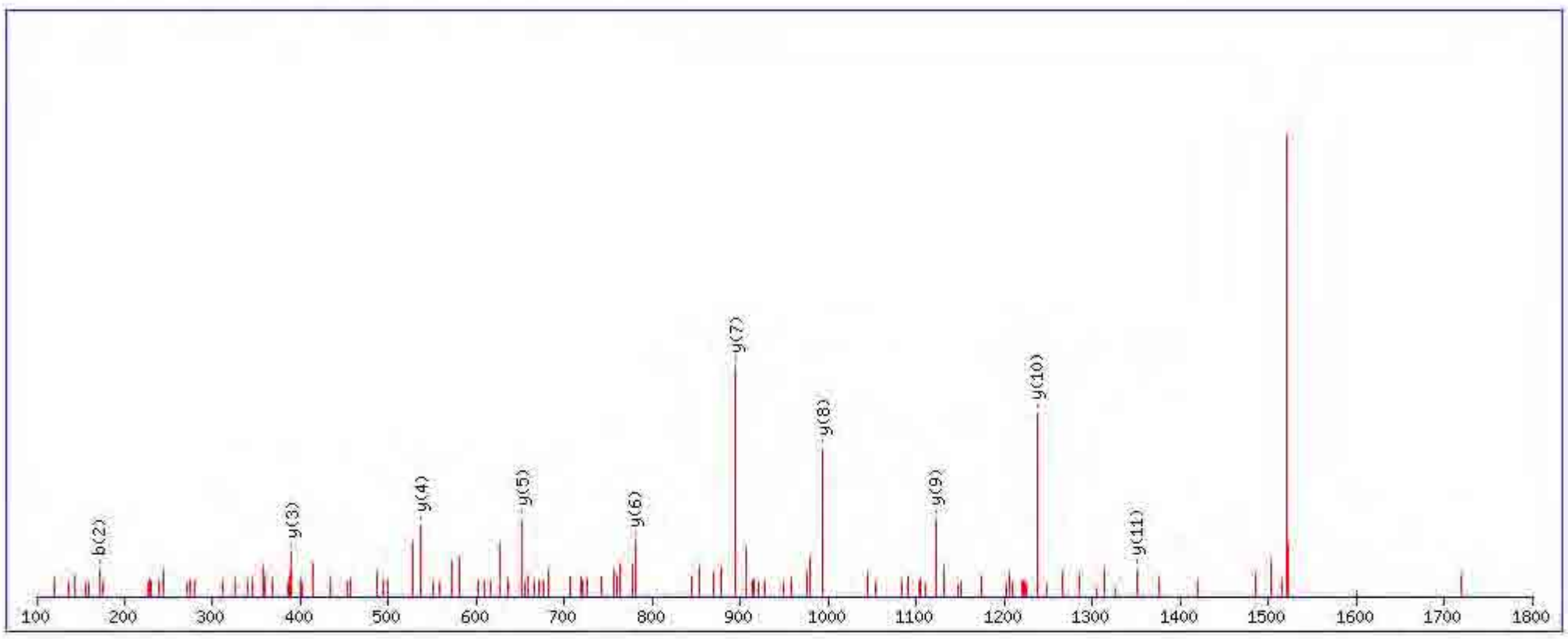
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLIDEVNQDFTNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

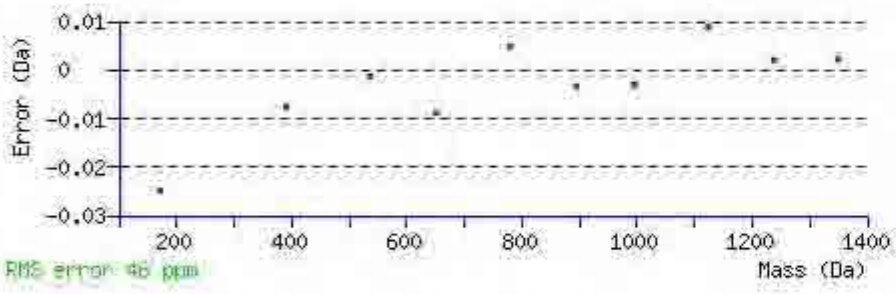
Match to Query 14963: 1519.738988 from(760.876770,2+) rtinseconds(1884) index(19223)
Title: Locus:1.1.1.1101.14
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

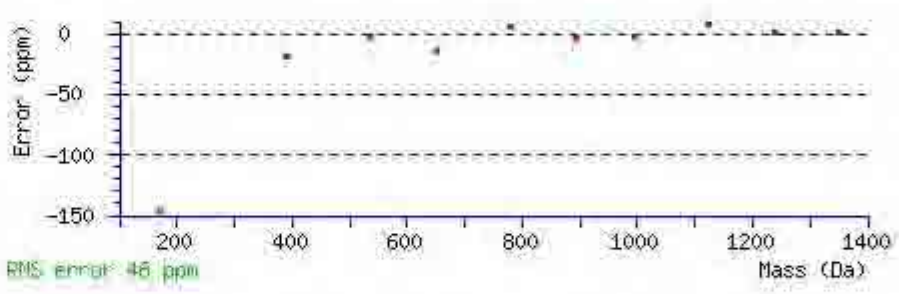
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1519.726685
Ions Score: 76 **Expect:** 6.5e-007
Matches : 10/122 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							13
2	171.112804	86.060040					L	1463.712498	732.359887	1446.685949	723.846613	1445.701933	723.354605	12
3	284.196868	142.602072					I	*1350.628434*	675.817855	1333.601885	667.304581	1332.617869	666.812572	11
4	399.223811	200.115544			381.213246	191.110261	D	*1237.544370*	619.275823	1220.517821	610.762549	1219.533805	610.270541	10
5	528.266404	264.636840			510.255839	255.631558	E	*1122.517427*	561.762352	1105.490878	553.249077	1104.506862	552.757069	9
6	627.334818	314.171047			609.324253	305.165765	V	*993.474834*	497.241055	976.448285	488.727780	975.464269	488.235773	8
7	741.377745	371.192511	724.351196	362.679236	723.367180	362.187228	N	*894.406420*	447.706848	877.379871	439.193574	876.395855	438.701566	7
8	869.436323	435.221800	852.409774	426.708525	851.425758	426.216517	Q	*780.363493*	390.685385	763.336944	382.172110	762.352928	381.680102	6
9	984.463266	492.735271	967.436717	484.221996	966.452701	483.729988	D	*652.304915*	326.656096	635.278366	318.142821	634.294350	317.650813	5
10	1131.531680	566.269478	1114.505131	557.756204	1113.521115	557.264196	F	*537.277972*	269.142624	520.251423	260.629350	519.267407	260.137342	4
11	1232.579359	616.793318	1215.552810	608.280043	1214.568794	607.788035	T	*390.209558*	195.608417	373.183009	187.095142	372.198993	186.603134	3
12	1346.622286	673.814781	1329.595737	665.301507	1328.611721	664.809499	N	289.161879	145.084577	272.135330	136.571303			2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLIDEVNQDFTNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.8	1519.726685	0.012303	GLIDEVNQDFTNR
9.2	1519.751846	-0.012858	GIEVEDLPQFTTR
5.1	1519.726685	0.012303	SSPGQAVELPDHNGL
3.2	1519.751877	-0.012889	SVIDPVPAPVGDSHV
3.1	1519.751877	-0.012889	SVIDPVPAPVGDSHV
2.7	1519.730713	0.008275	DPHYPDHDLGIIL
2.7	1519.737915	0.001073	TPPRPQGQRPEPE
2.3	1519.753189	-0.014201	GPPSSLPQRHFPGQ
2.3	1519.737915	0.001073	TPPRPQGQRPEPE
1.7	1519.749130	-0.010142	EPRAARPSSFQSR

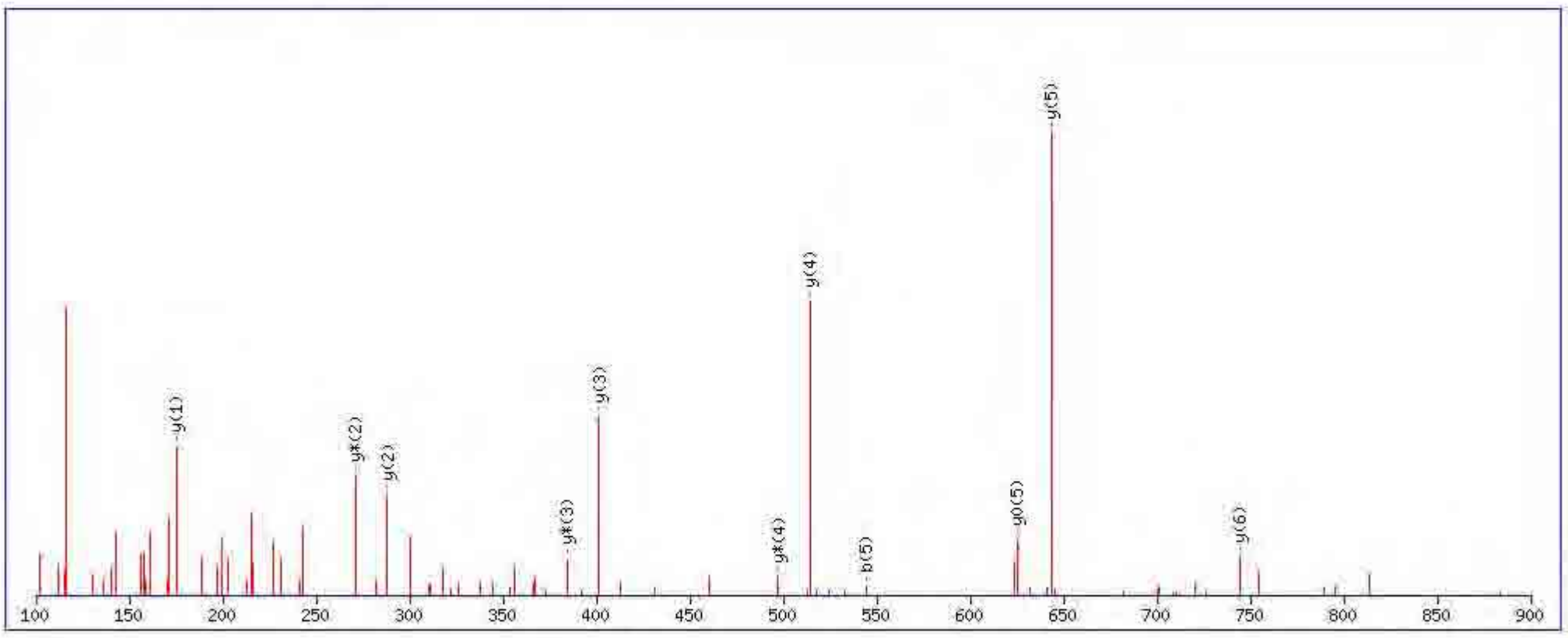
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELLIR**
Found in **H31T_HUMAN**, Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3

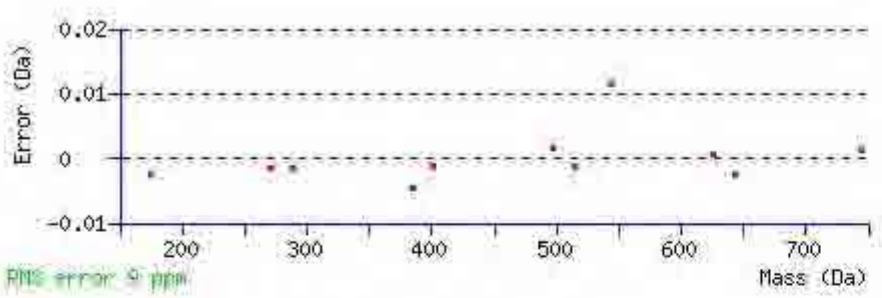
Match to Query 850: 830.485148 from(416.249850,2+) rtinseconds(1091) index(8809)
Title: Locus:1.1.1.663.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

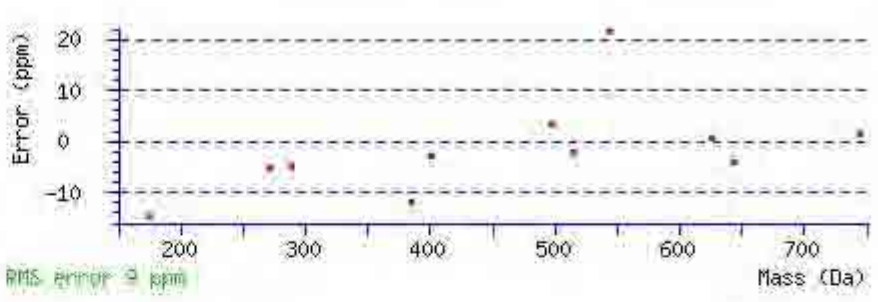
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 830.486145
Ions Score: 53 **Expect:** 0.00044
Matches : 11/52 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	189.086983	95.047129	171.076418	86.041847	T	*744.461416*	372.734346	727.434867	364.221072	726.450851	363.729064	6
3	318.129576	159.568426	300.119011	150.563144	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
4	431.213640	216.110458	413.203075	207.105176	L	*514.371144*	257.689210	497.344595	249.175936			4
5	544.297704	272.652490	526.287139	263.647208	L	*401.287080*	201.147178	384.260531	192.633904			3
6	657.381768	329.194522	639.371203	320.189240	I	*288.203016*	144.605146	271.176467	136.091872			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of STELLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	830.486145	-0.000997	STELLIR
22.5	830.486145	-0.000997	TESLLLR
21.3	830.486145	-0.000997	ESTLLIR
21.3	830.486160	-0.001012	TTDIILR
19.5	830.483643	0.001505	WMLLLR
18.8	830.486145	-0.000997	SSLLLNGK
18.0	830.486145	-0.000997	SLTEIIR
13.2	830.486145	-0.000997	TELSLLR
13.2	830.486145	-0.000997	TLESILR
11.7	830.490189	-0.005041	WTLLSLV

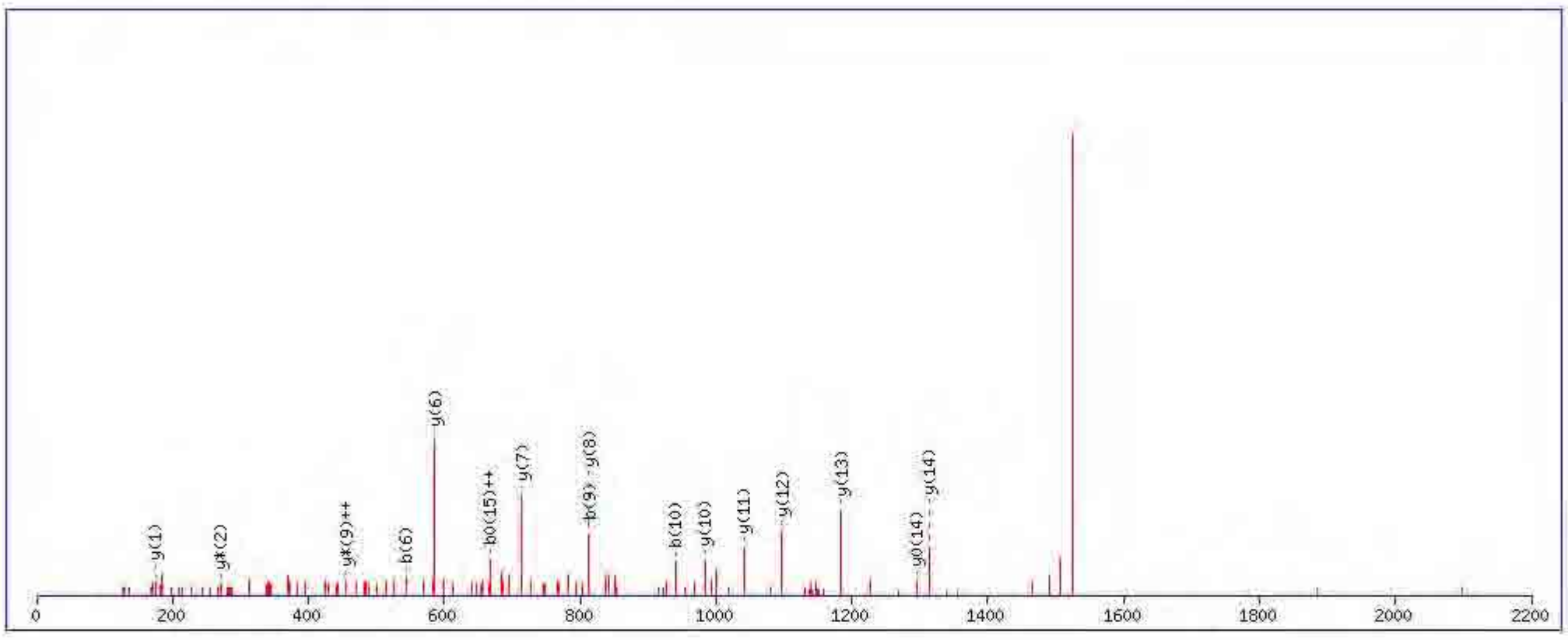
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVESGGGLVKPGGSLR**
Found in **HV319_HUMAN**, Ig heavy chain V-III region JON OS=Homo sapiens PE=1 SV=1

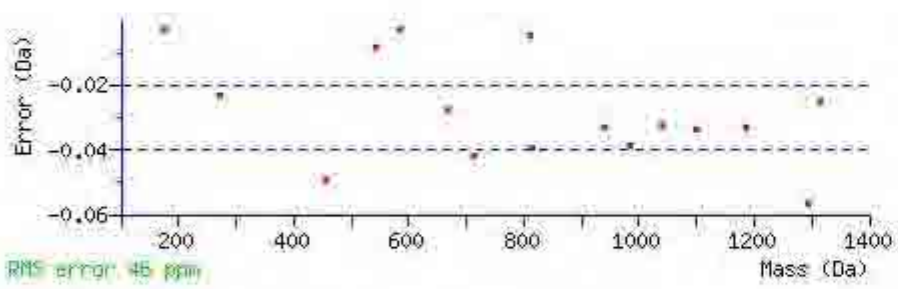
Match to Query 15114: 1524.863248 from(763.438900,2+) rtinseconds(1323) index(11823)
Title: Locus:1.1.1.792.17
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

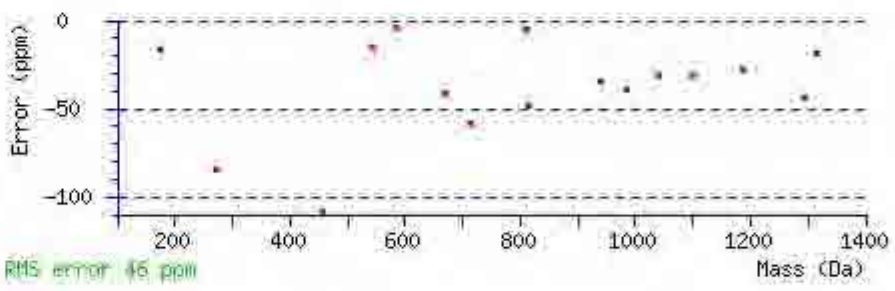
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1524.862396
Ions Score: 60 **Expect:** 5.4e-005
Matches : 16/154 fragment ions using 28 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							16
2	213.159754	107.083515					V	1412.785604	706.896440	1395.759055	698.383166	1394.775039	697.891157	15
3	342.202347	171.604811			324.191782	162.599529	E	*1313.717190*	657.362233	1296.690641	648.848958	1295.706625	648.356950	14
4	429.234375	215.120825			411.223810	206.115543	S	*1184.674597*	592.840937	1167.648048	584.327662	1166.664032	583.835654	13
5	486.255839	243.631557			468.245274	234.626275	G	*1097.642569*	549.324922	1080.616020	540.811648	1079.632004	540.319640	12
6	543.277303	272.142290			525.266738	263.137007	G	*1040.621105*	520.814191	1023.594556	512.300916	1022.610540	511.808908	11
7	600.298767	300.653022			582.288202	291.647739	G	*983.599641*	492.303458	966.573092	483.790184	965.589076	483.298176	10
8	713.382831	357.195054			695.372266	348.189771	L	926.578177	463.792726	909.551628	455.279452	908.567612	454.787444	9
9	812.451245	406.729261			794.440680	397.723978	V	*813.494113*	407.250694	796.467564	398.737420	795.483548	398.245412	8
10	940.546208	470.776742	923.519659	462.263467	922.535643	461.771459	K	*714.425699*	357.716487	697.399150	349.203213	696.415134	348.711205	7
11	1037.598972	519.303124	1020.572423	510.789850	1019.588407	510.297842	P	*586.330736*	293.669006	569.304187	285.155731	568.320171	284.663723	6
12	1094.620436	547.813856	1077.593887	539.300582	1076.609871	538.808573	G	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	5
13	1151.641900	576.324588	1134.615351	567.811313	1133.631335	567.319305	G	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
14	1238.673928	619.840602	1221.647379	611.327328	1220.663363	610.835319	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
15	1351.757992	676.382634	1334.731443	667.869359	1333.747427	667.377351	L	288.203016	144.605146	271.176467	136.091871			2
16							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LVESGGGLVKPGGSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.6	1524.862396	0.000852	LVESGGGLVKPGGSLR
13.2	1524.851166	0.012082	LAKVGTSAPVATPGPK
12.4	1524.851166	0.012082	LAKVGTSAPVATPGPK
8.0	1524.876282	-0.013034	ALKGLGSSPDLELLL
6.0	1524.851151	0.012097	GLKASLLDPVPEVR
5.3	1524.862350	0.000898	VVNEIEKQLNAIR
5.1	1524.855865	0.007383	LSTLAGIRVMVHGR
3.7	1524.855850	0.007398	GQRLQPMLVQALR
3.1	1524.869781	-0.006533	KGMIPPGTQLVKPK
2.8	1524.866425	-0.003177	PGTVATLRFQLLPP

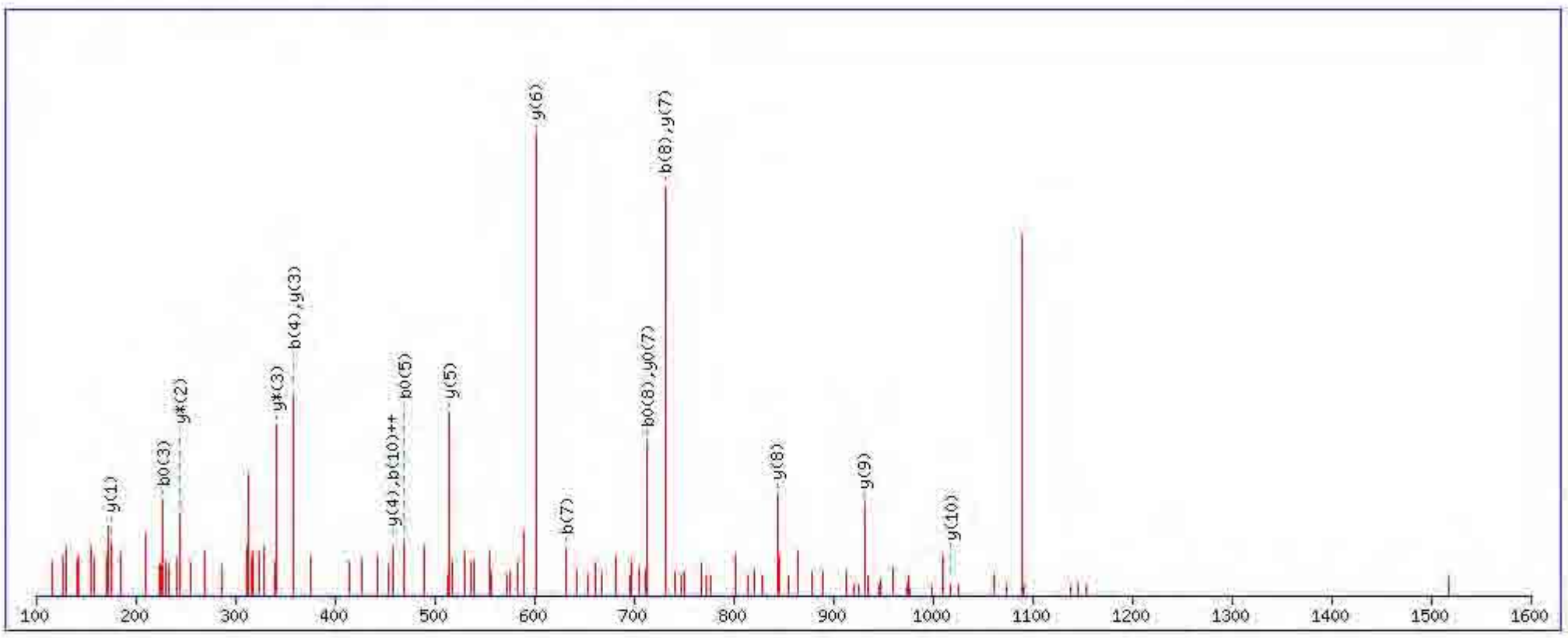
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASSLESGVPSR**
Found in **KV106_HUMAN**, Ig kappa chain V-I region EU OS=Homo sapiens PE=1 SV=1

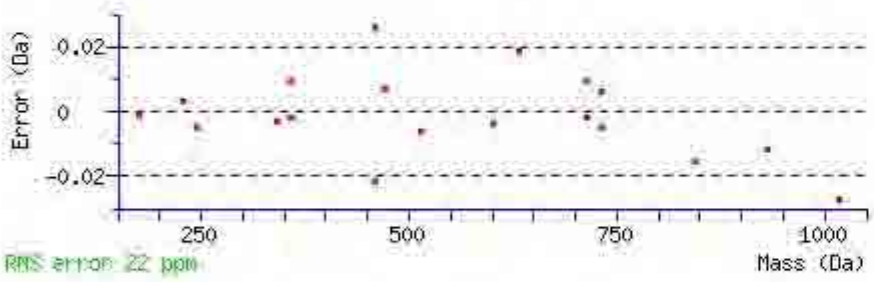
Match to Query 4657: 1088.540048 from(545.277300,2+) rtinseconds(780) index(5624)
Title: Locus:1.1.1.486.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

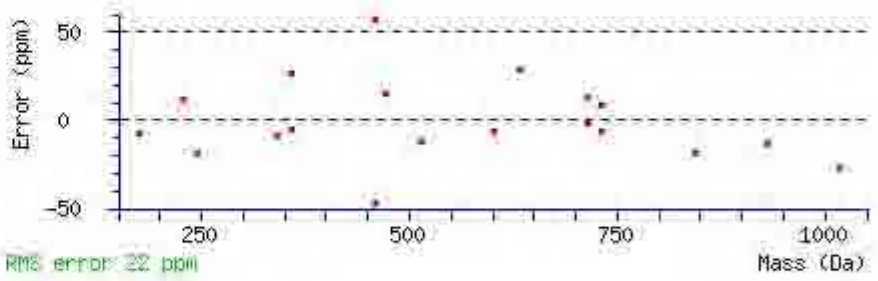
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1088.546188
Ions Score: 63 **Expect:** 0.00012
Matches : 19/96 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	159.076418	80.041847	141.065853	71.036564	S	*1018.516363*	509.761820	1001.489814	501.248545	1000.505798	500.756537	10
3	246.108446	123.557861	228.097881	114.552578	S	*931.484335*	466.245806	914.457786	457.732531	913.473770	457.240523	9
4	359.192510	180.099893	341.181945	171.094610	L	*844.452307*	422.729792	827.425758	414.216517	826.441742	413.724509	8
5	488.235103	244.621189	470.224538	235.615907	E	*731.368243*	366.187760	714.341694	357.674485	713.357678	357.182477	7
6	575.267131	288.137204	557.256566	279.131921	S	*602.325650*	301.666463	585.299101	293.153189	584.315085	292.661181	6
7	632.288595	316.647936	614.278030	307.642653	G	*515.293622*	258.150449	498.267073	249.637175	497.283057	249.145167	5
8	731.357009	366.182143	713.346444	357.176860	V	*458.272158*	229.639717	441.245609	221.126443	440.261593	220.634435	4
9	828.409773	414.708525	810.399208	405.703242	P	*359.203744*	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	915.441801	458.224539	897.431236	449.219256	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ASSLESGVPSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.7	1088.546188	-0.006140	ASSLESGVPSR
20.8	1088.534958	0.005090	EVATNSELVQ
18.8	1088.534943	0.005105	ASSLSESSPPK
17.9	1088.534943	0.005105	EDNEKDLVK
12.6	1088.539642	0.000406	ARLENMSPR
11.8	1088.546188	-0.006140	TASALGTESPR
10.7	1088.532440	0.007608	RMAEFPLEP
10.4	1088.546204	-0.006156	ASSLPSGVPSR
10.3	1088.546204	-0.006156	APGSLTSTPAR
10.2	1088.534958	0.005090	DTGKAEEPVK

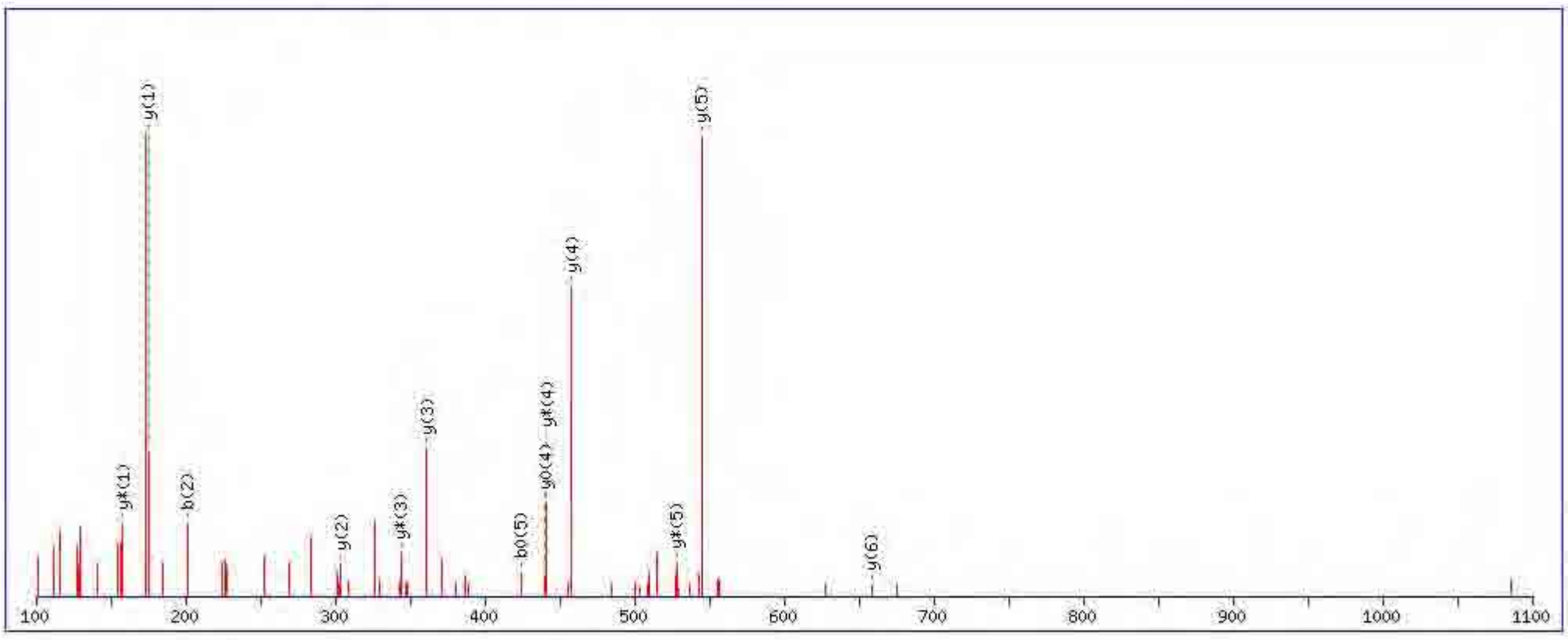
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLSPGER**
Found in **KV302_HUMAN**, Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1

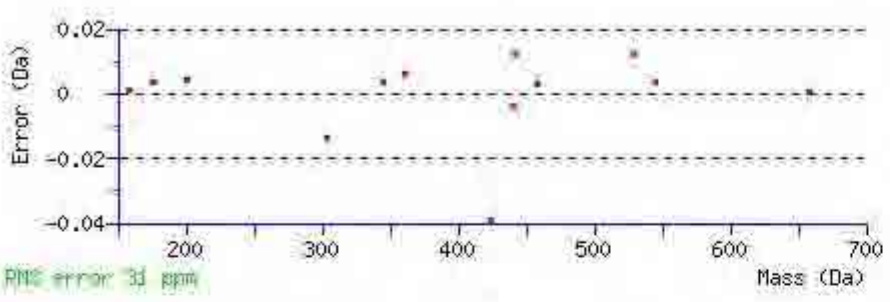
Match to Query 258: 744.377888 from(373.196220,2+) rtinseconds(359) index(749)
Title: Locus:1.1.1.249.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

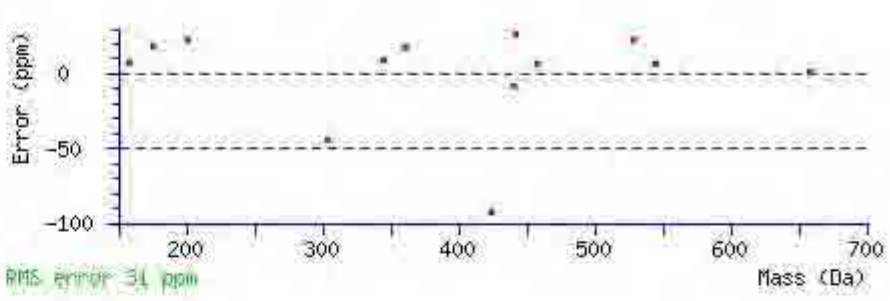
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 744.376602
Ions Score: 35 **Expect:** 0.072
Matches : 13/58 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	201.123368	101.065322	183.112803	92.060039	L	*658.351865*	329.679571	641.325316	321.166296	640.341300	320.674288	6
3	288.155396	144.581336	270.144831	135.576053	S	*545.267801*	273.137539	528.241252	264.624264	527.257236	264.132256	5
4	385.208160	193.107718	367.197595	184.102435	P	*458.235773*	229.621524	441.209224	221.108250	440.225208	220.616242	4
5	442.229624	221.618450	424.219059	212.613167	G	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
6	571.272217	286.139747	553.261652	277.134464	E	*304.161545*	152.584410	287.134996	144.071136	286.150980	143.579128	2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLSPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.5	744.376602	0.001286	SLSPGER
35.5	744.376602	0.001286	SLSPGZR
34.5	744.376617	0.001271	SPSPSVR
23.3	744.376602	0.001286	SLSGPER
22.6	744.376617	0.001271	SPSGPLR
22.6	744.376617	0.001271	SPSLPGR
22.6	744.376617	0.001271	SPSPGIR
21.5	744.376602	0.001286	LSSPDAR
21.5	744.376617	0.001271	PSSPSVR
21.5	744.376617	0.001271	PSSPVSR

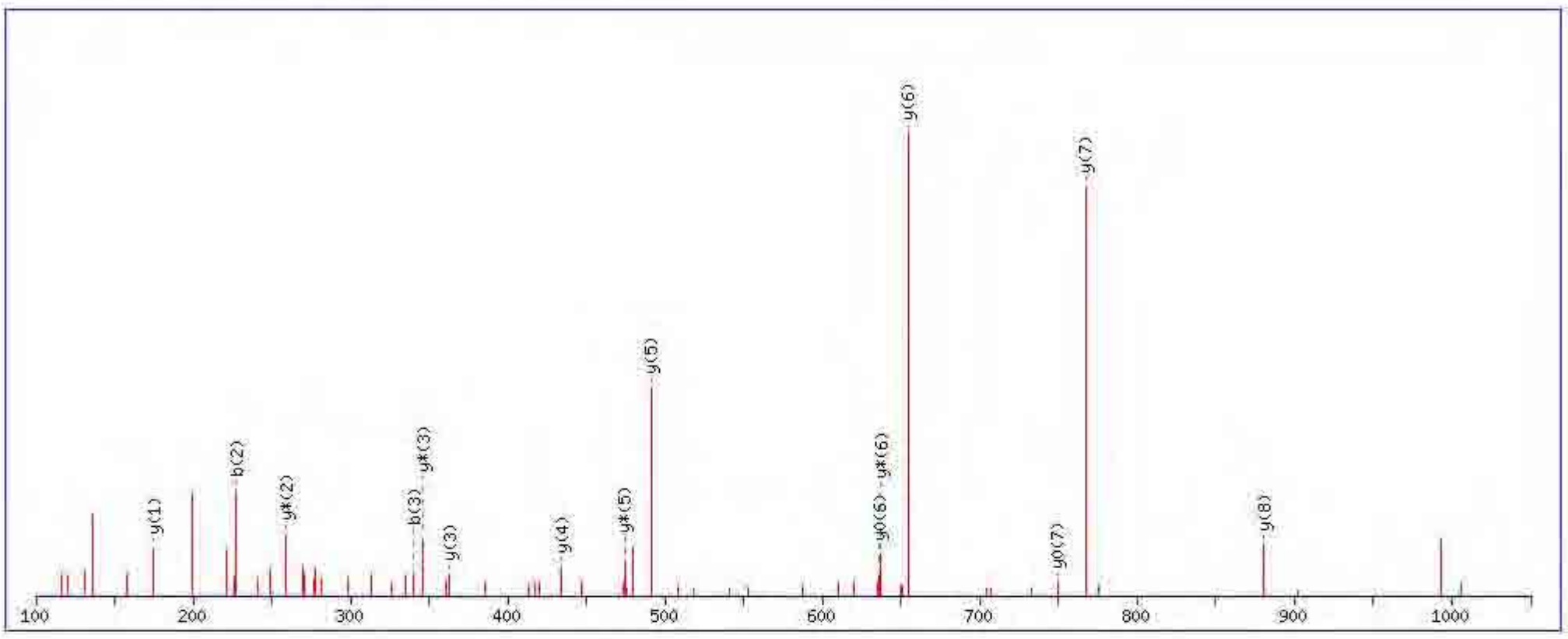
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

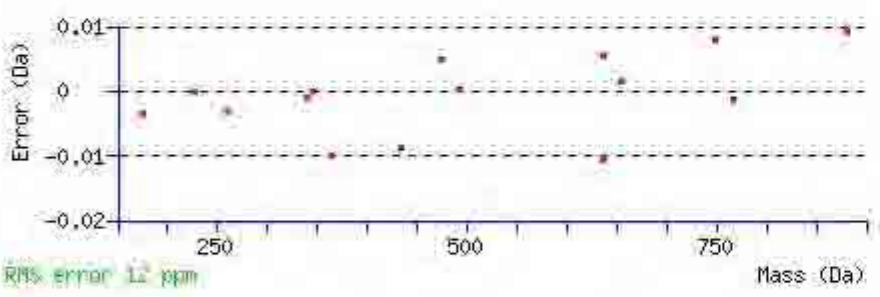
Match to Query 2979: 992.563128 from(497.288840,2+) rtinseconds(1238) index(10691)
Title: Locus:1.1.1.745.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

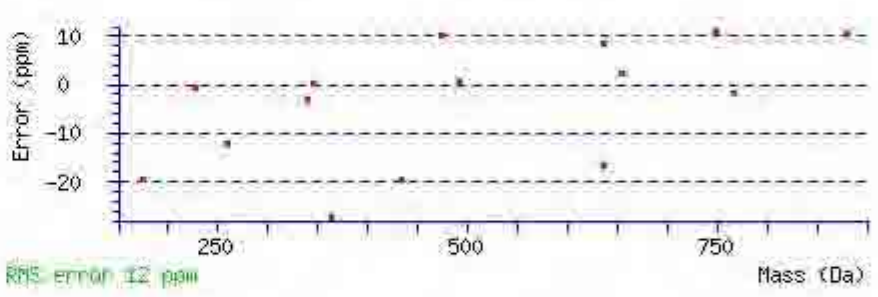
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 48 **Expect:** 0.0012
Matches : 15/66 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	*363.198659*	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	992.565460	-0.002332	LLIYGASTR
48.3	992.565460	-0.002332	LLIYGATSR
18.9	992.565475	-0.002347	PLLGPPDIR
16.2	992.554245	0.008883	ILPPLSPPQ
16.2	992.554245	0.008883	ILPPLSPPQ
15.8	992.565460	-0.002332	LILGPHESK
15.6	992.554245	0.008883	LPPPLSAPVA
15.6	992.554260	0.008868	LPPTPVGPAL
15.2	992.554245	0.008883	ILPPLSPPQ
15.2	992.565475	-0.002347	ILPSVSHKP

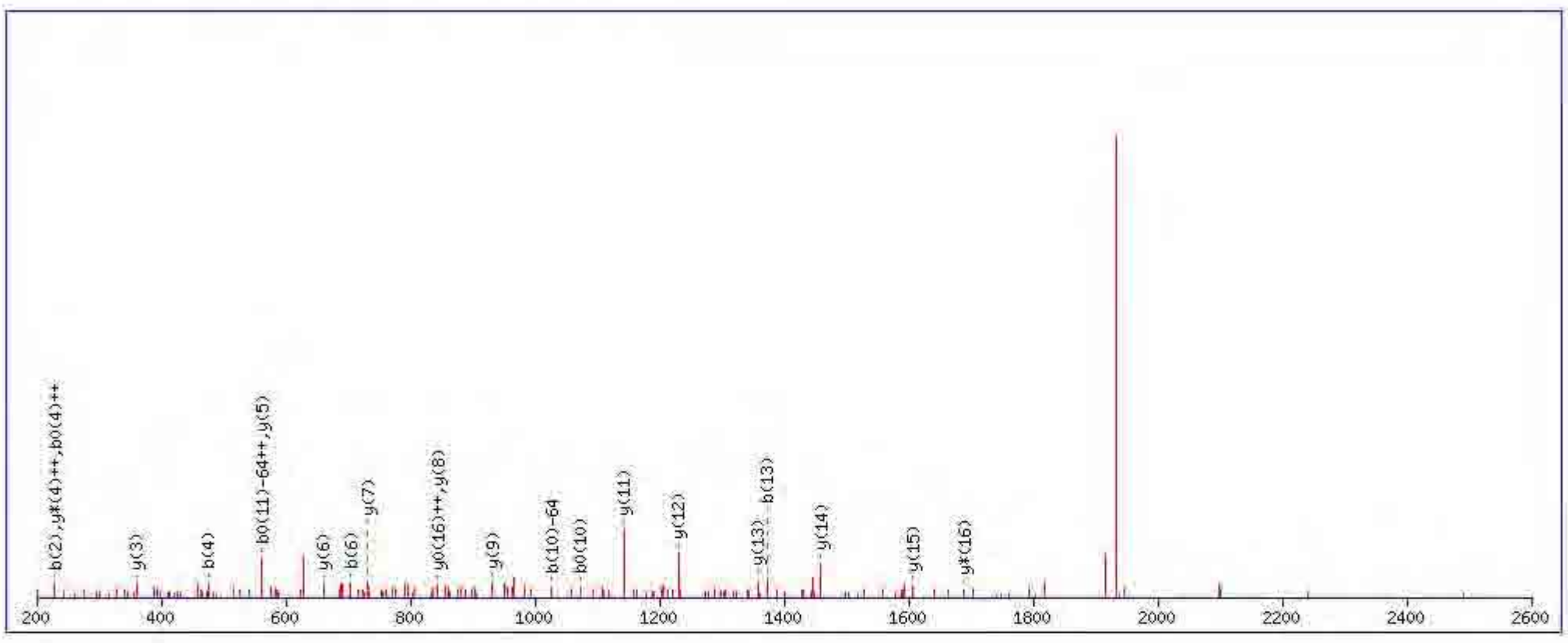
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIVMTQSPDSLAVSLGER**
Found in **KV401_HUMAN**, Ig kappa chain V-IV region (Fragment) OS=Homo sapiens GN=IGKV4-1 PE=4 SV=1

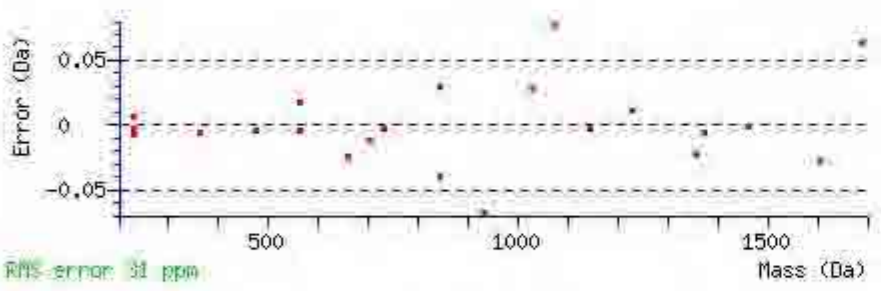
Match to Query 23815: 1932.943868 from(967.479210,2+) rtinseconds(1838) index(18608)
Title: Locus:1.1.1.1076.24
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

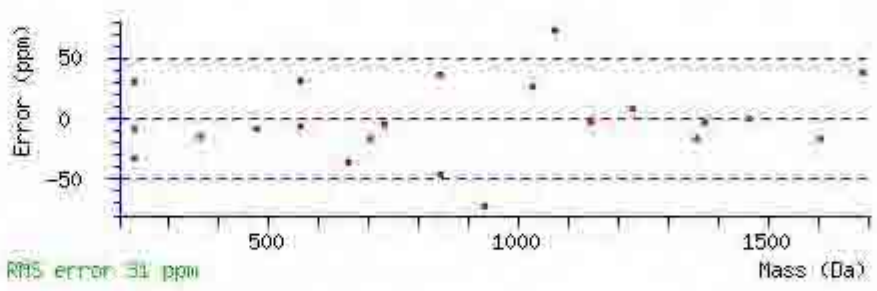
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1932.946259
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 68 **Expect:** 2.2e-006
Matches : 22/290 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							18
2	229.118283	115.062779			211.107718	106.057497	I	1818.926591	909.966933	1801.900042	901.453659	1800.916026	900.961651	17
3	328.186697	164.596986			310.176132	155.591704	V	1705.842527	853.424902	1688.815978	844.911627	1687.831962	844.419619	16
4	475.222097	238.114686			457.211532	229.109404	M	*1606.774113*	803.890695	1589.747564	795.377420	1588.763548	794.885412	15
5	576.269776	288.638526			558.259211	279.633243	T	*1459.738713*	730.372995	1442.712164	721.859720	1441.728148	721.367712	14
6	704.328354	352.667815	687.301805	344.154541	686.317789	343.662533	Q	*1358.691034*	679.849155	1341.664485	671.335881	1340.680469	670.843873	13
7	791.360382	396.183829	774.333833	387.670554	773.349817	387.178546	S	*1230.632456*	615.819866	1213.605907	607.306592	1212.621891	606.814584	12
8	888.413146	444.710211	871.386597	436.196936	870.402581	435.704928	P	*1143.600428*	572.303852	1126.573879	563.790578	1125.589863	563.298569	11
9	1003.440089	502.223683	986.413540	493.710408	985.429524	493.218400	D	1046.547664	523.777470	1029.521115	515.264196	1028.537099	514.772187	10
10	1090.472117	545.739697	1073.445568	537.226422	1072.461552	536.734414	S	*931.520721*	466.263999	914.494172	457.750724	913.510156	457.258716	9
11	1203.556181	602.281728	1186.529632	593.768454	1185.545616	593.276446	L	*844.488693*	422.747985	827.462144	414.234710	826.478128	413.742702	8
12	1274.593295	637.800285	1257.566746	629.287011	1256.582730	628.795003	A	*731.404629*	366.205953	714.378080	357.692678	713.394064	357.200670	7
13	1373.661709	687.334493	1356.635160	678.821218	1355.651144	678.329210	V	*660.367515*	330.687396	643.340966	322.174121	642.356950	321.682113	6
14	1460.693737	730.850507	1443.667188	722.337232	1442.683172	721.845224	S	*561.299101*	281.153189	544.272552	272.639914	543.288536	272.147906	5
15	1573.777801	787.392539	1556.751252	778.879264	1555.767236	778.387256	L	474.267073	237.637174	457.240524	229.123900	456.256508	228.631892	4
16	1630.799265	815.903270	1613.772716	807.389996	1612.788700	806.897988	G	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
17	1759.841858	880.424567	1742.815309	871.911293	1741.831293	871.419285	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
18							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DIVMTQSPDSLAVSLGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.2	1932.946259	-0.002391	DIVMTQSPDSLAVSLGER
19.1	1932.946259	-0.002391	DIVMTQSPDSLAVSLGER
7.4	1932.932968	0.010900	HPHSEQYPDLLPLEAR
4.1	1932.958160	-0.014292	GIVVTAYSPLGSPDRPWA
3.6	1932.946915	-0.003047	EDPFPEEVFPAVQGKTK
2.8	1932.962860	-0.018992	GARCSTKPRPPPGPWDVP
1.9	1932.928482	0.015386	VEVAQLNDVMDTMLERA
1.4	1932.961517	-0.017649	AGFDGIVVCEVPNNKLDK
0.5	1932.940384	0.003484	MPLTPEPPSGRVEGPPAW
0.4	1932.935013	0.008855	ECSLQVPEDELVSTLKQ

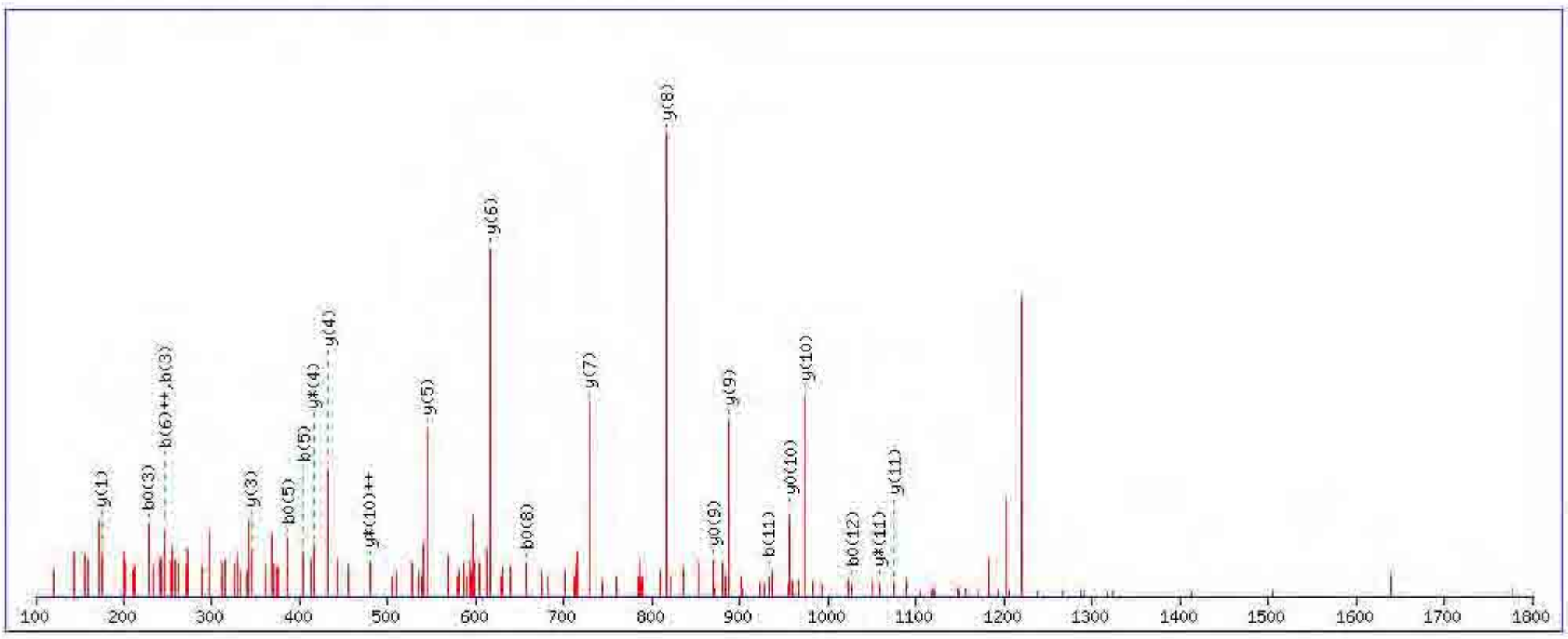
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGTSASLAISGLR**
Found in **LV102_HUMAN**, Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1

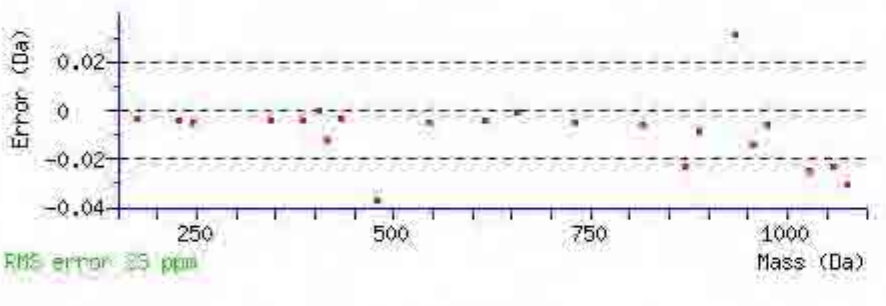
Match to Query 7597: 1218.655728 from(610.335140,2+) rtinseconds(1362) index(12335)
Title: Locus:1.1.1.814.9
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

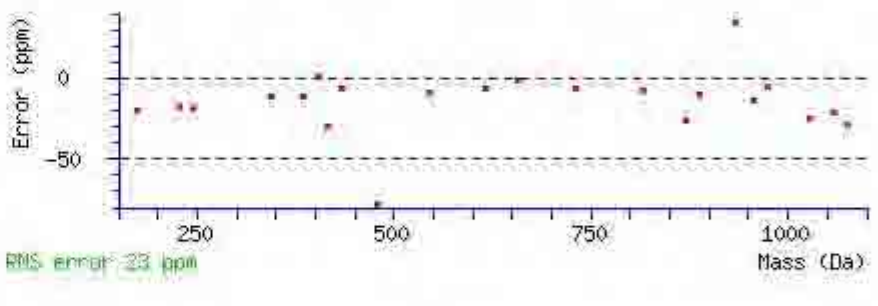
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1218.656799
Ions Score: 47 Expect: 0.0028
Matches : 23/114 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	145.060768	73.034022	127.050203	64.028740	G	1132.632063	566.819669	1115.605514	558.306395	1114.621498	557.814387	12
3	246.108447	123.557862	228.097882	114.552579	T	*1075.610599*	538.308937	1058.584050	529.795663	1057.600034	529.303655	11
4	333.140475	167.073875	315.129910	158.068593	S	*974.562920*	487.785098	957.536371	479.271823	956.552355	478.779815	10
5	404.177589	202.592432	386.167024	193.587150	A	*887.530892*	444.269084	870.504343	435.755809	869.520327	435.263801	9
6	491.209617	246.108446	473.199052	237.103164	S	*816.493778*	408.750527	799.467229	400.237252	798.483213	399.745244	8
7	604.293681	302.650479	586.283116	293.645196	L	*729.461750*	365.234513	712.435201	356.721238	711.451185	356.229230	7
8	675.330795	338.169036	657.320230	329.163753	A	*616.377686*	308.692481	599.351137	300.179206	598.367121	299.687198	6
9	788.414859	394.711068	770.404294	385.705785	I	*545.340572*	273.173924	528.314023	264.660649	527.330007	264.168641	5
10	875.446887	438.227082	857.436322	429.221799	S	*432.256508*	216.631892	415.229959	208.118617	414.245943	207.626609	4
11	932.468351	466.737814	914.457786	457.732531	G	*345.224480*	173.115878	328.197931	164.602603			3
12	1045.552415	523.279845	1027.541850	514.274563	L	288.203016	144.605146	271.176467	136.091871			2
13					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SGTSASLAISGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.2	1218.656799	-0.001071	SGTSASLAISGLR
18.9	1218.645554	0.010174	QLLISSSSASNL
17.8	1218.645554	0.010174	LNLSSTSPEKK
14.5	1218.645599	0.010129	QVPTSSVGTSIK
10.7	1218.660828	-0.005100	PNGLAFISSGLK
9.8	1218.646912	0.008816	PARGSFLSAGTR
9.1	1218.660828	-0.005100	INLPDKNVPPP
7.4	1218.660828	-0.005100	QLVKFSLDAAAG
7.2	1218.654297	0.001431	MGKSLSHLPLH
6.9	1218.656799	-0.001071	ILKSVTEGASAR

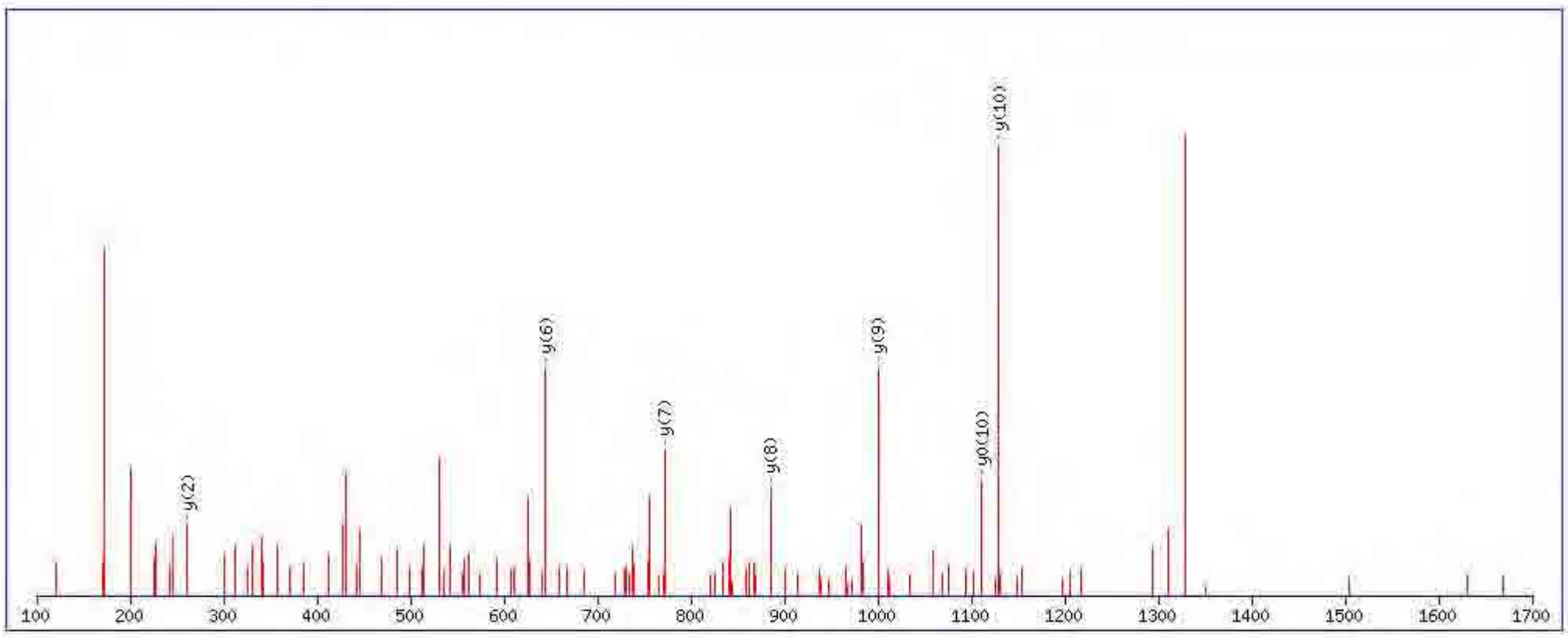
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAEDLQVGQVEL**
Found in **INS_HUMAN**, Insulin OS=Homo sapiens GN=INS PE=1 SV=1

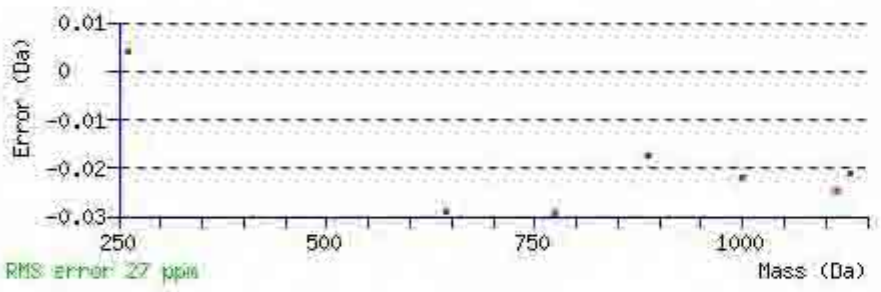
Match to Query 10691: 1328.657748 from(665.336150,2+) rtinseconds(1371) index(12459)
Title: Locus:1.1.1.819.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

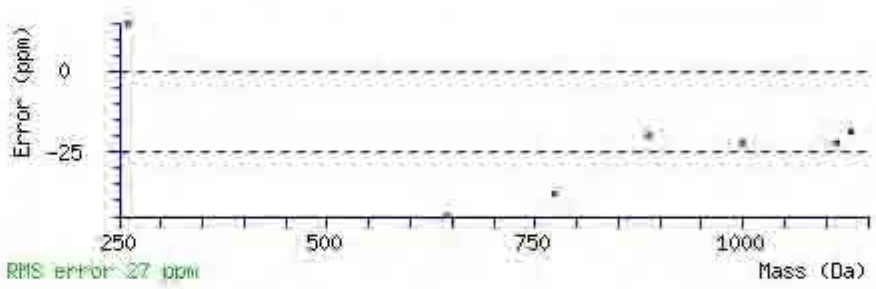
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1328.645966
Ions Score: 42 **Expect:** 0.0046
Matches : 7/114 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	201.086983	101.047130			183.076418	92.041847	A	1200.610660	600.808968	1183.584111	592.295694	1182.600095	591.803686	11
3	330.129576	165.568426			312.119011	156.563144	E	*1129.573546*	565.290411	1112.546997	556.777136	1111.562981	556.285128	10
4	445.156519	223.081898			427.145954	214.076615	D	*1000.530953*	500.769115	983.504404	492.255840	982.520388	491.763832	9
5	558.240583	279.623930			540.230018	270.618647	L	*885.504010*	443.255643	868.477461	434.742368	867.493445	434.250360	8
6	686.299161	343.653219	669.272612	335.139944	668.288596	334.647936	Q	*772.419946*	386.713611	755.393397	378.200336	754.409381	377.708328	7
7	785.367575	393.187426	768.341026	384.674151	767.357010	384.182143	V	*644.361368*	322.684322	627.334819	314.171047	626.350803	313.679039	6
8	842.389039	421.698158	825.362490	413.184883	824.378474	412.692875	G	545.292954	273.150115	528.266405	264.636841	527.282389	264.144833	5
9	970.447617	485.727447	953.421068	477.214172	952.437052	476.722164	Q	488.271490	244.639383	471.244941	236.126108	470.260925	235.634100	4
10	1069.516031	535.261654	1052.489482	526.748379	1051.505466	526.256371	V	360.212912	180.610094			342.202347	171.604811	3
11	1198.558624	599.782950	1181.532075	591.269676	1180.548059	590.777668	E	*261.144498*	131.075887			243.133933	122.070604	2
12							L	132.101905	66.554590					1





NCBI **BLAST** search of EAEDLQVGQVEL
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1328.645966	0.011782	EAEDLQVGQVEL
16.0	1328.645950	0.011798	SLDEISQPAQEL
14.8	1328.657196	0.000552	ENTSVLQQNPSL
14.3	1328.645981	0.011767	LSPPPSQSDQLL
13.6	1328.645966	0.011782	AEASATLTVQEPP
13.6	1328.645966	0.011782	AEASATLTVQEPP
11.9	1328.664597	-0.006849	MLAGPASGAPSPLL
11.8	1328.664581	-0.006833	MSLPPPKASPEK
11.1	1328.653366	0.004382	LPEMTAPLPPLS
9.0	1328.664597	-0.006849	MLAGPASGAPSPLL

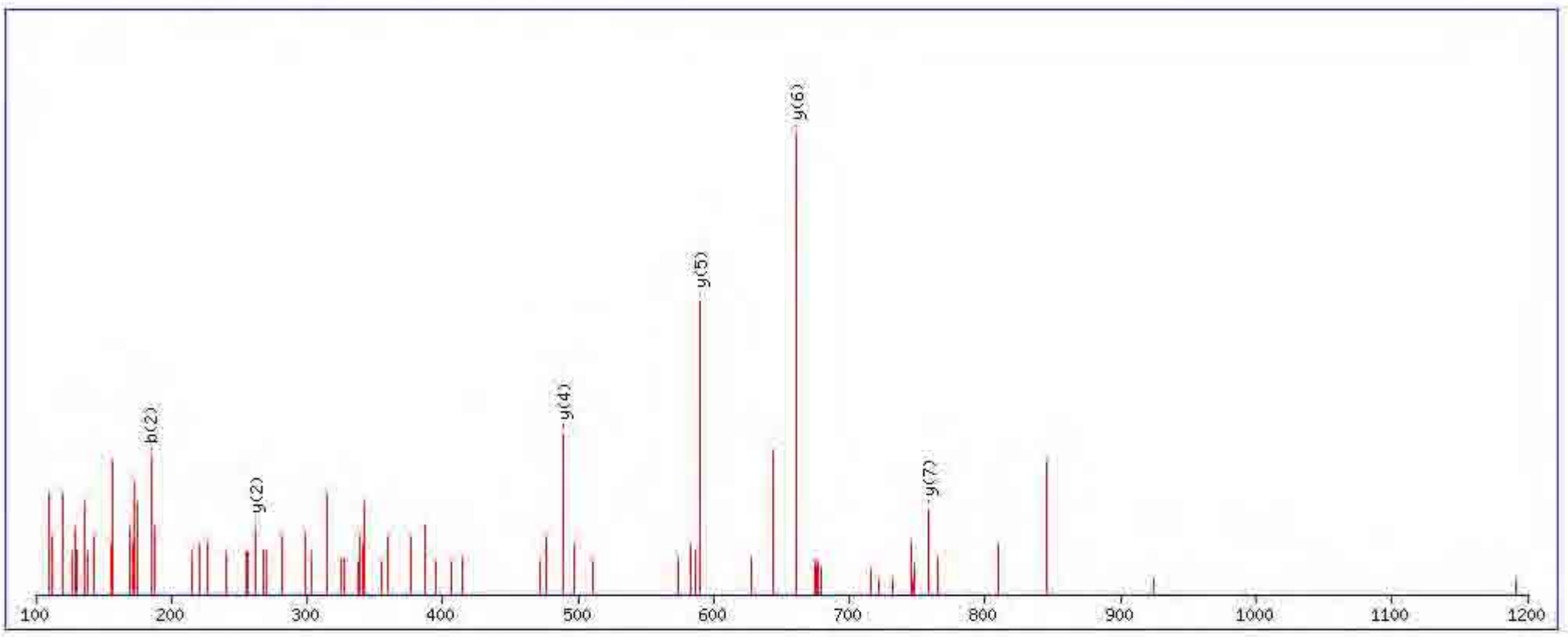
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPATVQSR**
Found in **K1C23_HUMAN**, Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2

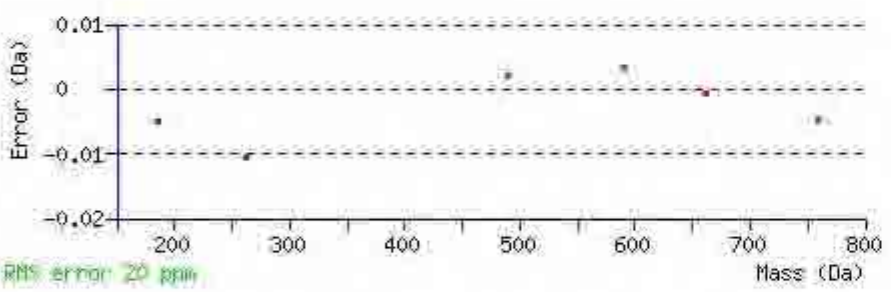
Match to Query 989: 844.436948 from(423.225750,2+) rtinseconds(809) index(5955)
Title: Locus:1.1.1.502.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

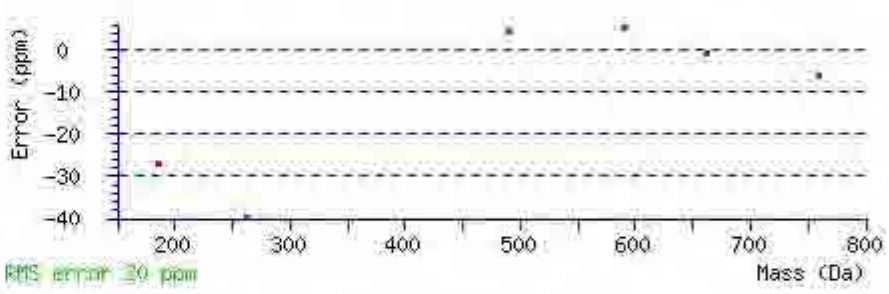
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 844.440277
Ions Score: 46 **Expect:** 0.0083
Matches : 6/72 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	185.092068	93.049672			167.081503	84.044389	P	*758.415529*	379.711403	741.388980	371.198128	740.404964	370.706120	7
3	256.129182	128.568229			238.118617	119.562947	A	*661.362765*	331.185021	644.336216	322.671746	643.352200	322.179738	6
4	357.176861	179.092068			339.166296	170.086786	T	*590.325651*	295.666464	573.299102	287.153189	572.315086	286.661181	5
5	456.245275	228.626275			438.234710	219.620993	V	*489.277972*	245.142624	472.251423	236.629350	471.267407	236.137342	4
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	Q	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
7	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPATVQSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	844.440277	-0.003329	SPATVQSR
29.2	844.440262	-0.003314	SPATADKR
15.2	844.429016	0.007932	SPASLNEK
15.2	844.440262	-0.003314	SPASSLQR
15.2	844.429031	0.007917	ALASQLQD
14.6	844.429031	0.007917	SPAASPATK
13.0	844.440262	-0.003314	SAPPSKSR
12.0	844.440262	-0.003314	SAPSAVARS
10.6	844.440262	-0.003314	IANLGDSR
9.6	844.429031	0.007917	APSTSSPAK

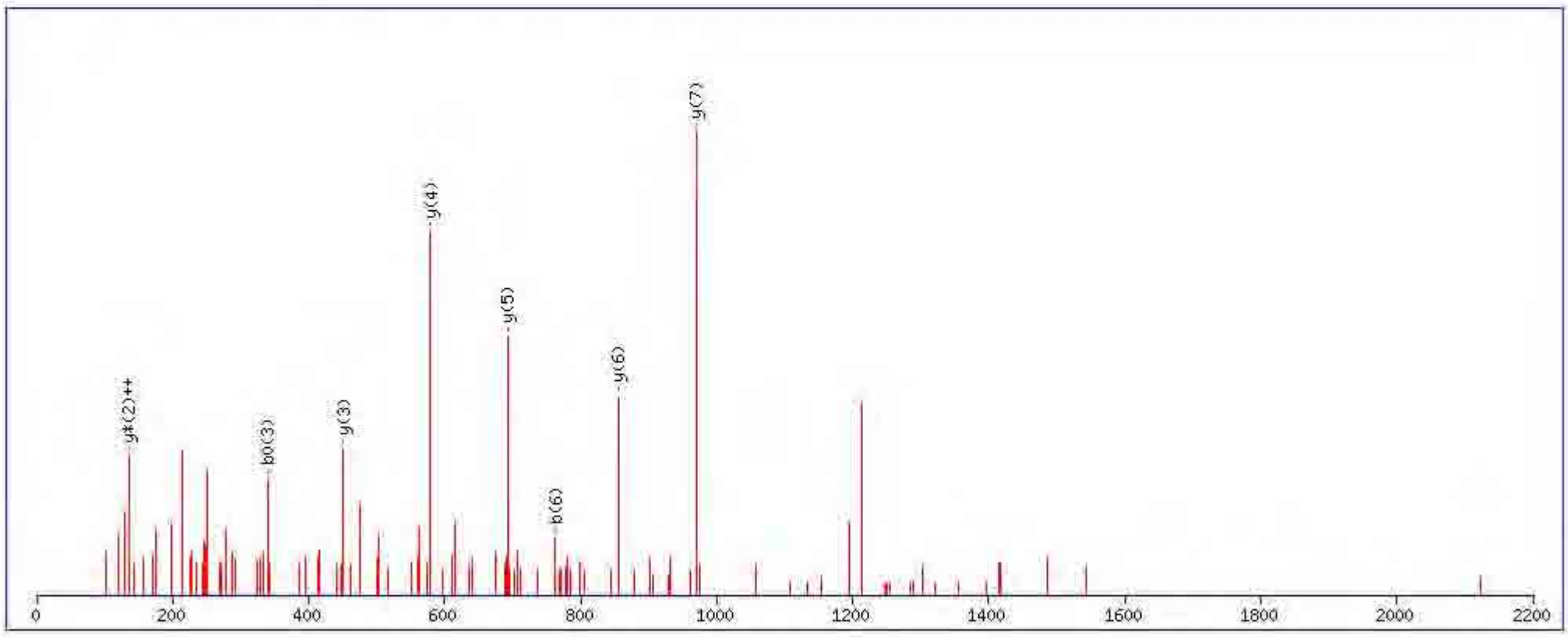
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIDYIQYLR**
Found in **OLFL1_HUMAN**, Olfactomedin-like protein 1 OS=Homo sapiens GN=OLFML1 PE=1 SV=2

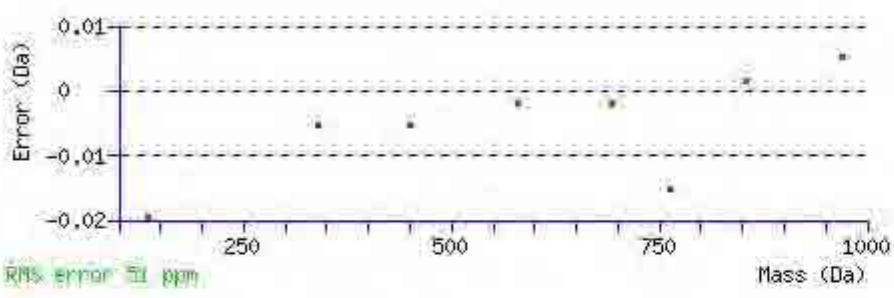
Match to Query 7413: 1211.617068 from(606.815810,2+) rtinseconds(1926) index(19789)
Title: Locus:1.1.1.1124.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

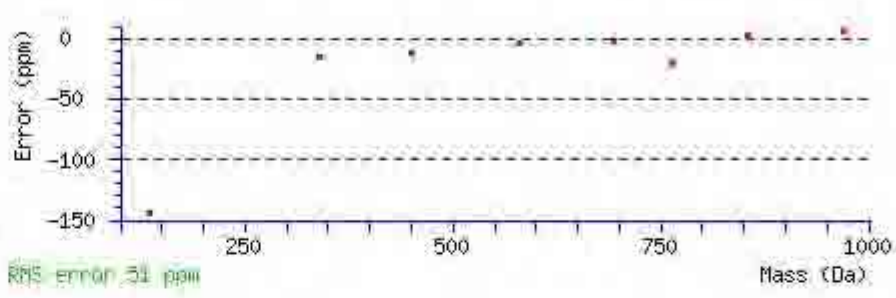
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1211.618607
Ions Score: 33 **Expect:** 0.0033
Matches : 8/74 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							9
2	243.133933	122.070605			225.123368	113.065322	I	1083.583323	542.295300	1066.556774	533.782025	1065.572758	533.290017	8
3	358.160876	179.584076			340.150311	170.578794	D	*970.499259*	485.753267	953.472710	477.239993	952.488694	476.747985	7
4	521.224205	261.115741			503.213640	252.110458	Y	*855.472316*	428.239796	838.445767	419.726521			6
5	634.308269	317.657773			616.297704	308.652490	I	*692.408987*	346.708131	675.382438	338.194857			5
6	762.366847	381.687062	745.340298	373.173787	744.356282	372.681779	Q	*579.324923*	290.166099	562.298374	281.652825			4
7	925.430176	463.218726	908.403627	454.705452	907.419611	454.213444	Y	*451.266345*	226.136810	434.239796	217.623536			3
8	1038.514240	519.760758	1021.487691	511.247483	1020.503675	510.755475	L	288.203016	144.605146	271.176467	136.091871			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIDYIQYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	1211.618607	-0.001539	EIDYIQYLR
6.4	1211.608078	0.008990	CLQQLLRDSH
6.3	1211.615967	0.001101	TPGGHPKPPHR
3.1	1211.614594	0.002474	KISHIAEQSPS
2.3	1211.625839	-0.008771	QNPLERLGTGGA
2.2	1211.614594	0.002474	LTNLHGAASLSE
1.0	1211.607391	0.009677	TIPYSDKLFE
0.3	1211.607407	0.009661	LTSIFPIAYDG

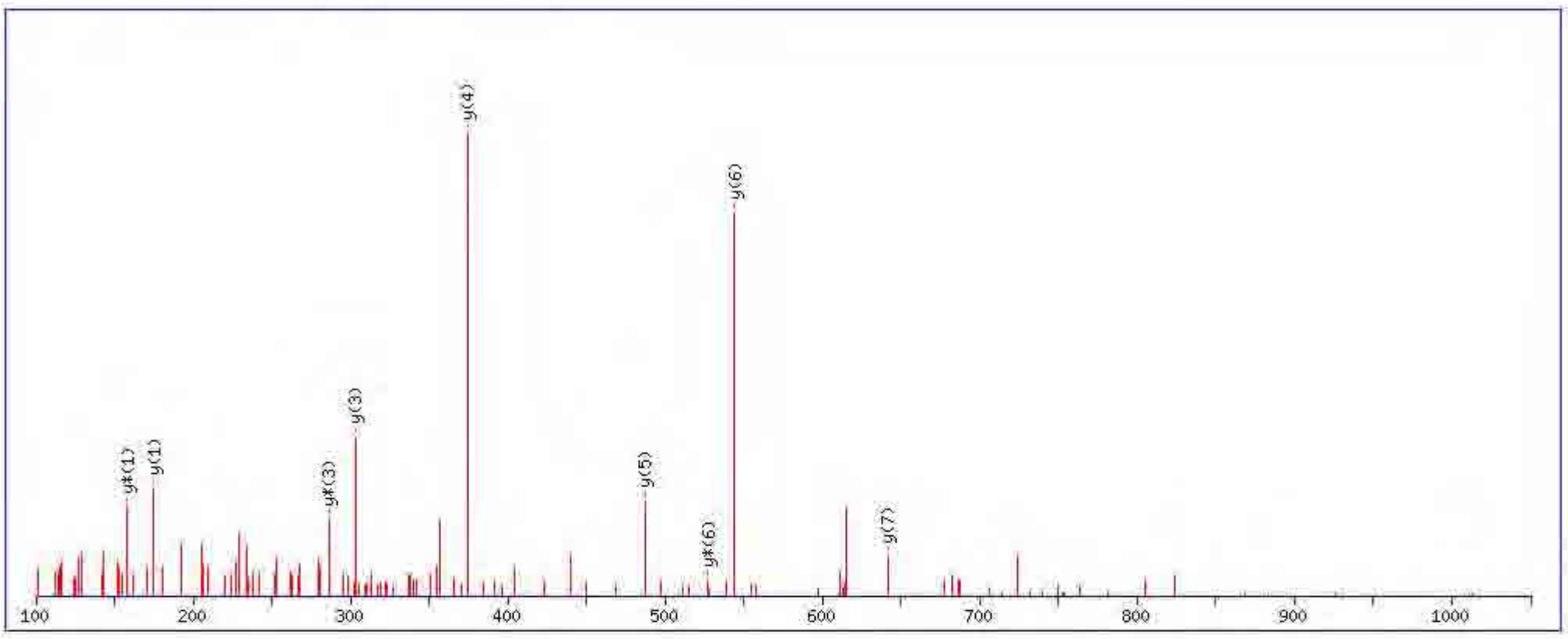
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PSPGPAAGR**
Found in **OTU7A_HUMAN**, OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=1 SV=1

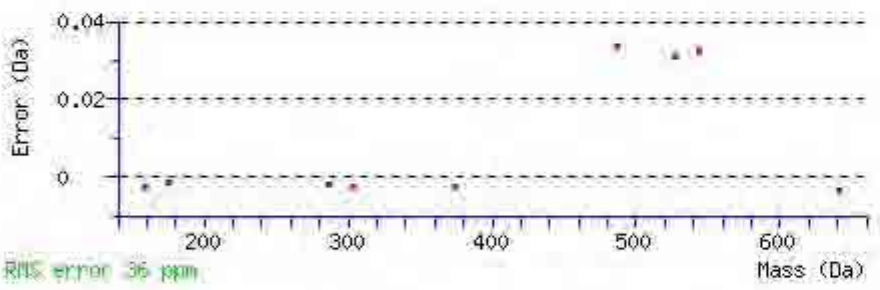
Match to Query 943: 840.413988 from(421.214270,2+) rtinseconds(342) index(639)
Title: Locus:1.1.1.239.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

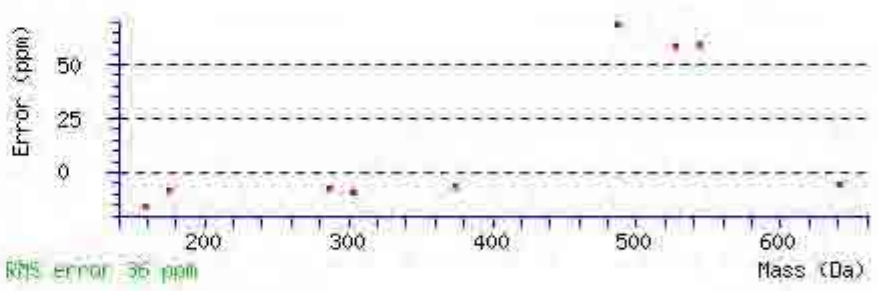
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 840.408981
Variable modifications:
P1 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 46 **Expect:** 0.0032
Matches : 9/64 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116			P							9
2	201.086983	101.047129	183.076418	92.041847	S	728.368579	364.687928	711.342030	356.174653	710.358014	355.682645	8
3	298.139747	149.573512	280.129182	140.568229	P	*641.336551*	321.171914	624.310002	312.658639			7
4	355.161211	178.084243	337.150646	169.078961	G	*544.283787*	272.645532	527.257238	264.132257			6
5	468.208890	234.608083	450.198325	225.602800	P	*487.262323*	244.134799	470.235774	235.621525			5
6	539.246004	270.126640	521.235439	261.121357	A	*374.214644*	187.610960	357.188095	179.097685			4
7	610.283118	305.645197	592.272553	296.639914	A	*303.177530*	152.092403	286.150981	143.579128			3
8	667.304582	334.155929	649.294017	325.150646	G	232.140416	116.573846	215.113867	108.060571			2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PSPGPAAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	840.408981	0.005007	PSPGPAAGR
32.4	840.408966	0.005022	EPAGAPQR
32.2	840.408981	0.005007	PSPGPAAGR
31.5	840.408981	0.005007	PPAPGAQR
31.2	840.408981	0.005007	PSGPPAGAR
30.9	840.408981	0.005007	PPAGSPAGR
22.4	840.408966	0.005022	PEASPGQR
19.9	840.408966	0.005022	EAPQPQR
19.9	840.408981	0.005007	SPPPQQR
19.8	840.408981	0.005007	PSGPPAGAR

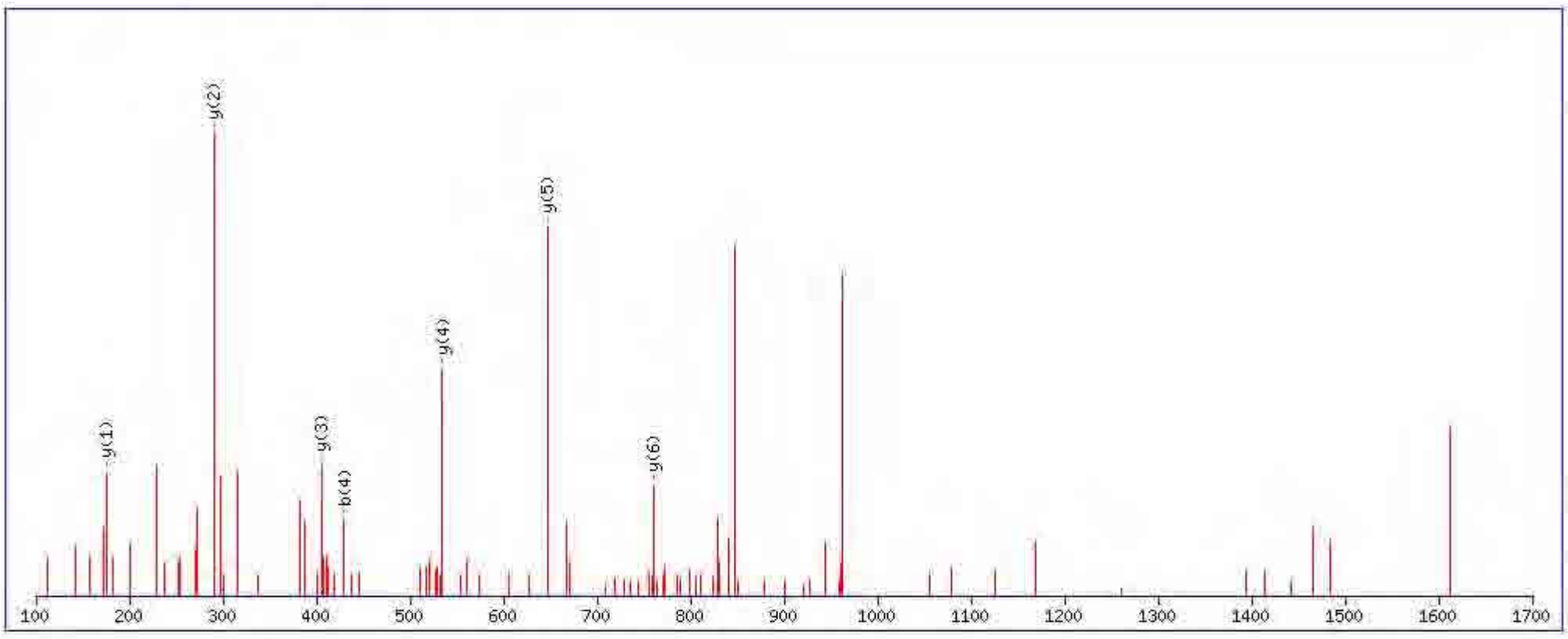
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTVIIEDDR**
Found in **PARD3_HUMAN**, Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2

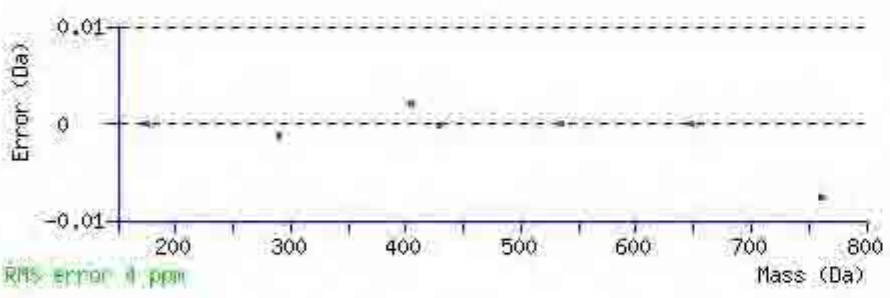
Match to Query 4360: 1074.522428 from(538.268490,2+) rtinseconds(1227) index(10542)
Title: Locus:1.1.1.739.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

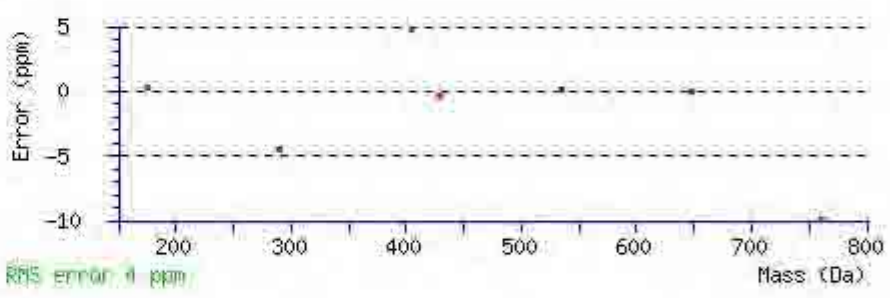
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.519318
Ions Score: 44 **Expect:** 0.0083
Matches : 7/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	217.081898	109.044587	199.071333	100.039304	T	960.499652	480.753464	943.473103	472.240190	942.489087	471.748182	8
3	316.150312	158.578794	298.139747	149.573512	V	859.451973	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	429.234376	215.120826	411.223811	206.115544	I	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
5	542.318440	271.662858	524.307875	262.657576	I	*647.299495*	324.153386	630.272946	315.640111	629.288930	315.148103	5
6	671.361033	336.184155	653.350468	327.178872	E	*534.215431*	267.611354	517.188882	259.098079	516.204866	258.606071	4
7	786.387976	393.697626	768.377411	384.692343	D	*405.172838*	203.090057	388.146289	194.576782	387.162273	194.084774	3
8	901.414919	451.211097	883.404354	442.205815	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DTVIIEDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	1074.519318	0.003110	DTVIIEDDR
31.9	1074.526688	-0.004260	LDSMAIEALP
29.4	1074.519287	0.003141	LEEGLEETR
24.9	1074.523331	-0.000903	EKLYPPSPP
22.8	1074.526703	-0.004275	GSPMEISLPI
19.1	1074.526688	-0.004260	LDSMAIEALP
18.8	1074.512772	0.009656	NSLNPEVMR
17.1	1074.523331	-0.000903	EKLYPPSPP
17.1	1074.513443	0.008985	PEWLDFPR
16.7	1074.520645	0.001783	LWTRNDDR

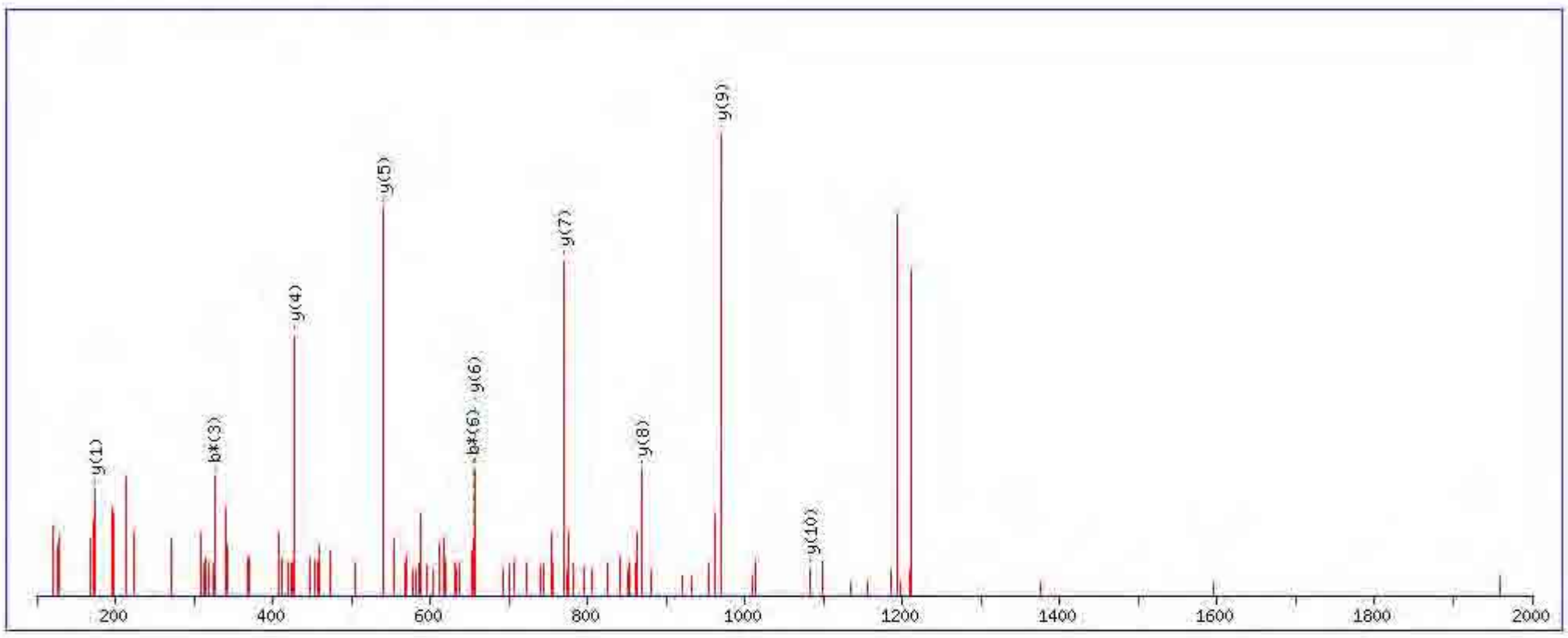
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QITVNDLPVGR**
Found in **PRDX1_HUMAN**, Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

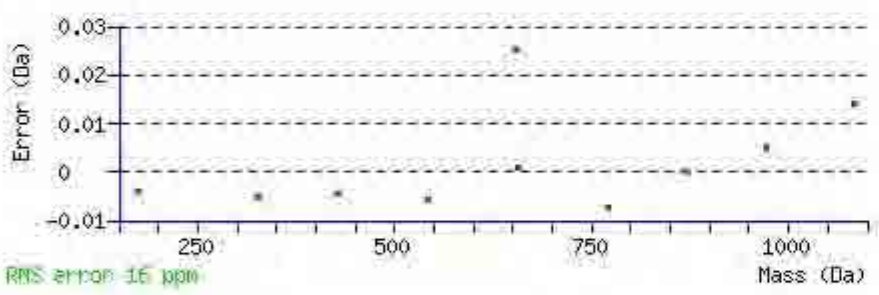
Match to Query 7391: 1210.663388 from(606.338970,2+) rtinseconds(1458) index(13586)
Title: Locus:1.1.1.867.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

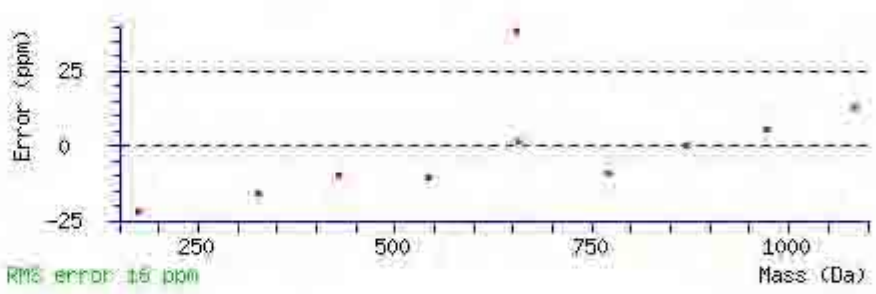
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1210.666992
Ions Score: 49 **Expect:** 0.00086
Matches : 10/106 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	242.149918	121.578597	225.123369	113.065323			I	*1083.615685*	542.311481	1066.589136	533.798206	1065.605120	533.306198	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	*970.531621*	485.769449	953.505072	477.256174	952.521056	476.764166	9
4	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	V	*869.483942*	435.245609	852.457393	426.732335	851.473377	426.240327	8
5	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	N	*770.415528*	385.711402	753.388979	377.198128	752.404963	376.706120	7
6	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	D	*656.372601*	328.689939	639.346052	320.176664	638.362036	319.684656	6
7	784.419945	392.713611	767.393396	384.200336	766.409380	383.708328	L	*541.345658*	271.176467	524.319109	262.663193			5
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	P	*428.261594*	214.634435	411.235045	206.121160			4
9	980.541123	490.774200	963.514574	482.260925	962.530558	481.768917	V	331.208830	166.108053	314.182281	157.594778			3
10	1037.562587	519.284932	1020.536038	510.771657	1019.552022	510.279649	G	232.140416	116.573846	215.113867	108.060571			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QITVNDLPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	1210.666992	-0.003604	QITVNDLPVGR
15.2	1210.657059	0.006329	KPEHYRLPR
10.0	1210.666977	-0.003589	LGKELQTGTHK
8.3	1210.667007	-0.003619	QVITPPTVGQR
7.7	1210.666992	-0.003604	KTLVPGPPGSSR
7.7	1210.666992	-0.003604	KTLVPGPPGSSR
7.3	1210.666992	-0.003604	QLTPGGGPLSLR
7.3	1210.666992	-0.003604	QPVQKGVKPQA
7.1	1210.667007	-0.003619	QVITPPTVGQR
7.1	1210.674362	-0.010974	KITEVALMGHL

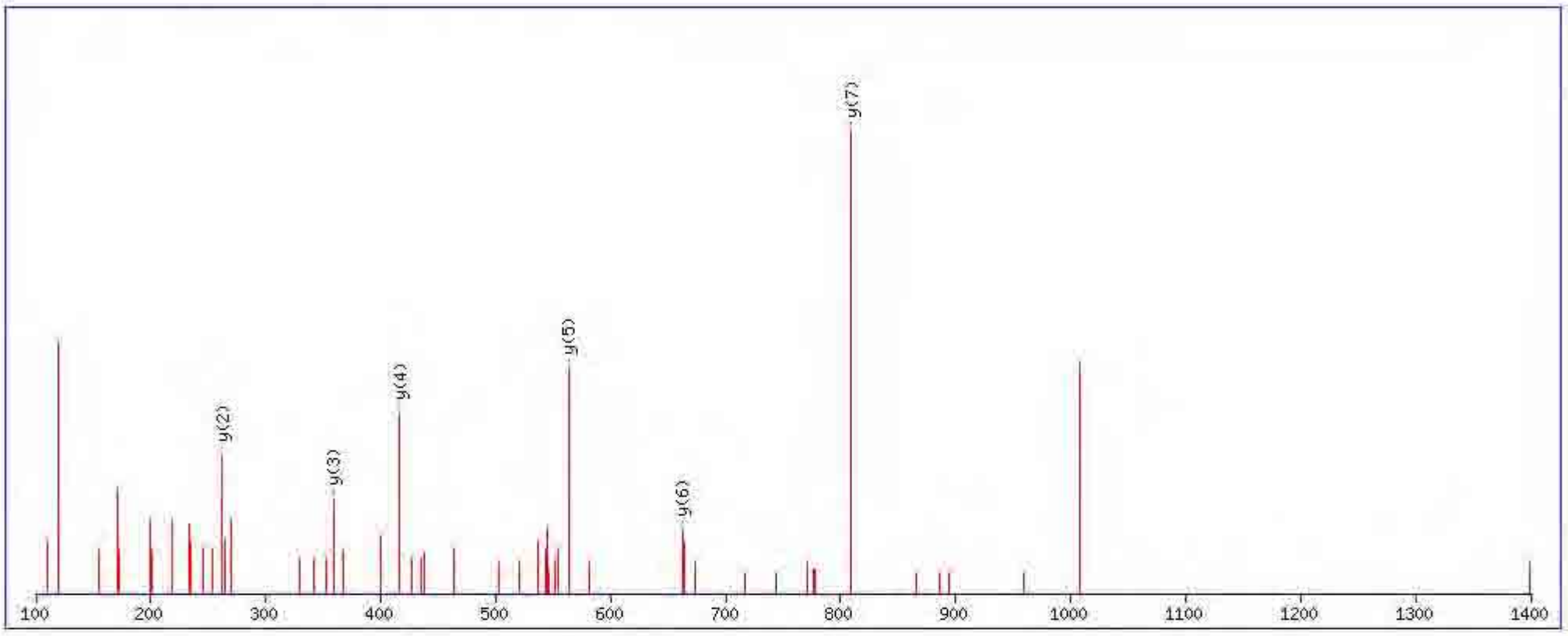
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVFVFGPDK**
Found in **PRDX6_HUMAN**, Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3

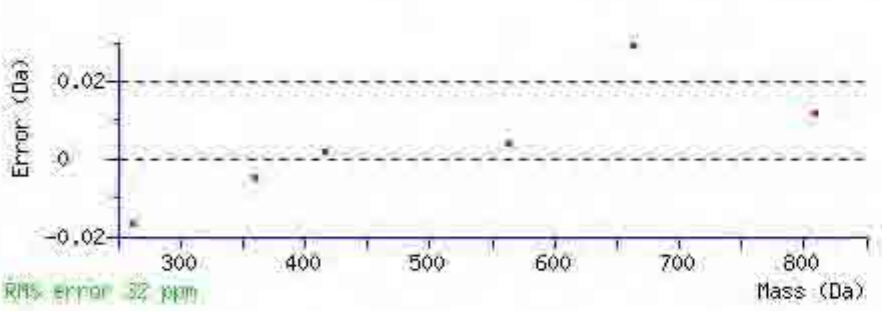
Match to Query 3214: 1006.548328 from(504.281440,2+) rtinseconds(1686) index(16584)
Title: Locus:1.1.1.994.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

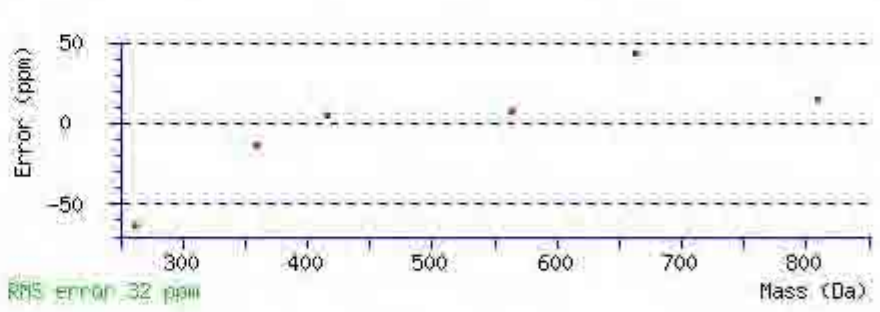
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1006.548798
Ions Score: 48 **Expect:** 0.0001
Matches : 6/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	199.144104	100.075690			V	908.487631	454.747454	891.461082	446.234179	890.477066	445.742171	8
3	346.212518	173.609897			F	*809.419217*	405.213247	792.392668	396.699972	791.408652	396.207964	7
4	445.280932	223.144104			V	*662.350803*	331.679040	645.324254	323.165765	644.340238	322.673757	6
5	592.349346	296.678311			F	*563.282389*	282.144833	546.255840	273.631558	545.271824	273.139550	5
6	649.370810	325.189043			G	*416.213975*	208.610626	399.187426	200.097351	398.203410	199.605343	4
7	746.423574	373.715425			P	*359.192511*	180.099893	342.165962	171.586619	341.181946	171.094611	3
8	861.450517	431.228897	843.439952	422.223614	D	*262.139747*	131.573511	245.113198	123.060237	244.129182	122.568229	2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VVFVFGPDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	1006.548798	-0.000470	VVFVFGPDK
5.0	1006.555969	-0.007641	TPAQPLAPGR
1.6	1006.555969	-0.007641	INIPPQRGP

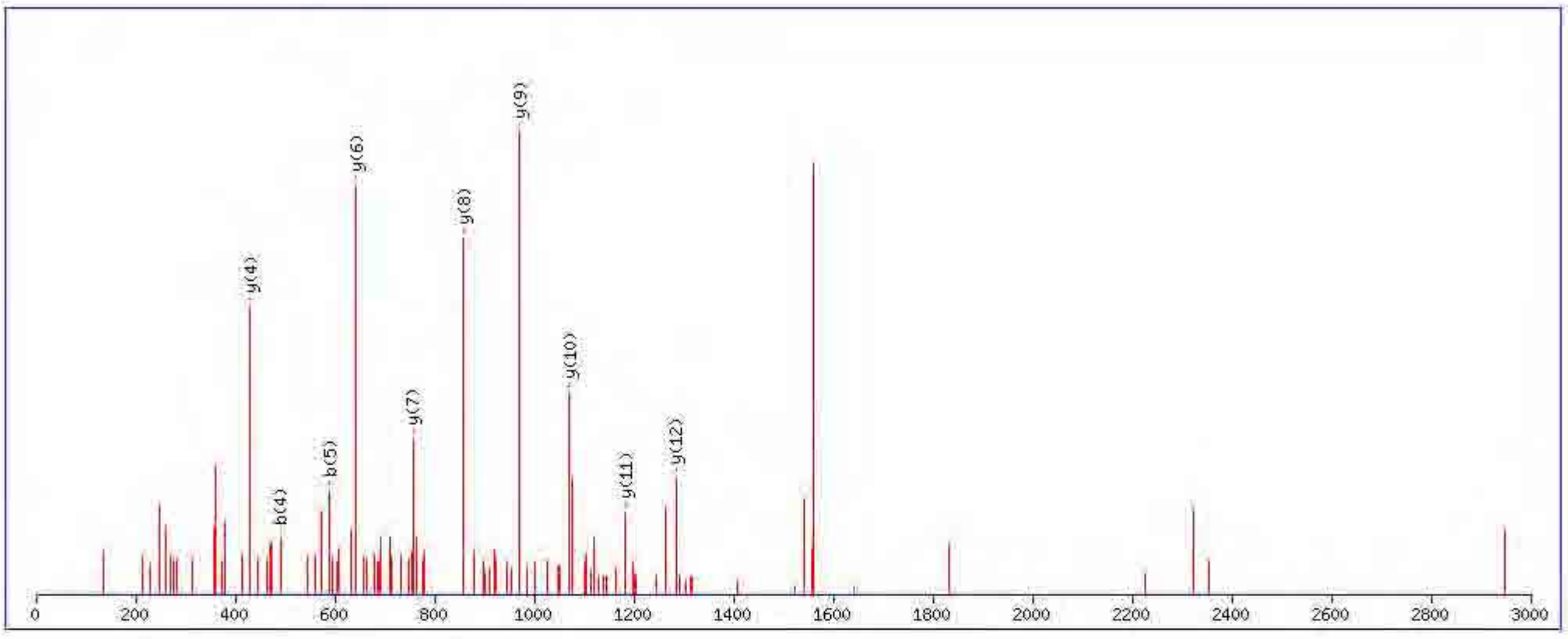
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYTLVLTDPDAPSR**
Found in **PEBP1_HUMAN**, Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3

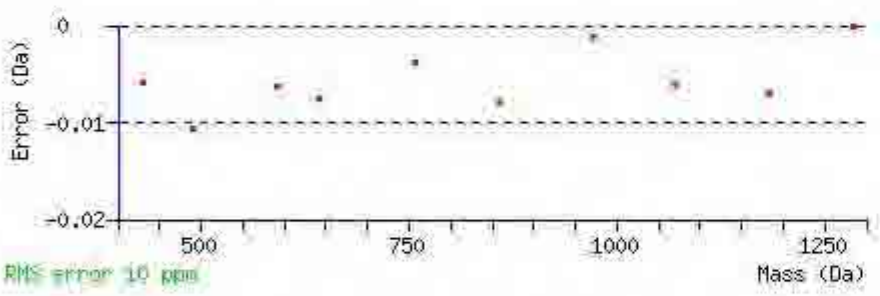
Match to Query 16245: 1559.805248 from(780.909900,2+) rtinseconds(1819) index(18350)
Title: Locus:1.1.1.1066.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

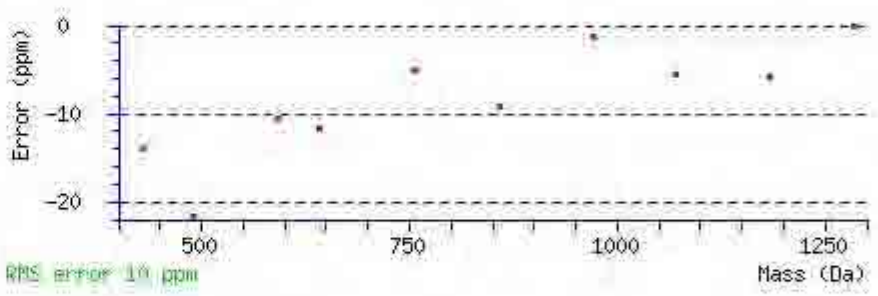
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1559.819519
Ions Score: 67 Expect: 2e-005
Matches : 10/124 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							14
2	277.154669	139.080973			Y	1447.742737	724.375007	1430.716188	715.861732	1429.732172	715.369724	13
3	378.202348	189.604812	360.191783	180.599530	T	*1284.679408*	642.843342	1267.652859	634.330068	1266.668843	633.838060	12
4	**491.286412**	246.146844	473.275847	237.141562	L	*1183.631729*	592.319503	1166.605180	583.806228	1165.621164	583.314220	11
5	**590.354826**	295.681051	572.344261	286.675769	V	*1070.547665*	535.777471	1053.521116	527.264196	1052.537100	526.772188	10
6	703.438890	352.223083	685.428325	343.217801	L	*971.479251*	486.243264	954.452702	477.729989	953.468686	477.237981	9
7	804.486569	402.746923	786.476004	393.741640	T	*858.395187*	429.701232	841.368638	421.187957	840.384622	420.695949	8
8	919.513512	460.260394	901.502947	451.255112	D	*757.347508*	379.177392	740.320959	370.664118	739.336943	370.172110	7
9	1016.566276	508.786776	998.555711	499.781494	P	*642.320565*	321.663921	625.294016	313.150646	624.310000	312.658638	6
10	1131.593219	566.300248	1113.582654	557.294965	D	545.267801	273.137539	528.241252	264.624264	527.257236	264.132256	5
11	1202.630333	601.818805	1184.619768	592.813522	A	*430.240858*	215.624067	413.214309	207.110793	412.230293	206.618785	4
12	1299.683097	650.345187	1281.672532	641.339904	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
13	1386.715125	693.861201	1368.704560	684.855918	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LYTLVLTDPDAPSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.3	1559.819519	-0.014271	LYTLVLTDPDAPSR
16.1	1559.797745	0.007503	VTLRTACPLVDDNK
7.1	1559.794373	0.010875	QLHTAYSGLVSSLQG
6.7	1559.813004	-0.007756	TMFLVHLPLSTNR
6.4	1559.793045	0.012203	TPLTKDVSLLDLDD
2.9	1559.797729	0.007519	LLALTSSDLGCQPSR
2.6	1559.798401	0.006847	EFALGPVSGPQAFPK
2.4	1559.804260	0.000988	SQVVVEESILQSDK
1.3	1559.790527	0.014721	CEIKGTEPIIVDPF
1.1	1559.799088	0.006160	HHTTLITCHRAGLT

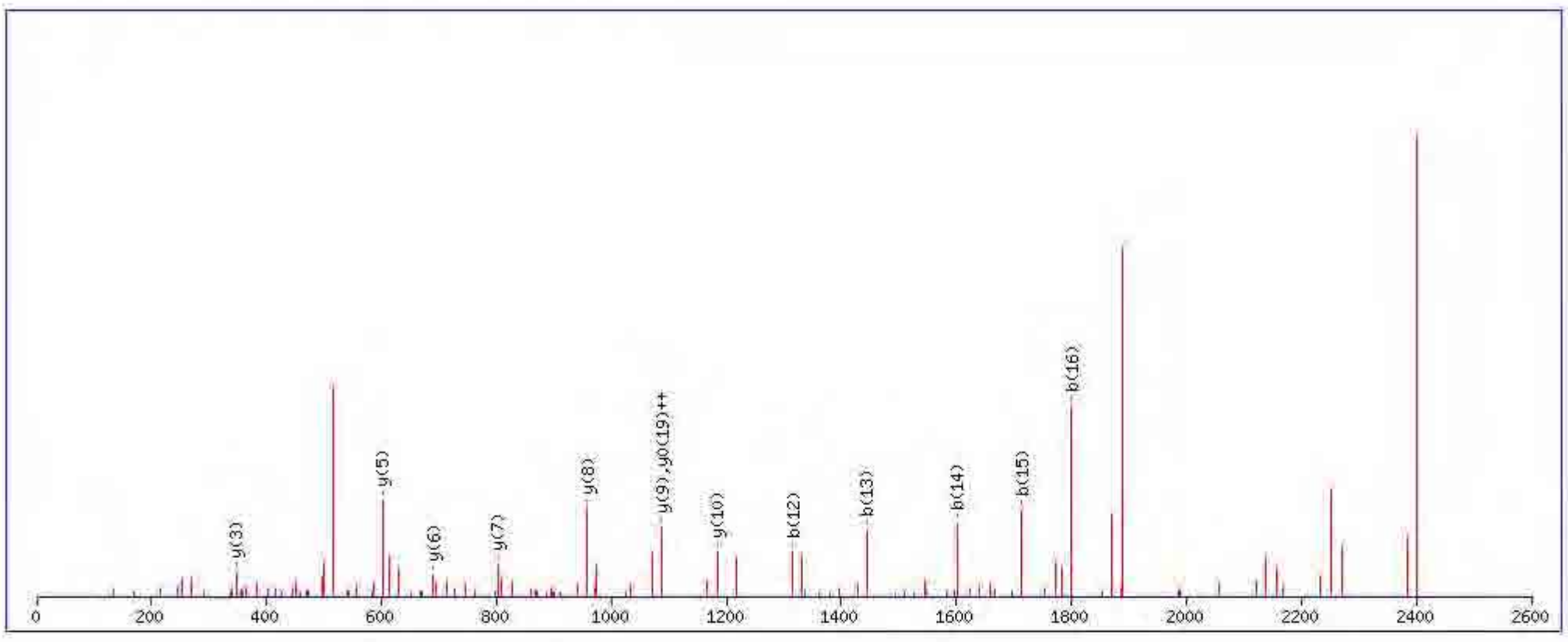
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPNHNMVSEVPPERPSVRATR**
Found in **PKHA6_HUMAN**, Pleckstrin homology domain-containing family A member 6 OS=Homo sapiens GN=PLEKHA6 PE=1 SV=4

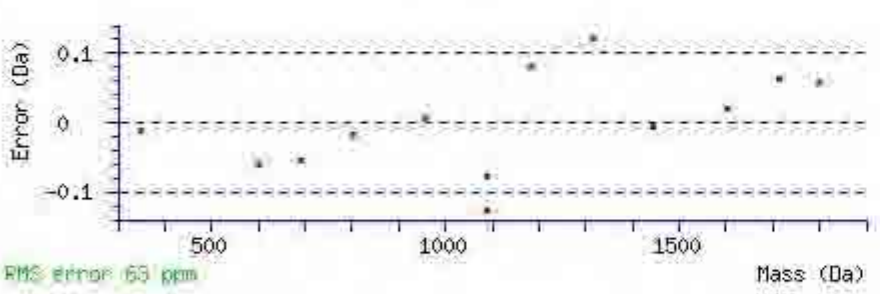
Match to Query 31351: 2401.239428 from(1201.626990,2+) rtinseconds(2917) index(32649)
Title: Locus:1.1.1.1651.25
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

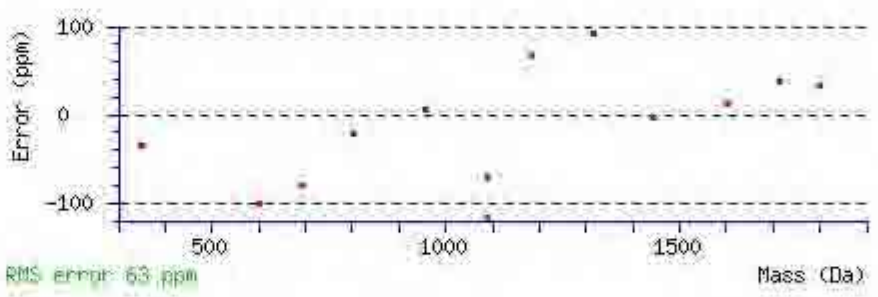
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 2401.228439
Variable modifications:
P15 : Oxidation (P)
Ions Score: 34 **Expect:** 0.0064
Matches : 13/220 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							21
2	211.144104	106.075690					P	2289.151673	1145.079474	2272.125124	1136.566200	2271.141108	1136.074192	20
3	325.187031	163.097153	308.160482	154.583879			N	2192.098909	1096.553092	2175.072360	1088.039818	2174.088344	1087.547810	19
4	462.245943	231.626609	445.219394	223.113335			H	2078.055982	1039.531629	2061.029433	1031.018354	2060.045417	1030.526346	18
5	576.288870	288.648073	559.262321	280.134798			N	1940.997070	971.002173	1923.970521	962.488899	1922.986505	961.996891	17
6	707.329355	354.168316	690.302806	345.655041			M	1826.954143	913.980710	1809.927594	905.467435	1808.943578	904.975427	16
7	806.397769	403.702522	789.371220	395.189248			V	1695.913658	848.460467	1678.887109	839.947193	1677.903093	839.455185	15
8	893.429797	447.218536	876.403248	438.705262	875.419232	438.213254	S	1596.845244	798.926260	1579.818695	790.412986	1578.834679	789.920978	14
9	1022.472390	511.739833	1005.445841	503.226558	1004.461825	502.734550	E	1509.813216	755.410246	1492.786667	746.896972	1491.802651	746.404964	13
10	1121.540804	561.274040	1104.514255	552.760766	1103.530239	552.268757	V	1380.770623	690.888950	1363.744074	682.375675	1362.760058	681.883667	12
11	1218.593568	609.800422	1201.567019	601.287148	1200.583003	600.795140	P	1281.702209	641.354743	1264.675660	632.841468	1263.691644	632.349460	11
12	**1315.646332**	658.326804	1298.619783	649.813530	1297.635767	649.321522	P	***1184.649445***	592.828361	1167.622896	584.315086	1166.638880	583.823078	10
13	**1444.688925**	722.848101	1427.662376	714.334826	1426.678360	713.842818	E	***1087.596681***	544.301979	1070.570132	535.788704	1069.586116	535.296696	9
14	**1600.790036**	800.898656	1583.763487	792.385382	1582.779471	791.893374	R	***958.554088***	479.780682	941.527539	471.267408	940.543523	470.775400	8
15	**1713.837715**	857.422496	1696.811166	848.909221	1695.827150	848.417213	P	***802.452977***	401.730127	785.426428	393.216852	784.442412	392.724844	7
16	**1800.869743**	900.938510	1783.843194	892.425235	1782.859178	891.933227	S	***689.405298***	345.206287	672.378749	336.693013	671.394733	336.201005	6
17	1899.938157	950.472717	1882.911608	941.959442	1881.927592	941.467434	V	***602.373270***	301.690273	585.346721	293.176999	584.362705	292.684991	5
18	2056.039268	1028.523272	2039.012719	1020.009998	2038.028703	1019.517990	R	503.304856	252.156066	486.278307	243.642791	485.294291	243.150783	4
19	2127.076382	1064.041829	2110.049833	1055.528554	2109.065817	1055.036547	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
20	2228.124061	1114.565668	2211.097512	1106.052394	2210.113496	1105.560386	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
21							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IPNHNMVSEVPPERPSVRATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	2401.228439	0.010989	IPNHNMVSEVPPERPSVRATR
9.7	2401.252899	-0.013471	ELEIHLWPSLEALDPGSLVGLN
9.7	2401.228439	0.010989	IPNHNMVSEVPPERPSVRATR
9.0	2401.253784	-0.014356	LVGLNVMCQLFLEPQLWSQLA
8.8	2401.239044	0.000384	PGSPGSPGLPGKPGPHGDLGFKGIK
5.5	2401.235184	0.004244	TPGPLPMLPPLIDPWDPGLTAR
5.2	2401.237656	0.001772	NKGEVFPTTEVLLQLASEALPN
4.8	2401.220596	0.018832	SGSGEVDLRECVVALSVVCRPAR
4.5	2401.219910	0.019518	TGSPAELCVVLNDEKVEGVWLK
4.0	2401.248871	-0.009443	DEPIFVGEISSSKPAISNILNR

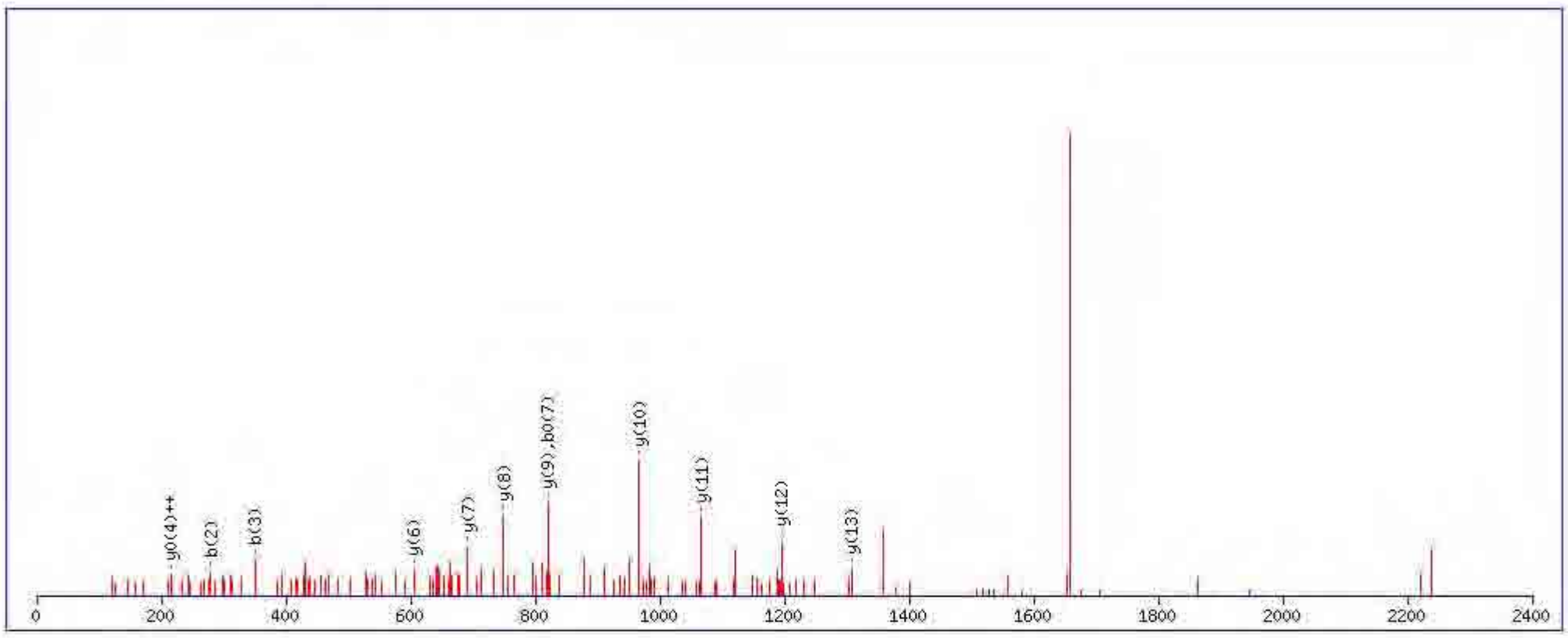
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDALEVFAGSGTSGQR**
Found in **PCOC1_HUMAN**, Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2

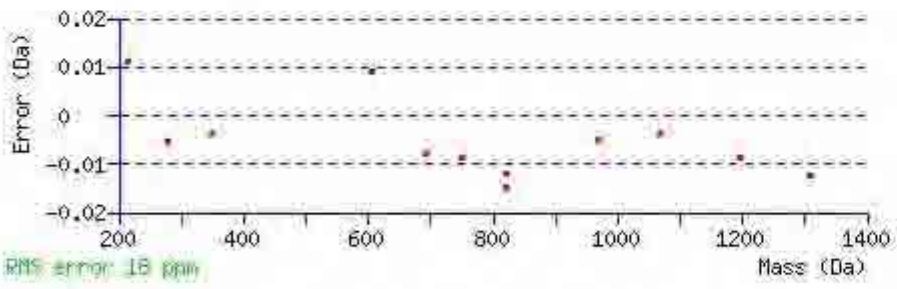
Match to Query 18385: 1656.777368 from(829.395960,2+) rtinseconds(1794) index(18006)
Title: Locus:1.1.1.1052.22
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

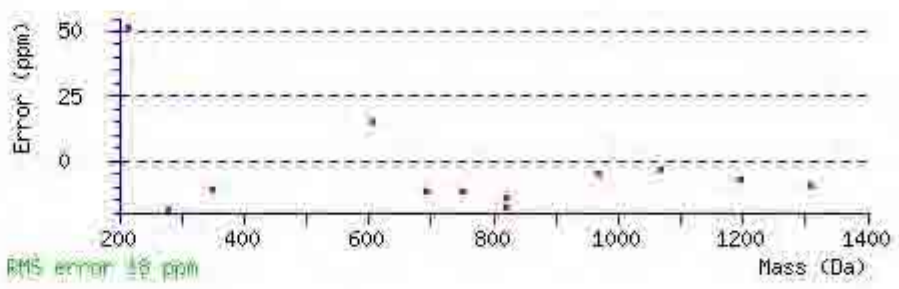
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1656.774368
Ions Score: 57 **Expect:** 7.6e-006
Matches : 12/144 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							16
2	279.097548	140.052412			261.086983	131.047130	D	1494.718313	747.862795	1477.691764	739.349520	1476.707748	738.857512	15
3	350.134662	175.570969			332.124097	166.565687	A	1379.691370	690.349323	1362.664821	681.836049	1361.680805	681.344041	14
4	463.218726	232.113001			445.208161	223.107719	L	*1308.654256*	654.830766	1291.627707	646.317492	1290.643691	645.825484	13
5	592.261319	296.634298			574.250754	287.629015	E	*1195.570192*	598.288734	1178.543643	589.775460	1177.559627	589.283452	12
6	691.329733	346.168505			673.319168	337.163222	V	*1066.527599*	533.767438	1049.501050	525.254163	1048.517034	524.762155	11
7	838.398147	419.702712			820.387582	410.697429	F	*967.459185*	484.233231	950.432636	475.719956	949.448620	475.227948	10
8	909.435261	455.221269			891.424696	446.215986	A	*820.390771*	410.699024	803.364222	402.185749	802.380206	401.693741	9
9	966.456725	483.732001			948.446160	474.726718	G	*749.353657*	375.180467	732.327108	366.667192	731.343092	366.175184	8
10	1053.488753	527.248015			1035.478188	518.242732	S	*692.332193*	346.669735	675.305644	338.156460	674.321628	337.664452	7
11	1110.510217	555.758747			1092.499652	546.753464	G	*605.300165*	303.153721	588.273616	294.640446	587.289600	294.148438	6
12	1211.557896	606.282586			1193.547331	597.277304	T	548.278701	274.642989	531.252152	266.129714	530.268136	265.637706	5
13	1298.589924	649.798600			1280.579359	640.793318	S	447.231022	224.119149	430.204473	215.605875	429.220457	215.113867	4
14	1355.611388	678.309332			1337.600823	669.304050	G	360.198994	180.603135	343.172445	172.089860			3
15	1483.669966	742.338621	1466.643417	733.825347	1465.659401	733.333339	Q	303.177530	152.092403	286.150981	143.579129			2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YDALEVFAGSGTSGQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	1656.774368	0.003000	YDALEVFAGSGTSGQR
2.3	1656.774399	0.002969	NSPQTPPGRDTPVFP

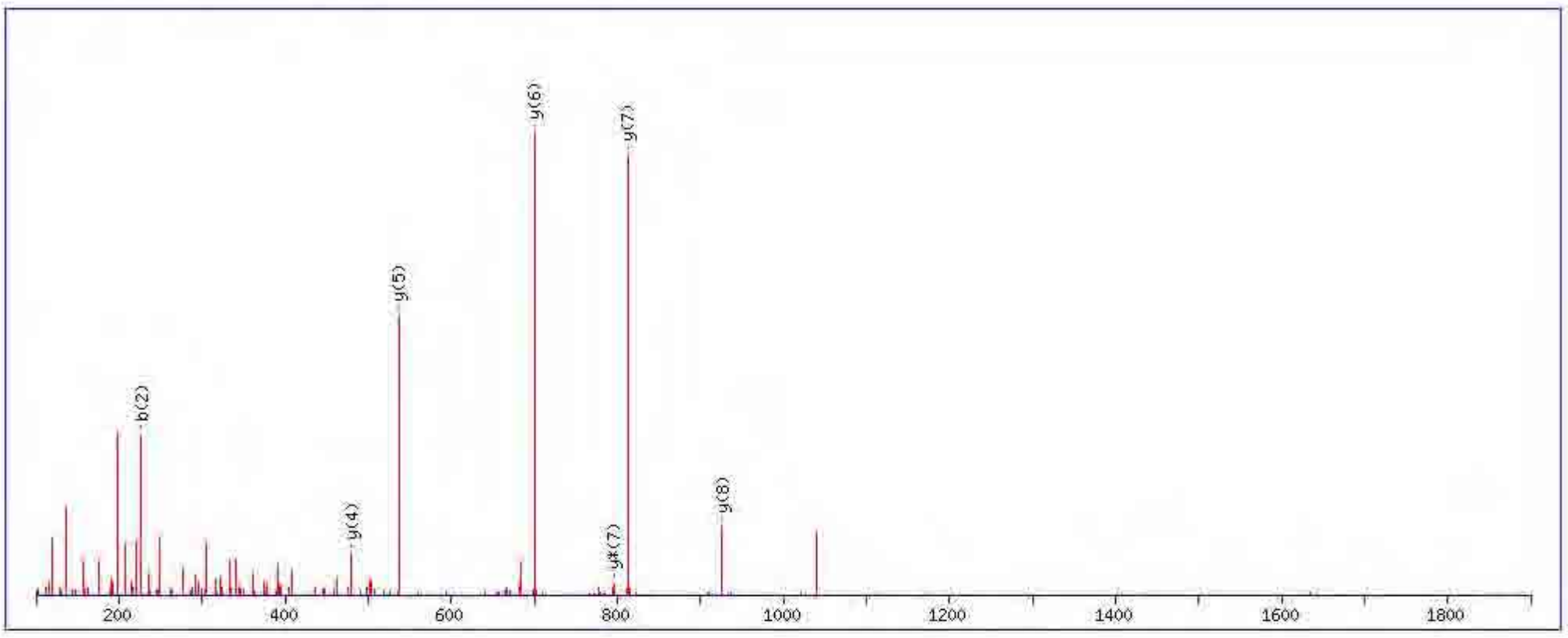
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIYGNISF**
Found in **RMI1_HUMAN**, RecQ-mediated genome instability protein 1 OS=Homo sapiens GN=RMI1 PE=1 SV=3

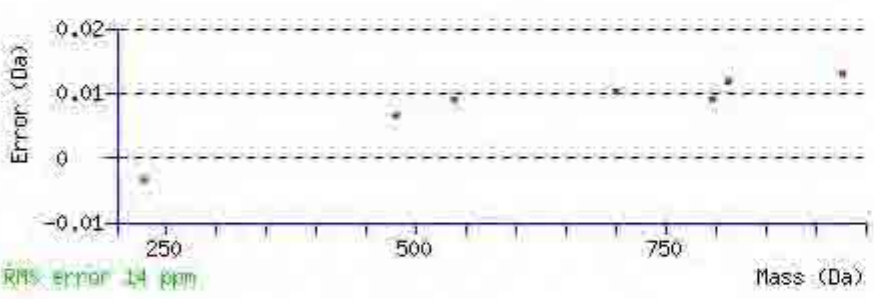
Match to Query 3732: 1038.582688 from(520.298620,2+) rtinseconds(1720) index(17035)
Title: Locus:1.1.1.1012.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

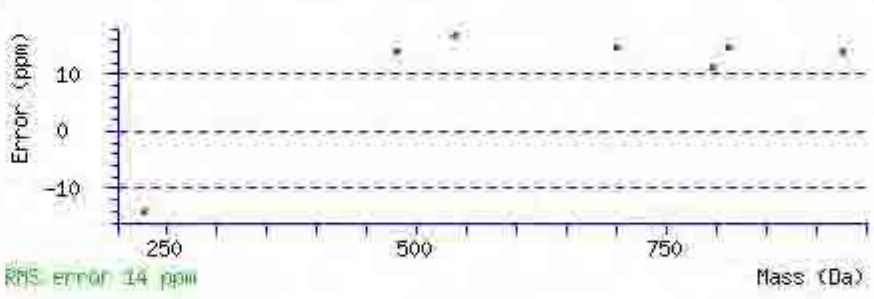
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1038.574966
Ions Score: 39 **Expect:** 0.01
Matches : 7/64 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							9
2	227.175404	114.091340					L	*926.498195*	463.752736	909.471646	455.239461	908.487630	454.747453	8
3	340.259468	170.633372					I	*813.414131*	407.210704	796.387582	398.697429	795.403566	398.205421	7
4	503.322797	252.165036					Y	*700.330067*	350.668672	683.303518	342.155397	682.319502	341.663389	6
5	560.344261	280.675769					G	*537.266738*	269.137007	520.240189	260.623733	519.256173	260.131725	5
6	674.387188	337.697232	657.360639	329.183958			N	*480.245274*	240.626275	463.218725	232.113000	462.234709	231.620992	4
7	787.471252	394.239264	770.444703	385.725990			I	366.202347	183.604811			348.191782	174.599529	3
8	874.503280	437.755278	857.476731	429.242004	856.492715	428.749996	S	253.118283	127.062779			235.107718	118.057497	2
9							F	166.086255	83.546765					1





NCBI **BLAST** search of ILIYGNISF
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	1038.574966	0.007722	ILIYGNISF
19.4	1038.582184	0.000504	PPLPTRQAK
14.5	1038.578339	0.004349	LLLGTYMTK
14.3	1038.582184	0.000504	PLPGATPAKR
13.8	1038.582153	0.000535	LLLNAENPR
13.8	1038.575653	0.007035	PLLTRMHR
13.6	1038.589584	-0.006896	PILVCPPLR
13.6	1038.589584	-0.006896	PILVCPPLR
12.0	1038.582184	0.000504	IPLQNGRLP
12.0	1038.586227	-0.003539	LIPHVQVFA

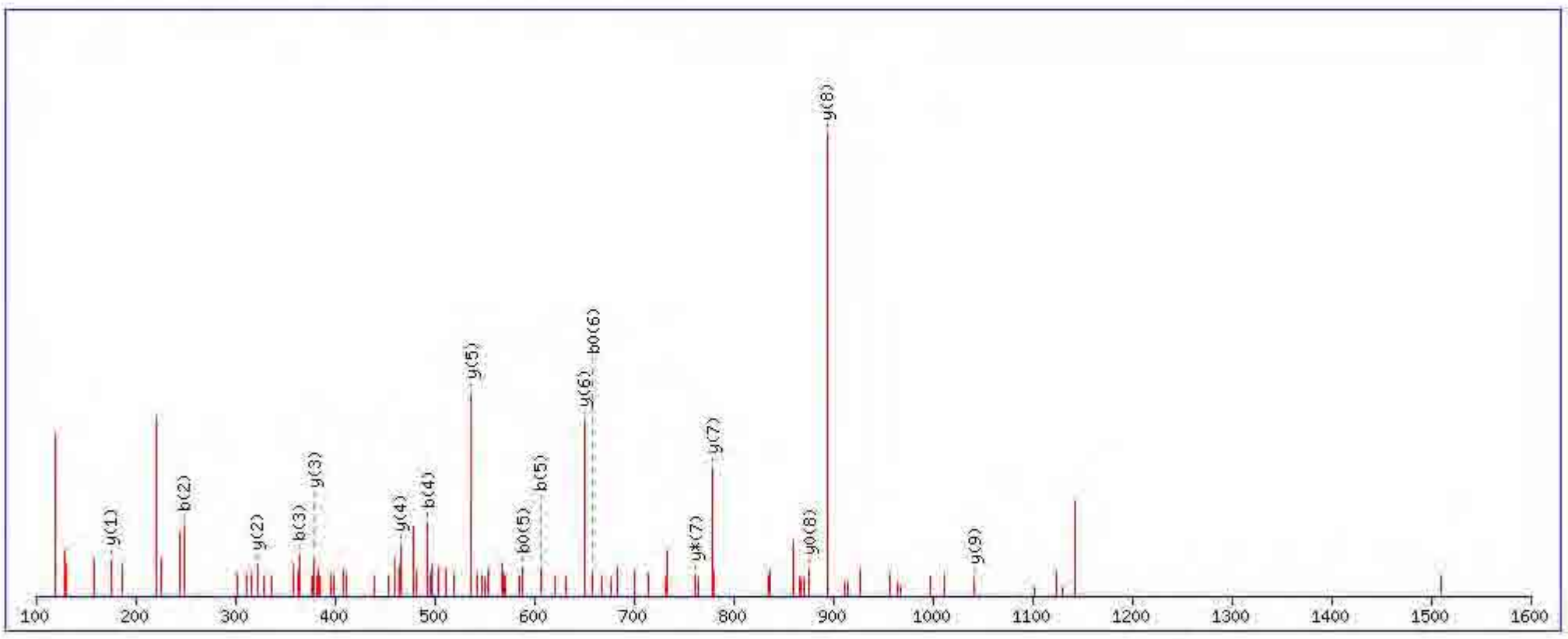
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFDEIASGFR**
Found in **GTR1_HUMAN**, Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2

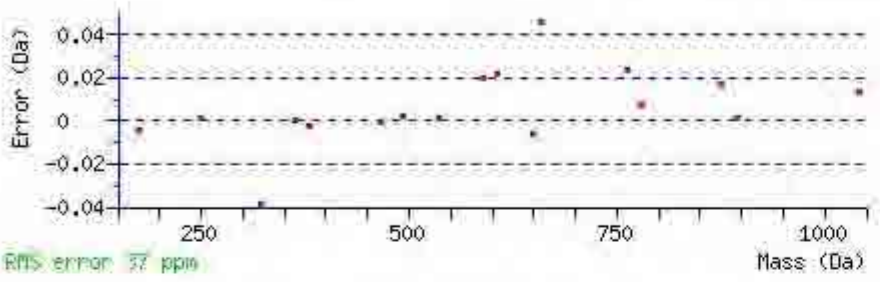
Match to Query 5762: 1141.539668 from(571.777110,2+) rtinseconds(1636) index(15910)
Title: Locus:1.1.1.967.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

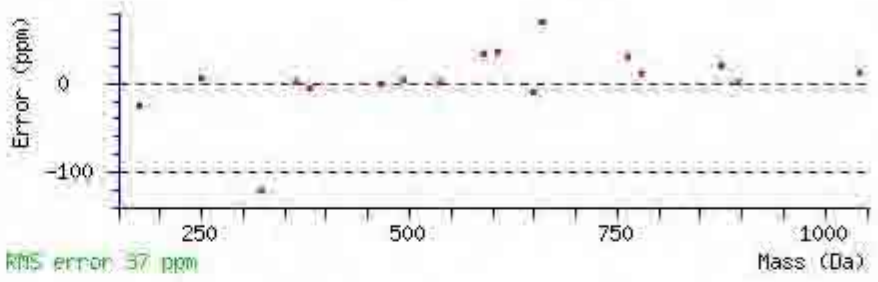
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1141.540390
Ions Score: 55 **Expect:** 0.00035
Matches : 17/84 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							10
2	249.123369	125.065322	231.112804	116.060040	F	1041.499986	521.253631	1024.473437	512.740357	1023.489421	512.248349	9
3	364.150312	182.578794	346.139747	173.573512	D	894.431572	447.719424	877.405023	439.206150	876.421007	438.714142	8
4	493.192905	247.100090	475.182340	238.094808	E	779.404629	390.205953	762.378080	381.692678	761.394064	381.200670	7
5	606.276969	303.642123	588.266404	294.636840	I	650.362036	325.684656	633.335487	317.171382	632.351471	316.679374	6
6	677.314083	339.160680	659.303518	330.155397	A	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	5
7	764.346111	382.676694	746.335546	373.671411	S	466.240858	233.624067	449.214309	225.110793	448.230293	224.618785	4
8	821.367575	411.187426	803.357010	402.182143	G	379.208830	190.108053	362.182281	181.594779			3
9	968.435989	484.721633	950.425424	475.716350	F	322.187366	161.597321	305.160817	153.084047			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TFDEIASGFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	1141.540390	-0.000722	TFDEIASGFR
17.3	1141.536377	0.003291	TFNQSSTRTT
14.2	1141.532532	0.007136	TNEFSMVLTT
10.2	1141.540390	-0.000722	EFSEIPGHQV
9.4	1141.543762	-0.004094	TGPPPALGGKEC
9.4	1141.543762	-0.004094	TGPPPALGGKEC
9.4	1141.543762	-0.004094	TGPPPALGGKEC
8.8	1141.540390	-0.000722	TVYEGPFASR
8.1	1141.532547	0.007121	MTDQAFVTLT
7.3	1141.543747	-0.004079	TFDAMKNSTK

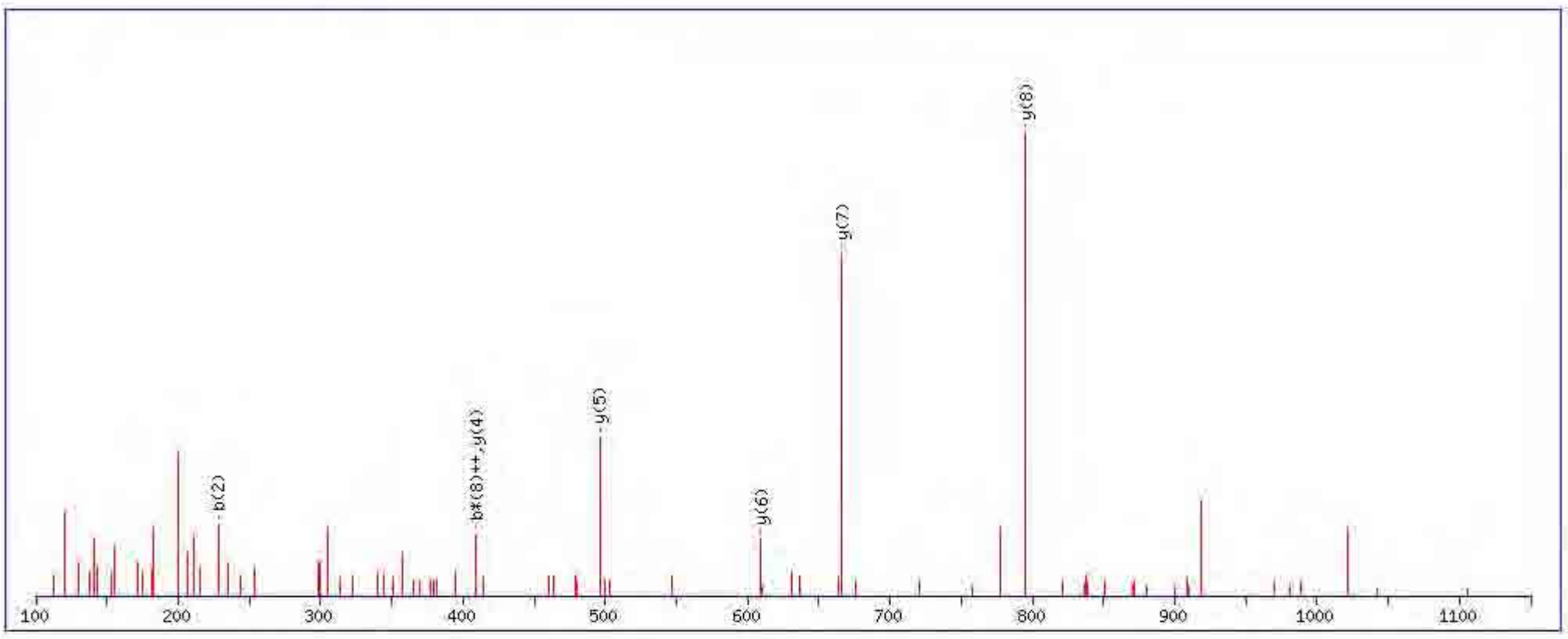
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RAEGLSGYAV**
Found in **TEPP_HUMAN**, Testis, prostate and placenta-expressed protein OS=Homo sapiens GN=TEPP PE=2 SV=3

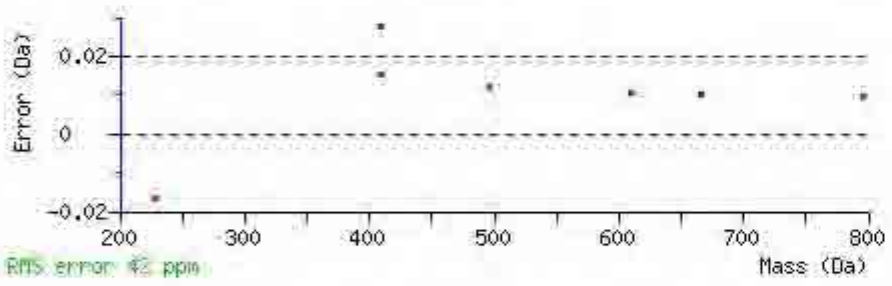
Match to Query 3450: 1021.514448 from(511.764500,2+) rtinseconds(1365) index(12379)
Title: Locus:1.1.1.816.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

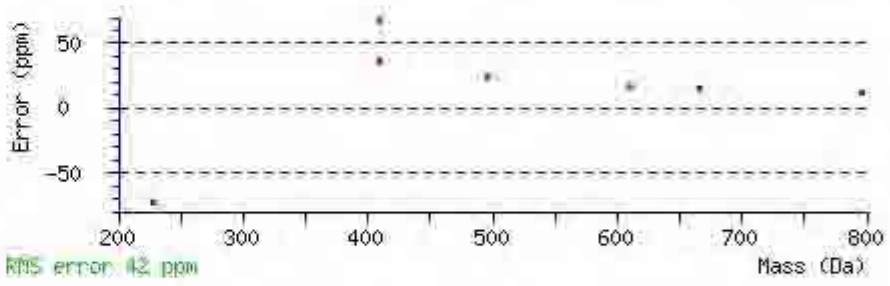
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1021.519241
Ions Score: 34 **Expect:** 0.0072
Matches : 7/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R					10
2	228.145501	114.576388	211.118952	106.063114			A	866.425425	433.716350	848.414860	424.711068	9
3	357.188094	179.097685	340.161545	170.584411	339.177529	170.092403	E	*795.388311*	398.197793	777.377746	389.192511	8
4	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	G	*666.345718*	333.676497	648.335153	324.671214	7
5	527.293622	264.150449	510.267073	255.637175	509.283057	255.145167	L	*609.324254*	305.165765	591.313689	296.160482	6
6	614.325650	307.666463	597.299101	299.153189	596.315085	298.661181	S	*496.240190*	248.623733	478.229625	239.618450	5
7	671.347114	336.177195	654.320565	327.663921	653.336549	327.171913	G	*409.208162*	205.107719			4
8	834.410443	417.708860	817.383894	409.195585	816.399878	408.703577	Y	352.186698	176.596987			3
9	905.447557	453.227417	888.421008	444.714142	887.436992	444.222134	A	189.123369	95.065322			2
10							V	118.086255	59.546765			1





NCBI **BLAST** search of RAEGLSGYAV
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	1021.519241	-0.004793	RAEGLSGYAV
10.1	1021.508041	0.006407	PATSGPTTFK
8.6	1021.508041	0.006407	TSPPPPGLAGP
8.6	1021.508041	0.006407	TSPPPPGLAGP
8.5	1021.519257	-0.004809	AQQPAVAQPP
8.5	1021.519257	-0.004809	AQQPAVAQPP
8.5	1021.519241	-0.004793	NLETFKDR
8.0	1021.511368	0.003080	VKECSSELK
7.9	1021.523300	-0.008852	LWGGPVPPAP
7.9	1021.523300	-0.008852	LWGGPVPPAP

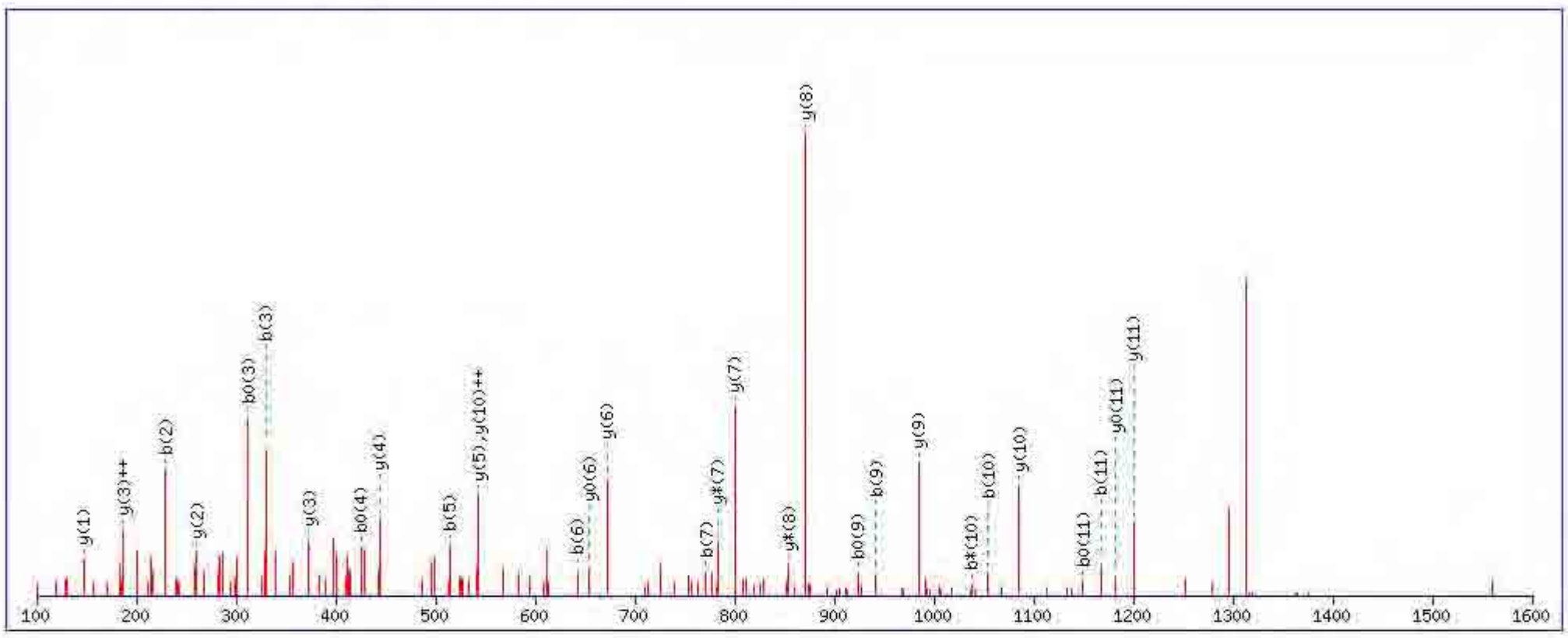
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

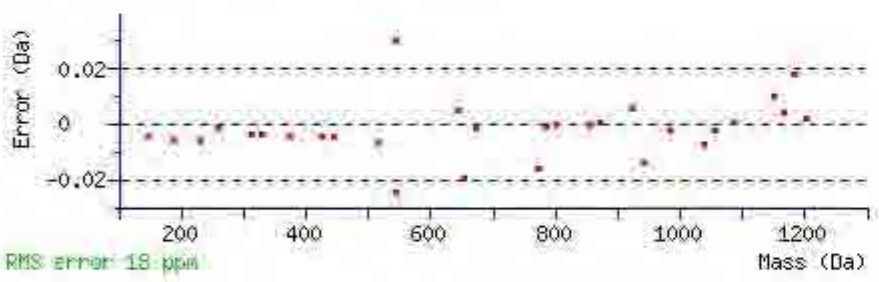
Match to Query 10123: 1312.764188 from(657.389370,2+) rtinseconds(2080) index(21801)
Title: Locus:1.1.1.1208.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

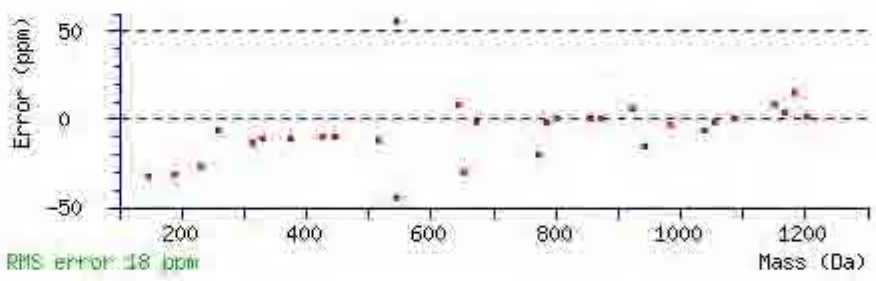
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1312.760193
Ions Score: 92 **Expect:** 3.6e-008
Matches : 30/110 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	**229.118283**	115.062779			211.107718	106.057497	D	*1200.683431*	600.845353	1183.656882	592.332079	1182.672866	591.840071	11
3	**330.165962**	165.586619			312.155397	156.581336	T	*1085.656488*	543.331882	1068.629939	534.818607	1067.645923	534.326599	10
4	443.250026	222.128651			425.239461	213.123369	L	*984.608809*	492.808042	967.582260	484.294768	966.598244	483.802760	9
5	**514.287140**	257.647208			496.276575	248.641926	A	*871.524745*	436.266010	854.498196	427.752736	853.514180	427.260728	8
6	**642.345718**	321.676497	625.319169	313.163223	624.335153	312.671215	Q	*800.487631*	400.747453	783.461082	392.234179	782.477066	391.742171	7
7	**771.388311**	386.197794	754.361762	377.684519	753.377746	377.192511	E	*672.429053*	336.718164	655.402504	328.204890	654.418488	327.712882	6
8	870.456725	435.732001	853.430176	427.218726	852.446160	426.726718	V	*543.386460*	272.196868	526.359911	263.683593			5
9	**941.493839**	471.250558	924.467290	462.737283	923.483274	462.245275	A	*444.318046*	222.662661	427.291497	214.149386			4
10	**1054.577903**	527.792589	1037.551354	519.279315	1036.567338	518.787307	L	*373.280932*	187.144104	356.254383	178.630829			3
11	**1167.661967**	584.334621	1150.635418	575.821347	1149.651402	575.329339	L	*260.196868*	130.602072	243.170319	122.088797			2
12							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDTLAQEVALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.5	1312.760193	0.003995	LDTLAQEVALLK
29.5	1312.760193	0.003995	ITSAAPLISSPLK
25.3	1312.760193	0.003995	ITSAAPLISSPLK
23.7	1312.771439	-0.007251	IDLTVLQRDLK
20.6	1312.760193	0.003995	KALEVTESPLVK
20.2	1312.761551	0.002637	LDRFGVRPLPK
18.7	1312.771423	-0.007235	LSQGQVLKLEAK
15.9	1312.771408	-0.007220	ASIELLARSLPK
15.6	1312.760193	0.003995	VEQLLASSLLQL
15.1	1312.771408	-0.007220	ILSNKNISAIIQ

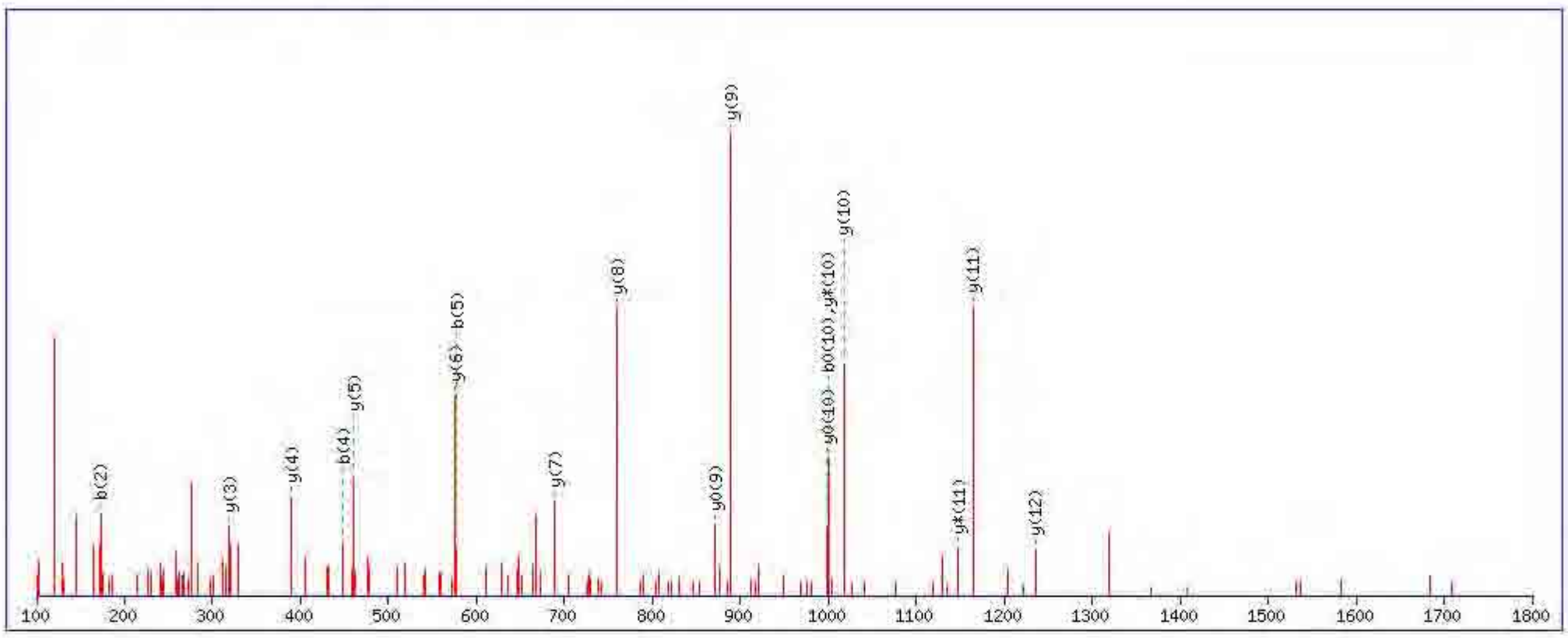
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

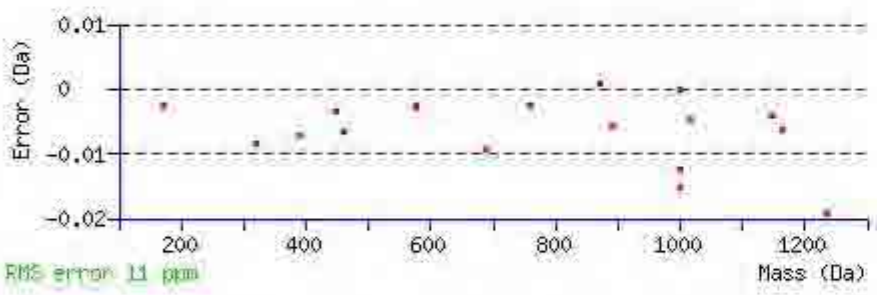
Match to Query 10840: 1335.630888 from(668.822720,2+) rtinseconds(1563) index(15039)
Title: Locus:1.1.1.925.13
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

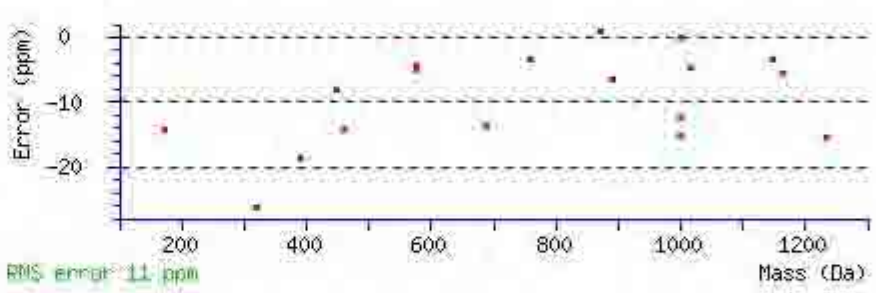
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 87 **Expect:** 1.3e-007
Matches : 18/136 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	*1235.590259*	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	*319.161211*	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.5	1335.630646	0.000242	TAFQEALDAAGDK
13.1	1335.638031	-0.007143	FIDISPAEMANL
11.0	1335.626633	0.004255	TASSSTEPSVSRQ
9.5	1335.630661	0.000227	TVTAWDSQTAEK
7.1	1335.620773	0.010115	GDFNPSAGWLTR
6.9	1335.641876	-0.010988	EQATKPSFESGR
6.0	1335.634033	-0.003145	TQTANMLSGPIST
5.7	1335.627533	0.003355	DGSRLCVGTLCGGV
5.7	1335.626648	0.004240	TAESSGGPSTSRVT
5.6	1335.634689	-0.003801	KFASVPEPEFPG

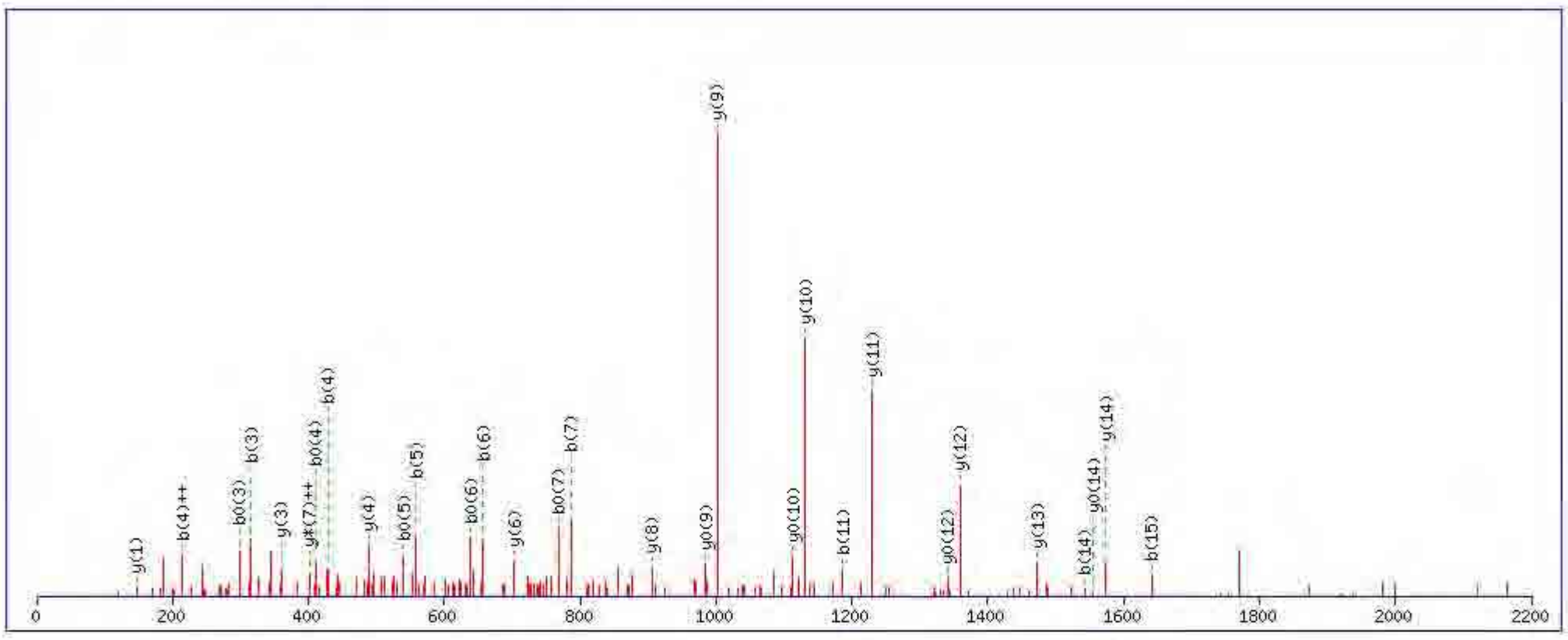
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TITLEVEPSDTIENVK**
Found in **RL40_HUMAN**, Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2

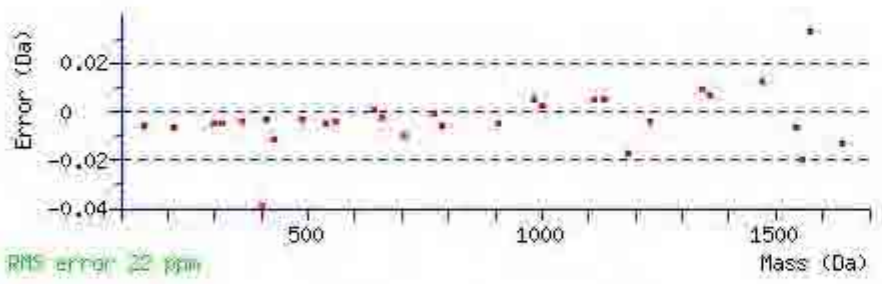
Match to Query 21048: 1786.917008 from(894.465780,2+) rtinseconds(1743) index(17354)
Title: Locus:1.1.1.1024.22
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

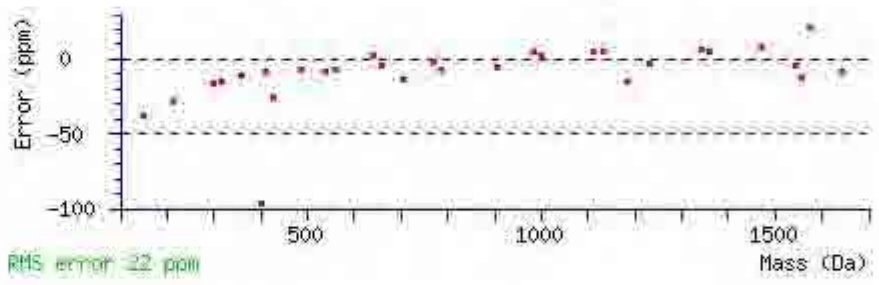
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1786.920013
Ions Score: 62 **Expect:** 0.00015
Matches : 31/148 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							16
2	*215.139019*	108.073147			197.128454	99.067865	I	1686.879623	843.943450	1669.853074	835.430175	1668.869058	834.938167	15
3	*316.186698*	158.596987			298.176133	149.591704	T	*1573.795559*	787.401418	1556.769010	778.888143	1555.784994	778.396135	14
4	*429.270762*	215.139019			411.260197	206.133737	L	*1472.747880*	736.877578	1455.721331	728.364304	1454.737315	727.872296	13
5	*558.313355*	279.660316			540.302790	270.655033	E	*1359.663816*	680.335546	1342.637267	671.822272	1341.653251	671.330264	12
6	*657.381769*	329.194523			639.371204	320.189240	V	*1230.621223*	615.814250	1213.594674	607.300975	1212.610658	606.808967	11
7	*786.424362*	393.715819			768.413797	384.710536	E	*1131.552809*	566.280043	1114.526260	557.766768	1113.542244	557.274760	10
8	883.477126	442.242201			865.466561	433.236919	P	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	9
9	970.509154	485.758215			952.498589	476.752932	S	*905.457452*	453.232364	888.430903	444.719090	887.446887	444.227082	8
10	1085.536097	543.271686			1067.525532	534.266404	D	818.425424	409.716350	801.398875	401.203076	800.414859	400.711068	7
11	*1186.583776*	593.795526			1168.573211	584.790243	T	*703.398481*	352.202879	686.371932	343.689604	685.387916	343.197596	6
12	1299.667840	650.337558			1281.657275	641.332275	I	602.350802	301.679039	585.324253	293.165765	584.340237	292.673757	5
13	1428.710433	714.858855			1410.699868	705.853572	E	*489.266738*	245.137007	472.240189	236.623733	471.256173	236.131725	4
14	*1542.753360*	771.880318	1525.726811	763.367044	1524.742795	762.875035	N	*360.224145*	180.615711	343.197596	172.102436			3
15	*1641.821774*	821.414525	1624.795225	812.901251	1623.811209	812.409243	V	246.181218	123.594247	229.154669	115.080973			2
16							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TITLEVEPSDTIENVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.5	1786.920013	-0.003005	TITLEVEPSDTIENVK
20.9	1786.902237	0.014771	MPSLEDLKELSPDLGK
18.2	1786.906952	0.010056	TLTLANGDRIPMAPSCK
15.7	1786.925415	-0.008407	TVDELVRHFFPDVTI
14.7	1786.900238	0.016770	WRPQPPAEGPGGELTVP
11.1	1786.931229	-0.014221	SVELSEQSLQELQAVK
9.1	1786.924713	-0.007705	ADMIKEGAAVIDVGINR
8.9	1786.928726	-0.011718	SNNIMILVDLKNEVW
8.9	1786.932571	-0.015563	EHGPNPILGSEALLGQR
8.0	1786.900223	0.016785	NDNPPTFIPPNYRVK

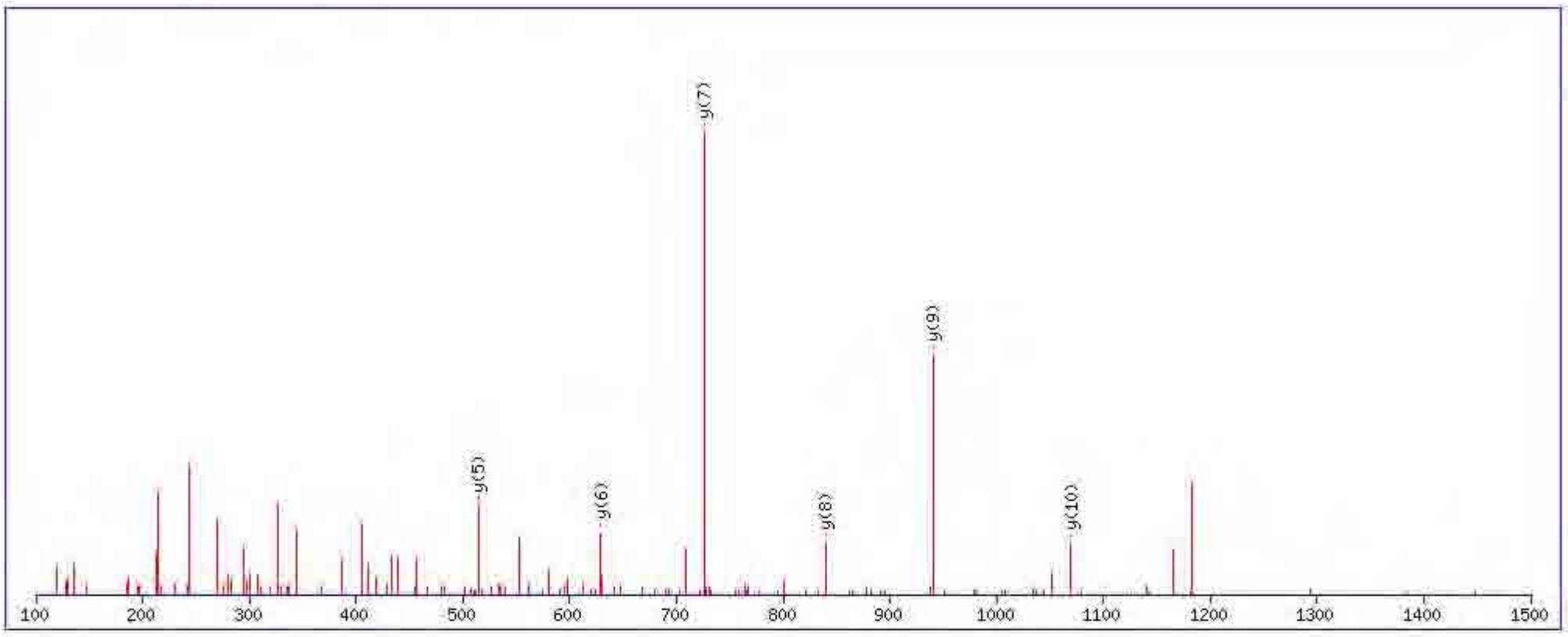
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NETIPDIPVSV**
Found in **ZN507_HUMAN**, Zinc finger protein 507 OS=Homo sapiens GN=ZNF507 PE=1 SV=2

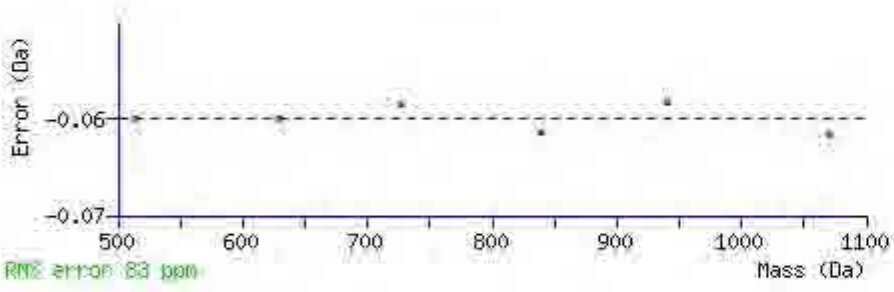
Match to Query 6733: 1182.602068 from(592.308310,2+) rtinseconds(1612) index(15652)
Title: Locus:1.1.1.953.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_5.mgf

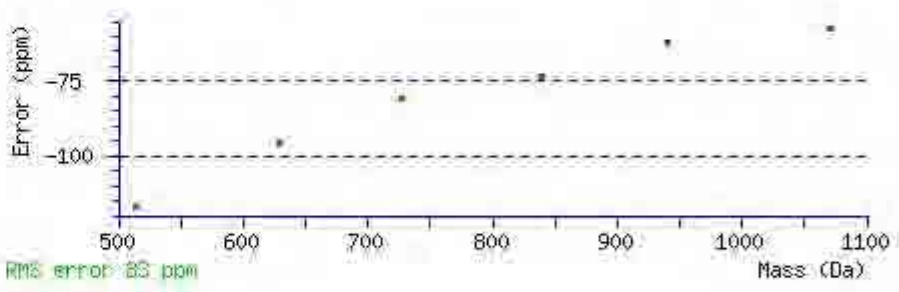
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1182.613220
Ions Score: 41 Expect: 0.0011
Matches : 6/96 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N					11
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	*1069.577568*	535.292422	1051.567003	526.287140	10
3	345.140475	173.073876	328.113926	164.560601	327.129910	164.068593	T	*940.534975*	470.771126	922.524410	461.765843	9
4	458.224539	229.615908	441.197990	221.102633	440.213974	220.610625	I	*839.487296*	420.247286	821.476731	411.242004	8
5	555.277303	278.142290	538.250754	269.629015	537.266738	269.137007	P	*726.403232*	363.705254	708.392667	354.699972	7
6	670.304246	335.655761	653.277697	327.142487	652.293681	326.650479	D	*629.350468*	315.178872	611.339903	306.173590	6
7	783.388310	392.197793	766.361761	383.684519	765.377745	383.192511	I	*514.323525*	257.665401	496.312960	248.660118	5
8	880.441074	440.724175	863.414525	432.210901	862.430509	431.718893	P	401.239461	201.123369	383.228896	192.118086	4
9	979.509488	490.258382	962.482939	481.745108	961.498923	481.253100	V	304.186697	152.596986	286.176132	143.591704	3
10	1066.541516	533.774396	1049.514967	525.261122	1048.530951	524.769114	S	205.118283	103.062780	187.107718	94.057497	2
11							V	118.086255	59.546766			1





NCBI **BLAST** search of NETIPDIPVSV
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.6	1182.613220	-0.011152	NETIPDIPVSV
8.6	1182.599289	0.002779	QDTIAHLERT
8.4	1182.592773	0.009295	CQPARGPPGLR
8.0	1182.613235	-0.011167	VLDTPSPPVNL
7.4	1182.599335	0.002733	GGPGVRVSPTPGA
5.1	1182.599304	0.002764	TLSQAPQPGPR
4.6	1182.596802	0.005266	GWTLMHPGRL
3.9	1182.596802	0.005266	GWTLMHPGRL
3.6	1182.610550	-0.008482	RPSTPRQGPVG
3.3	1182.613235	-0.011167	VPIPITNGLDP

Control – technical replicate # 4

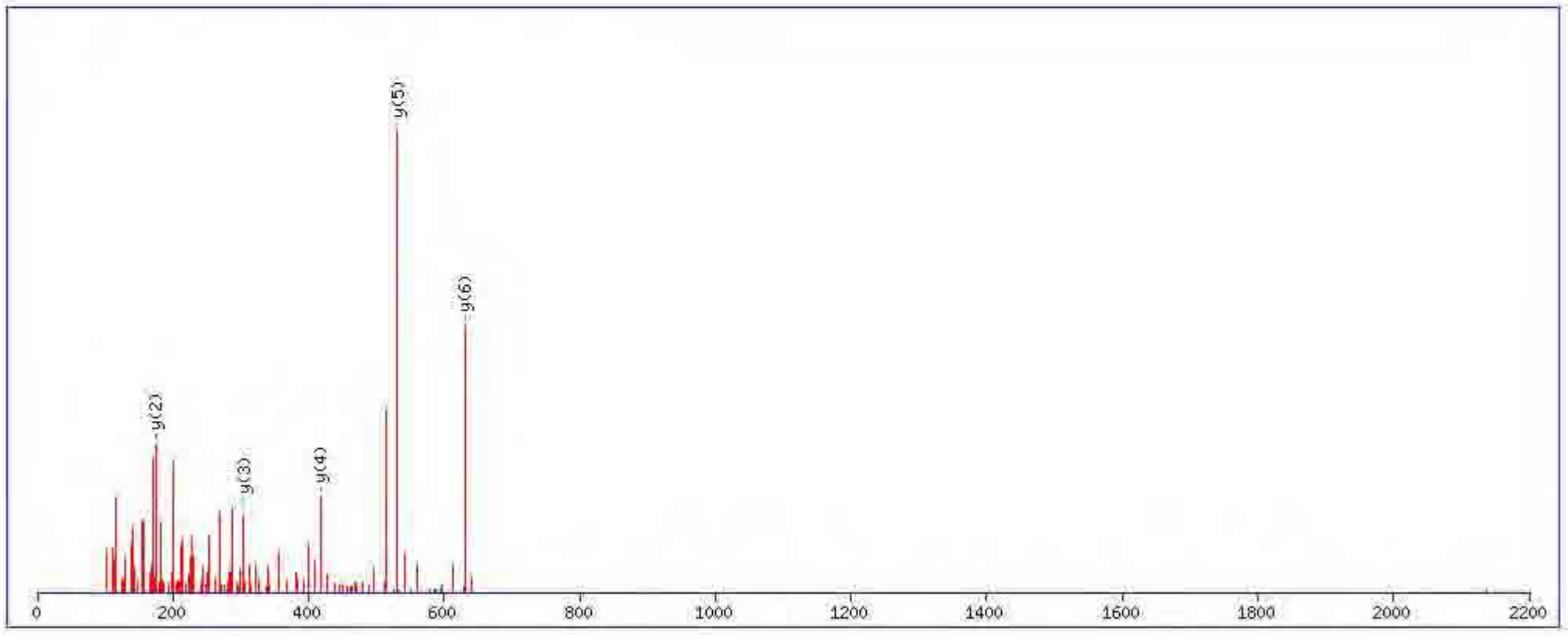
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNIEGV**
Found in **AASD1_HUMAN**, Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 PE=1 SV=2

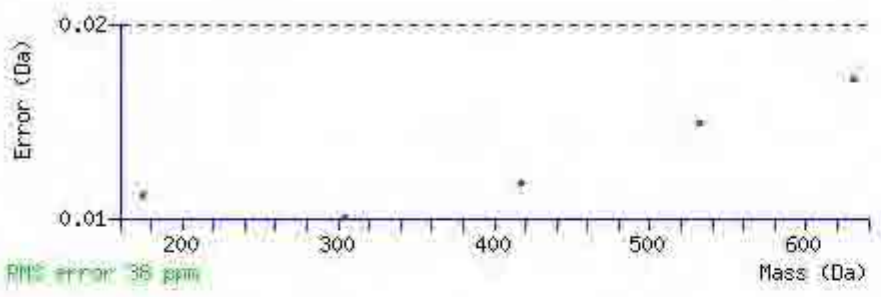
Match to Query 114: 728.408928 from(365.211740,2+) rtinseconds(718) index(4046)
Title: Locus:1.1.1.1059.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

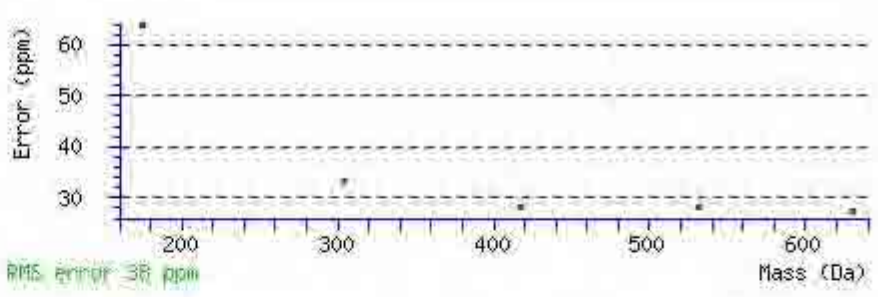
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 728.406860
Ions Score: 48 **Expect:** 0.0023
Matches : 5/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							7
2	199.144104	100.075690					V	*630.345717*	315.676497	613.319168	307.163222	612.335152	306.671214	6
3	313.187031	157.097153	296.160482	148.583879			N	*531.277303*	266.142290	514.250754	257.629015	513.266738	257.137007	5
4	426.271095	213.639186	409.244546	205.125911			I	*417.234376*	209.120826			399.223811	200.115544	4
5	555.313688	278.160482	538.287139	269.647208	537.303123	269.155200	E	*304.150312*	152.578794			286.139747	143.573512	3
6	612.335152	306.671214	595.308603	298.157940	594.324587	297.665932	G	*175.107719*	88.057497					2
7							V	118.086255	59.546765					1





NCBI **BLAST** search of VVNIEGV
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.1	728.406860	0.002068	VVNIEGV
30.2	728.406860	0.002068	VVNITSP
30.2	728.406860	0.002068	VVNLAVD
19.4	728.411560	-0.002632	VVPRCR
16.0	728.411560	-0.002632	VVRCPR
15.7	728.404144	0.004784	RRPER
11.6	728.406845	0.002083	LAQIEGV
7.1	728.406860	0.002068	VVPTADK
7.1	728.406860	0.002068	VVPTEKG
7.0	728.406860	0.002068	VVILGDN

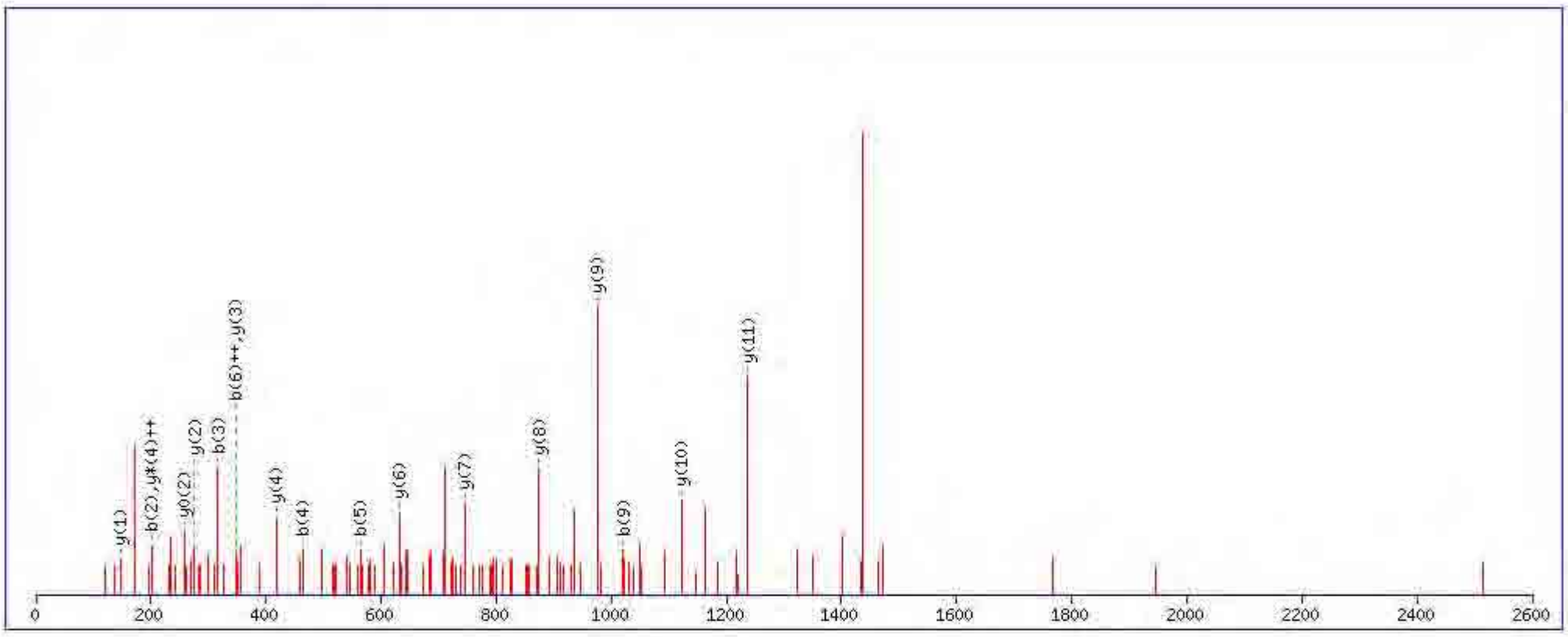
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLDFTELDVAAEK**
Found in **ANGT_HUMAN**, Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1

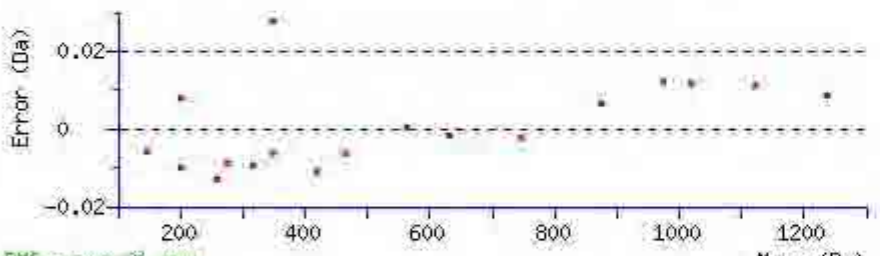
Match to Query 12564: 1436.697168 from(719.355860,2+) rtinseconds(2001) index(19180)
Title: Locus:1.1.1.1773.11
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

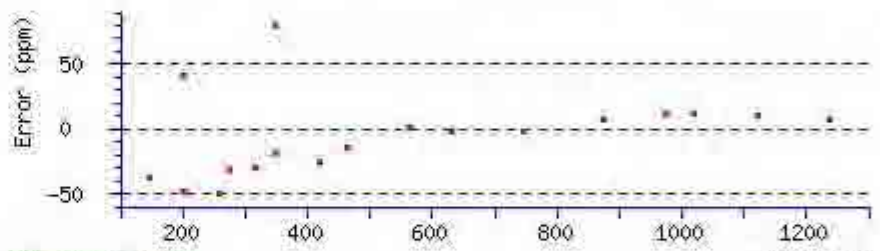
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1436.703476
Ions Score: 51 Expect: 6.8e-005
Matches : 18/118 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	**201.123368**	101.065322	183.112803	92.060039	L	1350.678739	675.843008	1333.652190	667.329733	1332.668174	666.837725	12
3	**316.150311**	158.578793	298.139746	149.573511	D	*1237.594675*	619.300976	1220.568126	610.787701	1219.584110	610.295693	11
4	**463.218725**	232.113001	445.208160	223.107718	F	*1122.567732*	561.787504	1105.541183	553.274230	1104.557167	552.782222	10
5	**564.266404**	282.636840	546.255839	273.631558	T	*975.499318*	488.253297	958.472769	479.740023	957.488753	479.248015	9
6	693.308997	347.158137	675.298432	338.152854	E	*874.451639*	437.729458	857.425090	429.216183	856.441074	428.724175	8
7	806.393061	403.700169	788.382496	394.694886	L	*745.409046*	373.208161	728.382497	364.694887	727.398481	364.202879	7
8	921.420004	461.213640	903.409439	452.208358	D	*632.324982*	316.666129	615.298433	308.152855	614.314417	307.660847	6
9	**1020.488418**	510.747847	1002.477853	501.742565	V	517.298039	259.152658	500.271490	250.639383	499.287474	250.147375	5
10	1091.525532	546.266404	1073.514967	537.261122	A	*418.229625*	209.618451	401.203076	201.105176	400.219060	200.613168	4
11	1162.562646	581.784961	1144.552081	572.779679	A	*347.192511*	174.099894	330.165962	165.586619	329.181946	165.094611	3
12	1291.605239	646.306258	1273.594674	637.300975	E	*276.155397*	138.581337	259.128848	130.068062	258.144832	129.576054	2
13					K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SLDFTELDVAAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.6	1436.703476	-0.006308	SLDFTELDVAAEK
5.8	1436.692917	0.004251	SIQSSEMIATNTR
5.6	1436.700790	-0.003622	PSDHDLKPNAATR
4.8	1436.700974	-0.003806	MALFPAFAGLSEAP
4.3	1436.685745	0.011423	ISGPIPPDPTLCPD
4.1	1436.700821	-0.003653	RPSTGETFVQSGR
3.4	1436.696945	0.000223	PSDFDIEMALRK
2.8	1436.689560	0.007608	VTFQGETENREK
2.7	1436.696976	0.000192	AERMGFTEVTPVT
2.4	1436.706833	-0.009665	VTEDIKMSLEEK

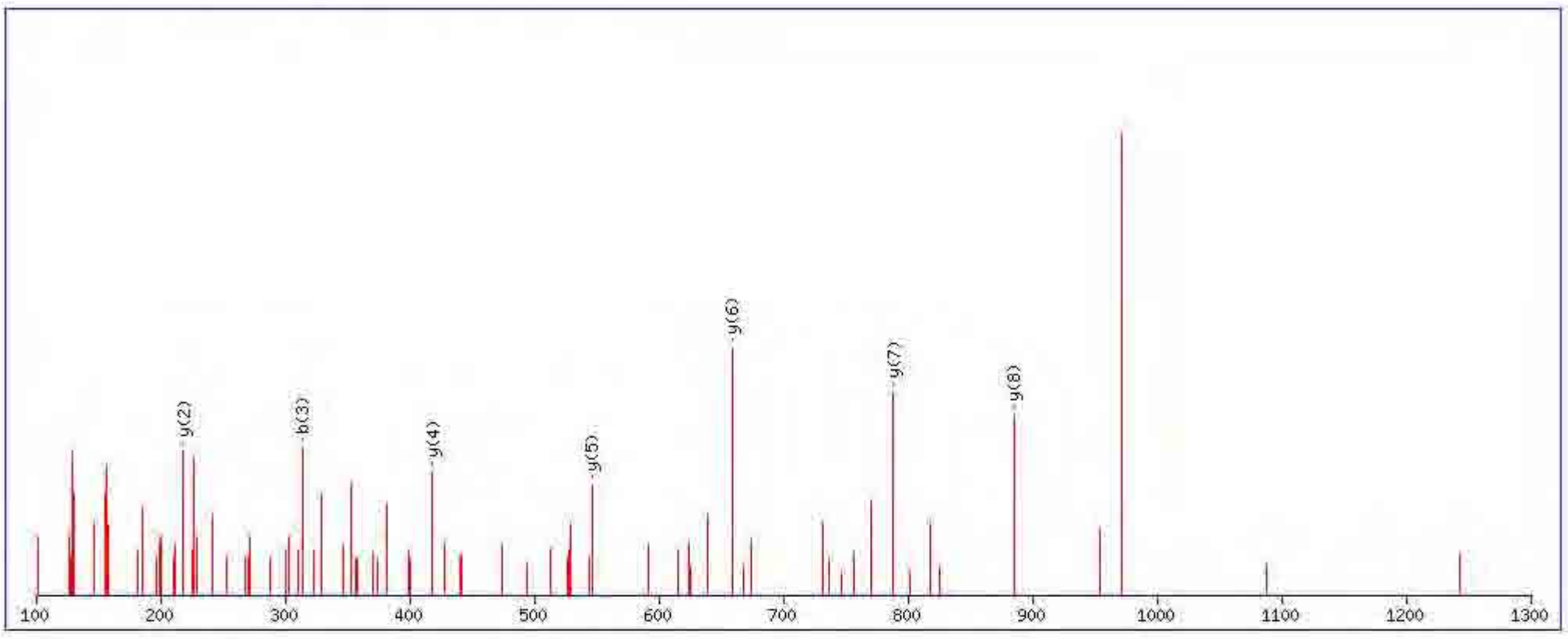
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPELQAEAK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

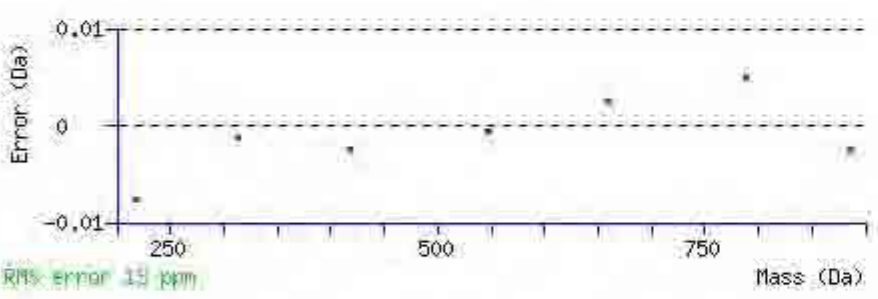
Match to Query 2647: 971.492968 from(486.753760,2+) rtinseconds(656) index(3532)
Title: Locus:1.1.1.1024.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

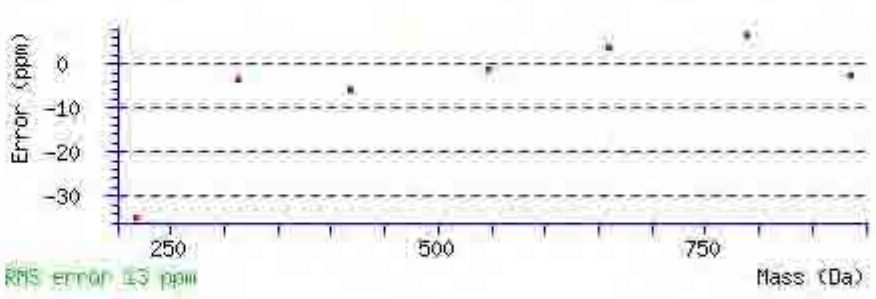
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 971.492340
Ions Score: 53 **Expect:** 0.002
Matches : 7/84 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	185.092068	93.049672			167.081503	84.044389	P	*885.467624*	443.237450	868.441075	434.724176	867.457059	434.232168	8
3	314.134661	157.570968			296.124096	148.565686	E	*788.414860*	394.711068	771.388311	386.197794	770.404295	385.705786	7
4	427.218725	214.113001			409.208160	205.107718	L	*659.372267*	330.189772	642.345718	321.676497	641.361702	321.184489	6
5	555.277303	278.142290	538.250754	269.629015	537.266738	269.137007	Q	*546.288203*	273.647740	529.261654	265.134465	528.277638	264.642457	5
6	626.314417	313.660847	609.287868	305.147572	608.303852	304.655564	A	*418.229625*	209.618450	401.203076	201.105176	400.219060	200.613168	4
7	755.357010	378.182143	738.330461	369.668869	737.346445	369.176861	E	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	826.394124	413.700700	809.367575	405.187426	808.383559	404.695418	A	*218.149918*	109.578597	201.123369	101.065322			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SPELQAEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	971.492340	0.000628	SPELQAEAK
21.9	971.492355	0.000613	SPEKLPQSS
17.8	971.492371	0.000597	QPSVTPEKA
15.2	971.492371	0.000597	SSENGALPVV
14.9	971.492371	0.000597	SPSVASPSPK
13.7	971.492355	0.000613	QISISEPQA
11.9	971.492371	0.000597	SPSVASPSPK
11.9	971.492340	0.000628	SEPAKEPAK
11.6	971.492355	0.000613	ESPKPSPAK
10.9	971.492371	0.000597	SPVASPSSPK

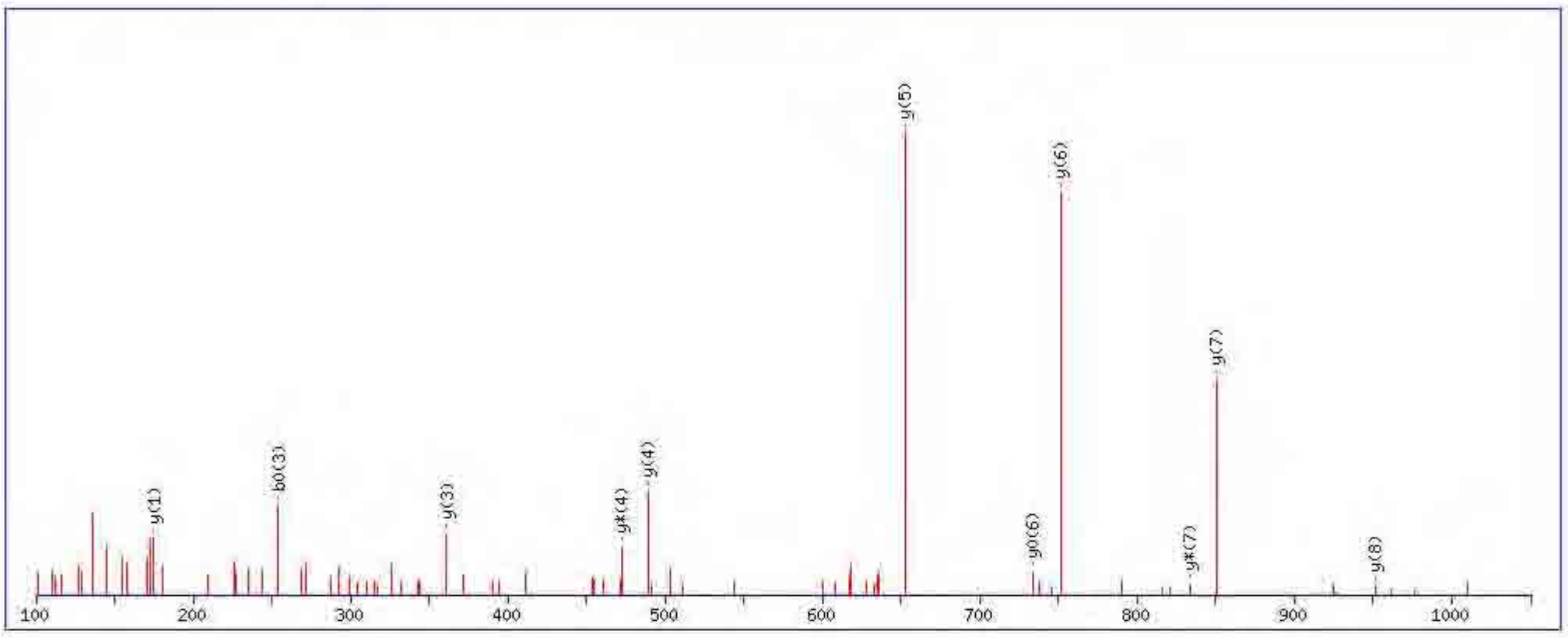
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATVVYQGER**
Found in **APOH_HUMAN**, Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3

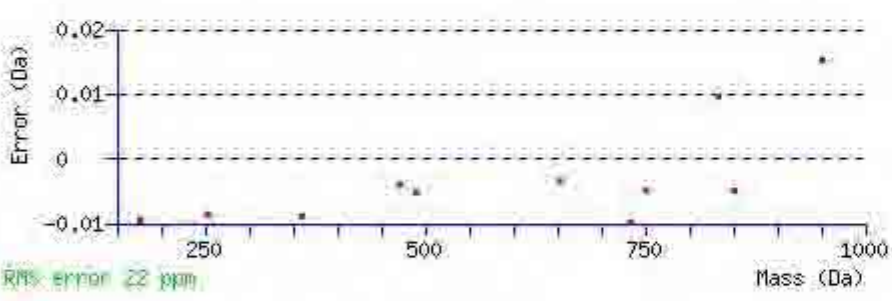
Match to Query 3428: 1021.514788 from(511.764670,2+) rtinseconds(754) index(4530)
Title: Locus:1.1.1.1079.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

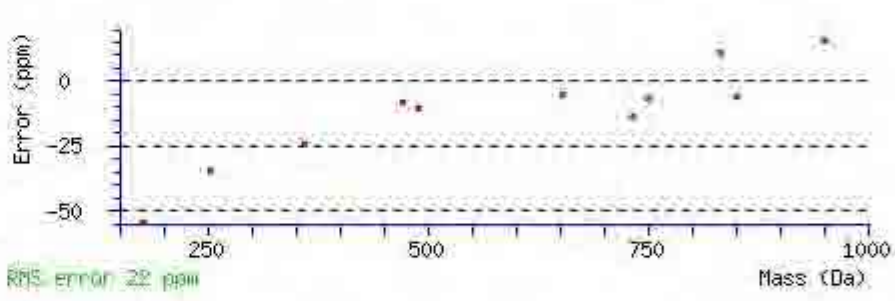
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1021.519257
Ions Score: 55 **Expect:** 0.00025
Matches : 11/82 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							9
2	173.092069	87.049672			155.081504	78.044390	T	*951.489423*	476.248350	934.462874	467.735075	933.478858	467.243067	8
3	272.160483	136.583879			254.149918	127.578597	V	*850.441744*	425.724510	833.415195	417.211236	832.431179	416.719228	7
4	371.228897	186.118087			353.218332	177.112804	V	*751.373330*	376.190303	734.346781	367.677029	733.362765	367.185021	6
5	534.292226	267.649751			516.281661	258.644469	Y	*652.304916*	326.656096	635.278367	318.142822	634.294351	317.650814	5
6	662.350804	331.679040	645.324255	323.165766	644.340239	322.673758	Q	*489.241587*	245.124432	472.215038	236.611157	471.231022	236.119149	4
7	719.372268	360.189772	702.345719	351.676498	701.361703	351.184490	G	*361.183009*	181.095143	344.156460	172.581868	343.172444	172.089860	3
8	848.414861	424.711069	831.388312	416.197794	830.404296	415.705786	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ATVVYQGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.7	1021.519257	-0.004469	ATVVYQGER
15.3	1021.522644	-0.007856	ATVSMGITVR
14.5	1021.519257	-0.004469	PASYVQVSR
14.4	1021.519272	-0.004484	TGPVPAPPDR
13.4	1021.519226	-0.004438	QELYKADR
11.6	1021.519257	-0.004469	ASPVQHALPS
9.7	1021.508011	0.006777	QELYGALTQ
8.2	1021.519241	-0.004453	ATFPSEKAR
7.6	1021.519257	-0.004469	PDLQPSPPR
7.4	1021.512726	0.002062	QPAMHAVPR

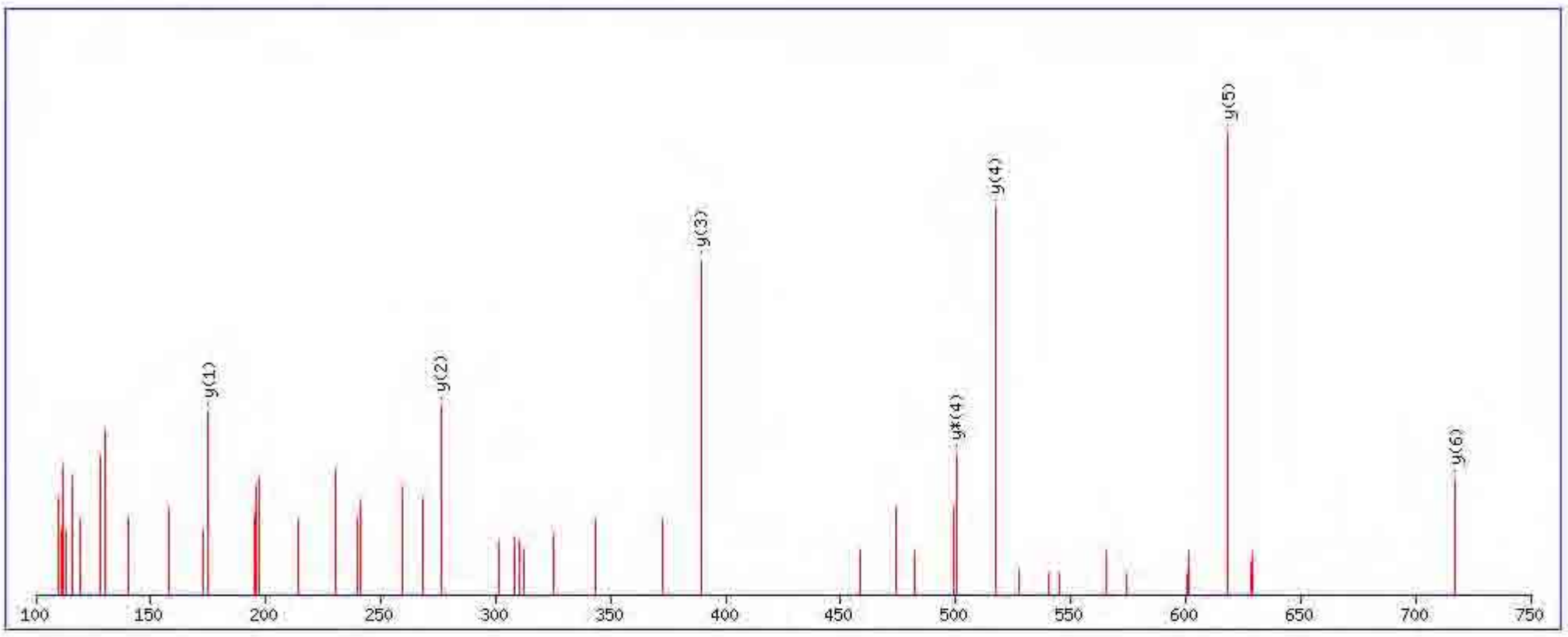
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQTVTKLTR**
Found in **CIB3_HUMAN**, Calcium and integrin-binding family member 3 OS=Homo sapiens GN=CIB3 PE=2 SV=3

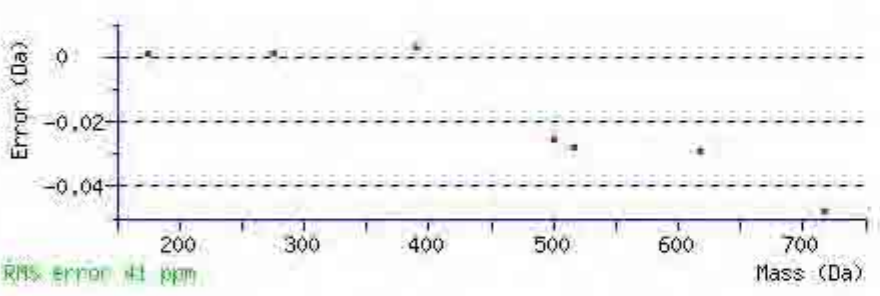
Match to Query 54: 1074.613392 from(359.211740,3+) rtinseconds(464) index(1269)
Title: Locus:1.1.1.916.2
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

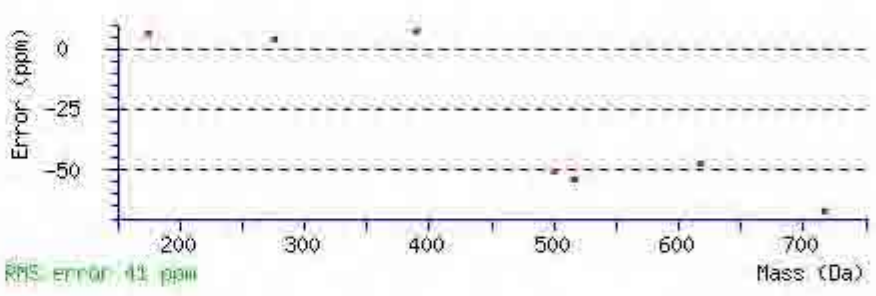
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.603317
Ions Score: 63 **Expect:** 0.00019
Matches : 7/92 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							9
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	946.568008	473.787642	929.541459	465.274368	928.557443	464.782360	8
3	359.156126	180.081701	342.129577	171.568427	341.145561	171.076419	T	818.509430	409.758353	801.482881	401.245079	800.498865	400.753071	7
4	458.224540	229.615908	441.197991	221.102634	440.213975	220.610626	V	*717.461751*	359.234514	700.435202	350.721239	699.451186	350.229231	6
5	559.272219	280.139748	542.245670	271.626473	541.261654	271.134465	T	*618.393337*	309.700307	601.366788	301.187032	600.382772	300.695024	5
6	687.367182	344.187229	670.340633	335.673955	669.356617	335.181947	K	*517.345658*	259.176467	500.319109	250.663193	499.335093	250.171185	4
7	800.451246	400.729261	783.424697	392.215987	782.440681	391.723979	L	*389.250695*	195.128985	372.224146	186.615711	371.240130	186.123703	3
8	901.498925	451.253101	884.472376	442.739826	883.488360	442.247818	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EQTVTKLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.8	1074.603317	0.010075	EQTVTKLTR
27.6	1074.603302	0.010090	QISETLKTR
18.7	1074.603317	0.010075	TSSLKPAVTR
17.3	1074.603317	0.010075	IKDTTGTALR
13.9	1074.607330	0.006062	FKPQALLDK
13.9	1074.607315	0.006077	FQLKIAELN
13.9	1074.610718	0.002674	KMLQLVGVTA
13.9	1074.607330	0.006062	QFLGALDLAK
13.9	1074.621933	-0.008541	AVSAVMKTIR
13.9	1074.603302	0.010090	VAASTEKTLR

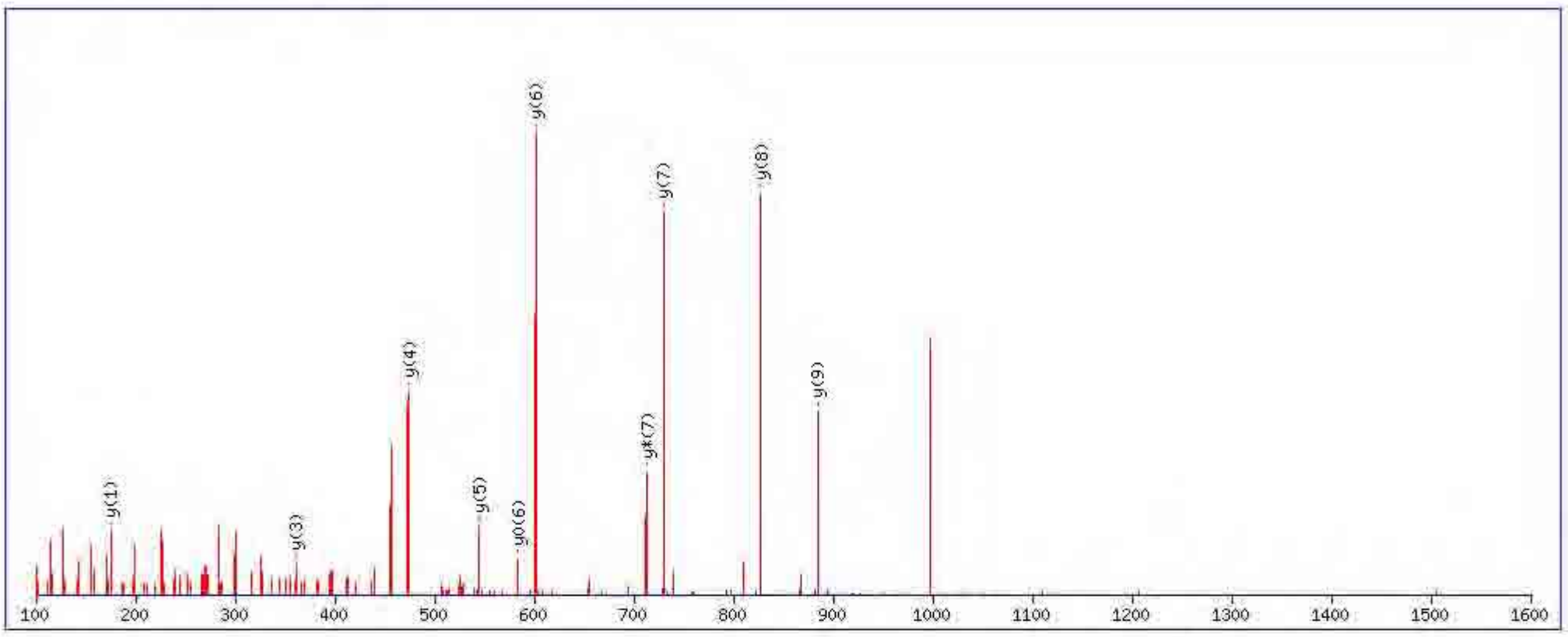
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPKGAPGER**
Found in **CO9A3_HUMAN**, Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2

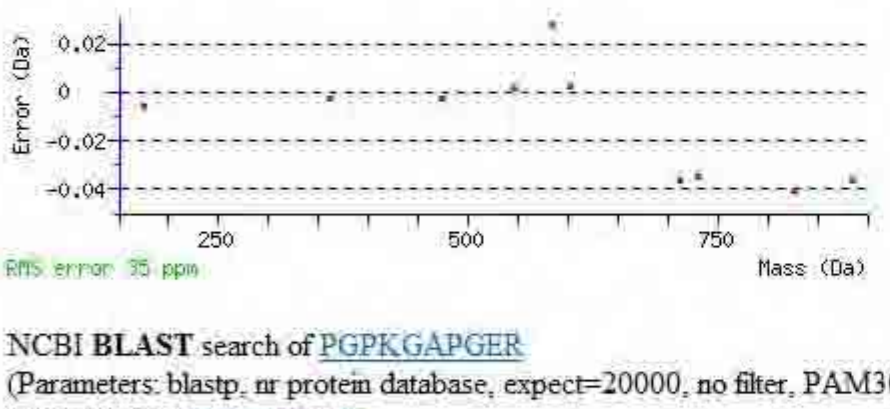
Match to Query 3019: 996.496088 from(499.255320,2+) rtinseconds(609) index(3039)
Title: Locus:1.1.1.997.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

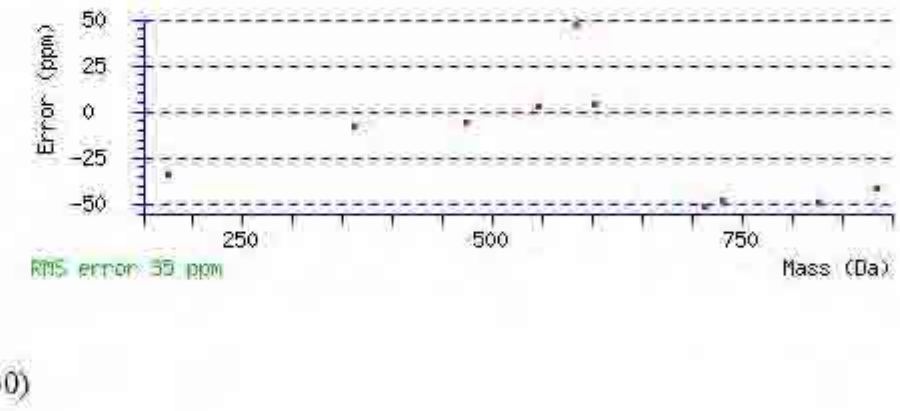
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 996.498856
Variable modifications:
P1 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 63 **Expect:** 9.5e-005
Matches : 10/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116					P							10
2	171.076419	86.041847					G	*884.458457*	442.732867	867.431908	434.219592	866.447892	433.727584	9
3	268.129183	134.568229					P	*827.436993*	414.222135	810.410444	405.708860	809.426428	405.216852	8
4	396.224146	198.615711	379.197597	190.102436			K	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	7
5	453.245610	227.126443	436.219061	218.613168			G	*602.289266*	301.648271	585.262717	293.134997	584.278701	292.642989	6
6	524.282724	262.645000	507.256175	254.131726			A	*545.267802*	273.137539	528.241253	264.624265	527.257237	264.132257	5
7	637.330403	319.168840	620.303854	310.655565			P	*474.230688*	237.618982	457.204139	229.105708	456.220123	228.613700	4
8	694.351867	347.679572	677.325318	339.166297			G	*361.183009*	181.095143	344.156460	172.581868	343.172444	172.089860	3
9	823.394460	412.200868	806.367911	403.687594	805.383895	403.195586	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PGPKGAPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.8	996.498856	-0.002768	PGPKGAPGER
34.4	996.498856	-0.002768	PGPAGPKGER
33.5	996.498856	-0.002768	PGPKGAPGER
23.9	996.487625	0.008463	IGPEVPDDR
23.2	996.487625	0.008463	PGPKGDPGEK
20.2	996.498871	-0.002783	PGPSGPPGKR
19.8	996.498871	-0.002783	LGPPQGGSPR
19.8	996.498871	-0.002783	PGQPGLPGSR
19.6	996.498856	-0.002768	PGPQAGAGAGAK
15.7	996.487640	0.008448	PPGEAGVGGPK

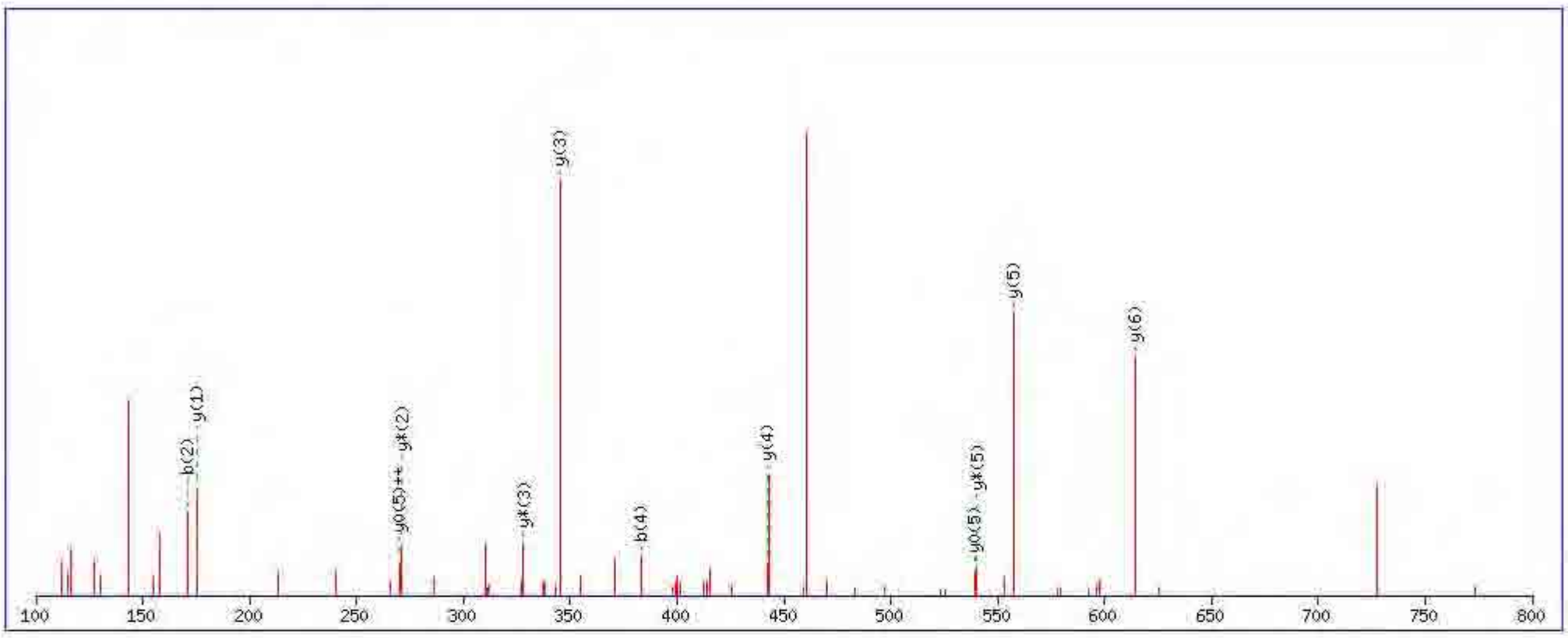
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDPGPR**
Found in **CO7A1_HUMAN**, Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2

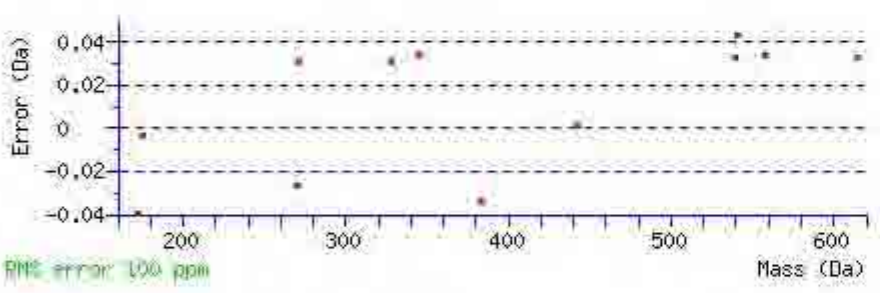
Match to Query 96: 726.361028 from(364.187790,2+) rtinseconds(491) index(1646)
Title: Locus:1.1.1.931.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

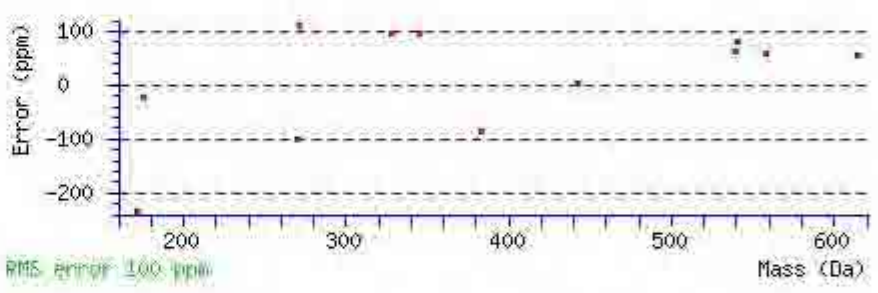
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 726.366058
Variable modifications:
P6 : Oxidation (P)
Ions Score: 40 **Expect:** 0.013
Matches : 12/48 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							7
2	171.112804	86.060040			G	*614.289266*	307.648271	597.262717	299.134997	596.278701	298.642989	6
3	286.139747	143.573512	268.129182	134.568229	D	*557.267802*	279.137539	540.241253	270.624265	539.257237	270.132257	5
4	383.192511	192.099894	365.181946	183.094611	P	*442.240859*	221.624068	425.214310	213.110793			4
5	440.213975	220.610626	422.203410	211.605343	G	*345.188095*	173.097685	328.161546	164.584411			3
6	553.261654	277.134465	535.251089	268.129183	P	288.166631	144.586953	271.140082	136.073679			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LGDPGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	726.366058	-0.005030	PGPDGLR
40.2	726.366058	-0.005030	LGDPGPR
40.2	726.366058	-0.005030	PGDPGLR
27.8	726.366058	-0.005030	PGPPTSR
26.7	726.366058	-0.005030	PGPGDLR
26.3	726.366074	-0.005046	PGVPGPR
26.3	726.366074	-0.005046	PGPVGPR
24.6	726.366074	-0.005046	PGVPPGR
24.3	726.366058	-0.005030	LGPPGDR
24.3	726.366058	-0.005030	PGPAPTR

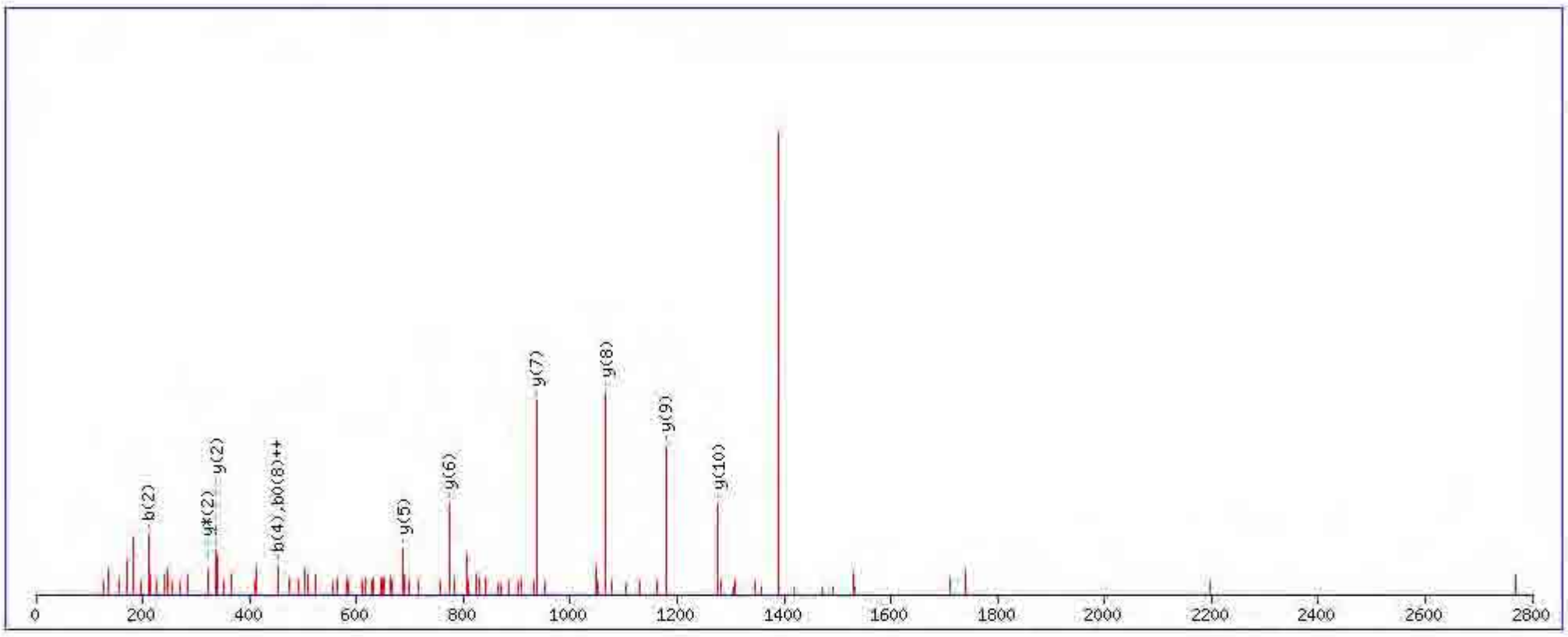
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

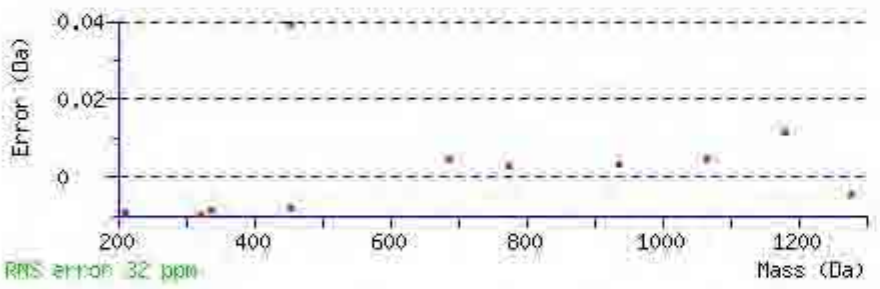
Match to Query 11729: 1388.667608 from(695.341080,2+) rtinseconds(1671) index(14809)
Title: Locus:1.1.1.1593.15
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

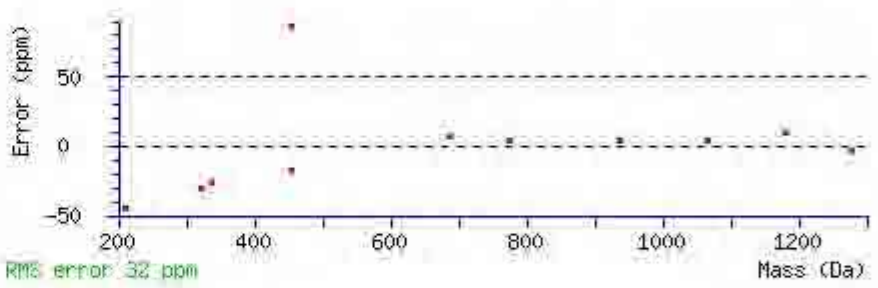
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 58 **Expect:** 0.00017
Matches : 11/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	*1276.584445*	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	*1179.531681*	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	*1066.447617*	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	*937.405024*	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	*774.341695*	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	*687.309667*	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	524.246338	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	*338.182281*	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.0	1388.661194	0.006414	LPLEYSYGEYR
16.8	1388.667114	0.000494	PPPELTDTATSTK
12.1	1388.671082	-0.003474	IPELEEAELFAE
8.1	1388.667114	0.000494	PPPELTDTATSTK
7.3	1388.667953	-0.000345	IPELLASGMVDNM
6.9	1388.679703	-0.012095	LPGQGVHSQGQGPGA
2.8	1388.664612	0.002996	PPPPAPDMTFKK
2.5	1388.679169	-0.011561	SKIHMQEMELK
2.5	1388.679184	-0.011576	QCLNKMPPGEIK
2.5	1388.679184	-0.011576	QCLNKMPPGEIK

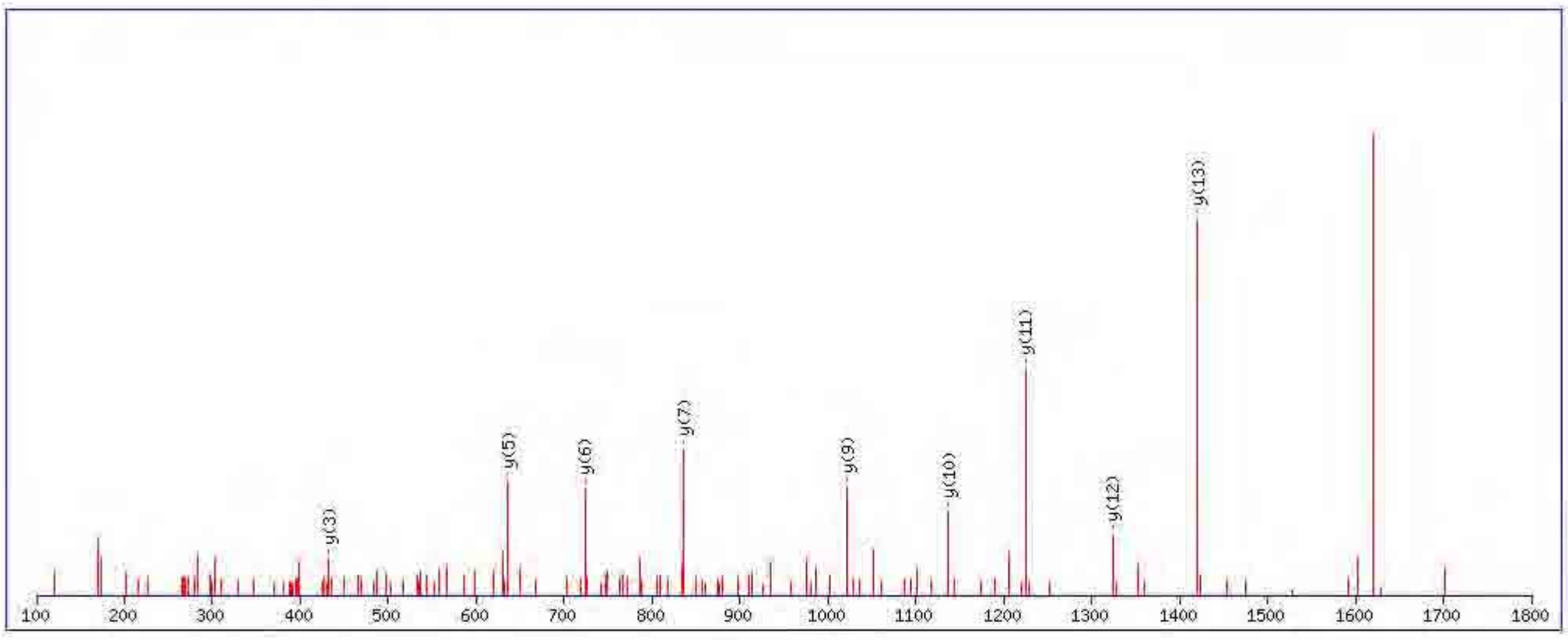
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFEQR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

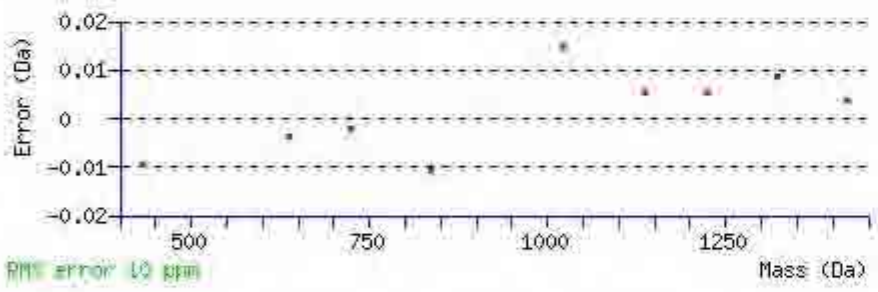
Match to Query 16750: 1619.814568 from(810.914560,2+) rtinseconds(2043) index(19722)
Title: Locus:1.1.1.1796.12
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

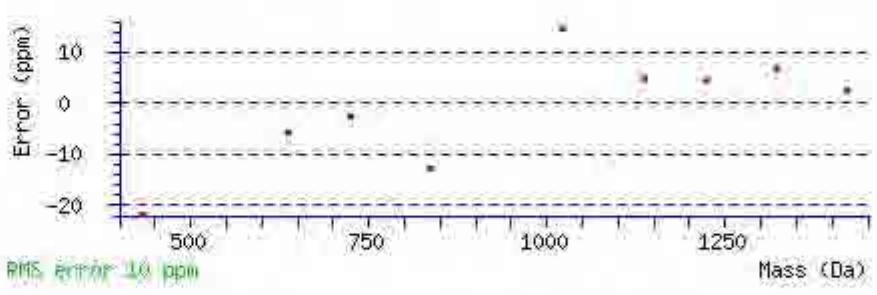
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1619.815506
Ions Score: 71 **Expect:** 4.9e-007
Matches : 9/138 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							15
2	201.123368	101.065322			183.112803	92.060039	L	1533.790748	767.399012	1516.764199	758.885738	1515.780183	758.393730	14
3	298.176132	149.591704			280.165567	140.586422	P	*1420.706684*	710.856980	1403.680135	702.343706	1402.696119	701.851698	13
4	397.244546	199.125911			379.233981	190.120629	V	*1323.653920*	662.330598	1306.627371	653.817324	1305.643355	653.325316	12
5	484.276574	242.641925			466.266009	233.636643	S	*1224.585506*	612.796391	1207.558957	604.283117	1206.574941	603.791109	11
6	599.303517	300.155397			581.292952	291.150114	D	*1137.553478*	569.280377	1120.526929	560.767103	1119.542913	560.275095	10
7	686.335545	343.671411			668.324980	334.666128	S	*1022.526535*	511.766906	1005.499986	503.253631	1004.515970	502.761623	9
8	785.403959	393.205618			767.393394	384.200335	V	935.494507	468.250892	918.467958	459.737617	917.483942	459.245609	8
9	898.488023	449.747650			880.477458	440.742367	L	*836.426093*	418.716685	819.399544	410.203410	818.415528	409.711402	7
10	985.520051	493.263664			967.509486	484.258381	S	*723.342029*	362.174653	706.315480	353.661378	705.331464	353.169370	6
11	1042.541515	521.774395			1024.530950	512.769113	G	*636.310001*	318.658639	619.283452	310.145364	618.299436	309.653356	5
12	1189.609929	595.308603			1171.599364	586.303320	F	579.288537	290.147907	562.261988	281.634632	561.277972	281.142624	4
13	1318.652522	659.829899			1300.641957	650.824617	E	*432.220123*	216.613700	415.193574	208.100425	414.209558	207.608417	3
14	1446.711100	723.859188	1429.684551	715.345914	1428.700535	714.853906	Q	303.177530	152.092403	286.150981	143.579129			2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLPVSDSVLSGFEQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.3	1619.815506	-0.000938	SLPVSDSVLSGFEQR
3.8	1619.819565	-0.004997	TVPVQPAFSTVPFSQ
2.9	1619.808960	0.005608	CGKAFNQSSTLSIHK
2.3	1619.807648	0.006920	VISSVISVSMSSNPPT
2.2	1619.826950	-0.012382	VTPVEVMPVFPDFK
2.2	1619.826950	-0.012382	VTPVEVMPVFPDFK
1.7	1619.807648	0.006920	VISSVISVSMSSNPPT
1.2	1619.819565	-0.004997	TVPVQPAFSTVPFSQ
1.2	1619.826950	-0.012382	VTPVEVMPVFPDFK
1.0	1619.819519	-0.004951	LPPPGPPPLFENEGK

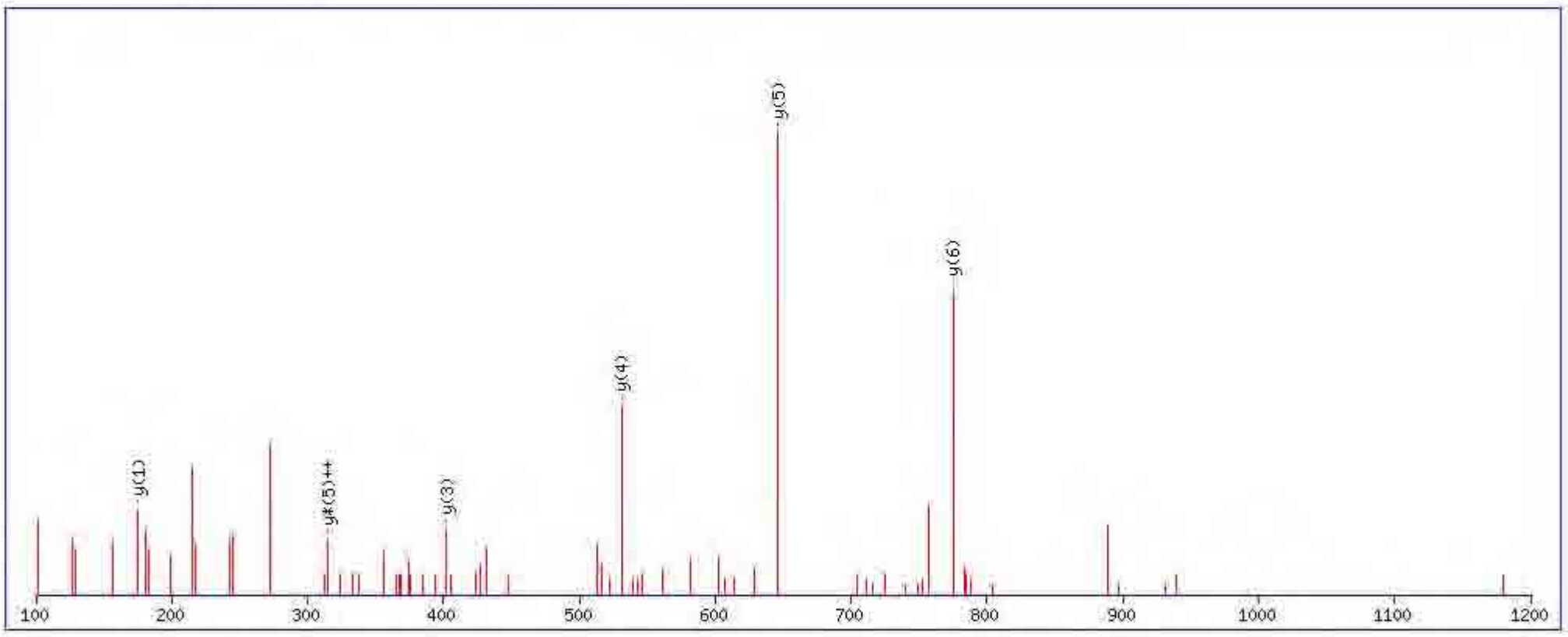
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDERAR**
Found in **EVPL_HUMAN**, Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3

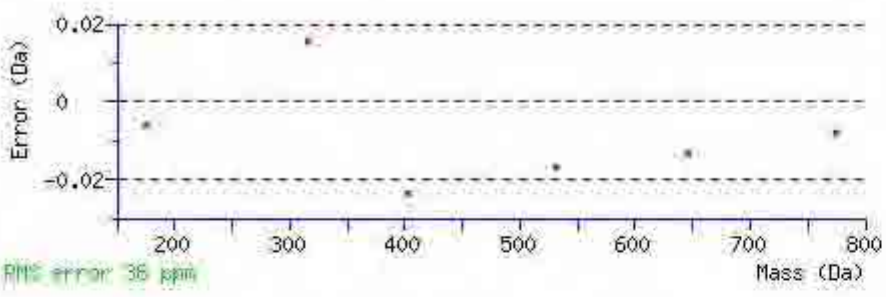
Match to Query 1428: 887.447188 from(444.730870,2+) rtinseconds(808) index(5091)
Title: Locus:1.1.1.1110.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

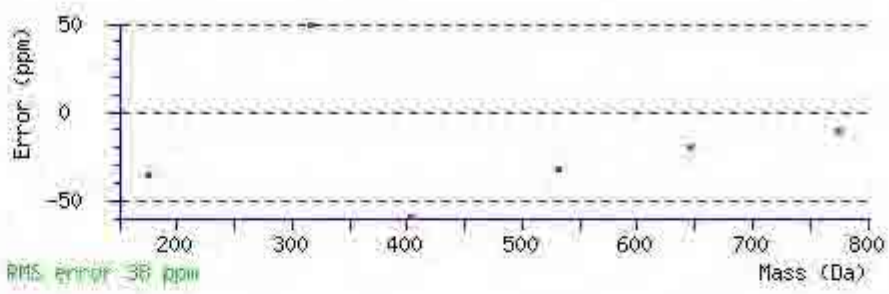
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 887.446060
Ions Score: 43 **Expect:** 0.01
Matches : 6/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							7
2	243.133933	122.070605			225.123368	113.065322	E	*775.369306*	388.188291	758.342757	379.675017	757.358741	379.183009	6
3	358.160876	179.584076			340.150311	170.578794	D	*646.326713*	323.666995	629.300164	*315.153720*	628.316148	314.661712	5
4	487.203469	244.105373			469.192904	235.100090	E	*531.299770*	266.153523	514.273221	257.640249	513.289205	257.148241	4
5	643.304580	322.155928	626.278031	313.642654	625.294015	313.150646	R	*402.257177*	201.632227	385.230628	193.118952			3
6	714.341694	357.674485	697.315145	349.161211	696.331129	348.669203	A	246.156066	123.581671	229.129517	115.068397			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LEDERAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.1	887.446060	0.001128	LEDERAR
30.2	887.450104	-0.002916	IEDVAWR
27.7	887.446060	0.001128	IEDARER
27.7	887.446075	0.001113	LEDRSPR
27.7	887.450104	-0.002916	LEDWVAR
27.7	887.446075	0.001113	PEDRISR
27.7	887.446075	0.001113	PEDSRLR
27.5	887.453476	-0.006288	PEKMVPR
26.3	887.453461	-0.006273	IMPELNR
26.3	887.453461	-0.006273	IMPELNR

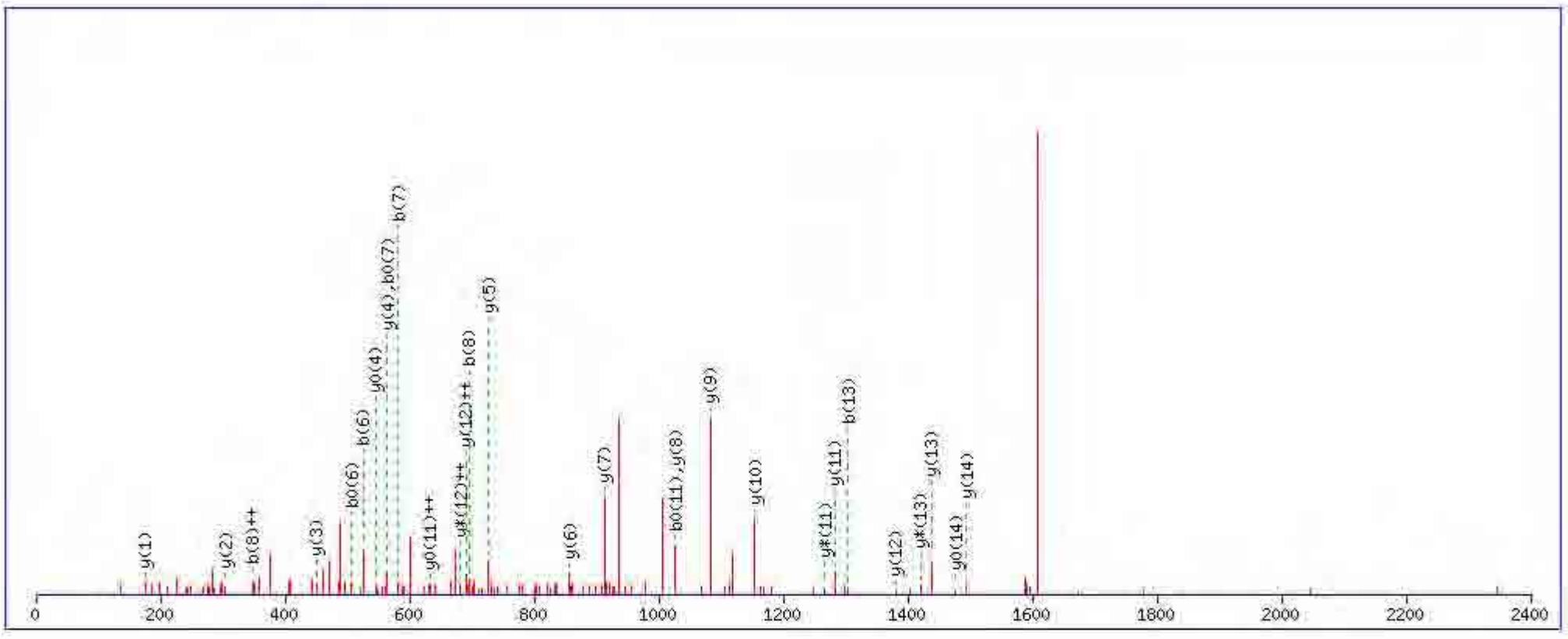
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGGPEAGLGEYLFER**
Found in **FRIL_HUMAN**, Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2

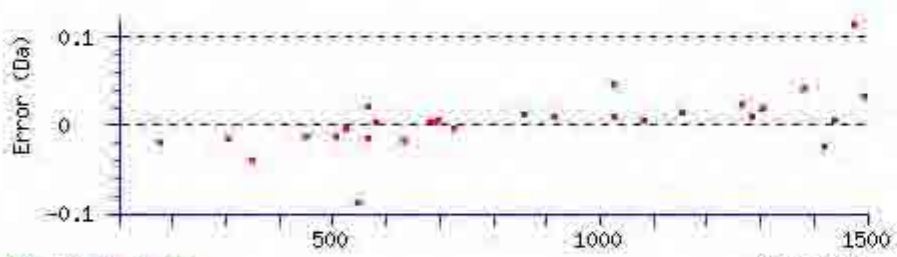
Match to Query 16490: 1606.804708 from(804.409630,2+) rtinseconds(2226) index(22165)
Title: Locus:1.1.1.1895.17
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

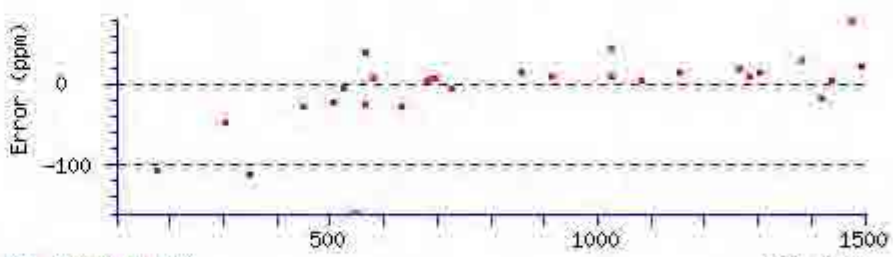
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1606.799103
Ions Score: 64 **Expect:** 2.4e-005
Matches : 29/130 fragment ions using 96 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							15
2	171.112804	86.060040			G	*1494.722336*	747.864806	1477.695787	739.351532	1476.711771	738.859524	14
3	228.134268	114.570772			G	*1437.700872*	719.354074	1420.674323	710.840800	1419.690307	710.348792	13
4	325.187032	163.097154			P	*1380.679408*	690.843342	1363.652859	682.330068	1362.668843	681.838060	12
5	454.229625	227.618450	436.219060	218.613168	E	*1283.626644*	642.316960	1266.600095	633.803686	1265.616079	633.311678	11
6	525.266739	263.137008	507.256174	254.131725	A	*1154.584051*	577.795664	1137.557502	569.282389	1136.573486	568.790381	10
7	582.288203	291.647740	564.277638	282.642457	G	*1083.546937*	542.277107	1066.520388	533.763832	1065.536372	533.271824	9
8	695.372267	348.189772	677.361702	339.184489	L	*1026.525473*	513.766375	1009.498924	505.253100	1008.514908	504.761092	8
9	752.393731	376.700504	734.383166	367.695221	G	*913.441409*	457.224343	896.414860	448.711068	895.430844	448.219060	7
10	881.436324	441.221800	863.425759	432.216518	E	*856.419945*	428.713611	839.393396	420.200336	838.409380	419.708328	6
11	1044.499653	522.753465	1026.489088	513.748182	Y	*727.377352*	364.192314	710.350803	355.679040	709.366787	355.187032	5
12	1157.583717	579.295497	1139.573152	570.290214	L	*564.314023*	282.660650	547.287474	274.147375	546.303458	273.655367	4
13	1304.652131	652.829704	1286.641566	643.824421	F	*451.229959*	226.118618	434.203410	217.605343	433.219394	217.113335	3
14	1433.694724	717.351000	1415.684159	708.345718	E	*304.161545*	152.584411	287.134996	144.071136	286.150980	143.579128	2
15					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LGGPEAGLGEYLFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.1	1606.799103	0.005605	LGGPEAGLGEYLFER
13.8	1606.817749	-0.013041	KLSCSFLVGALPWNG
13.8	1606.803162	0.001546	YVWQGPTSAPILFP
12.2	1606.795258	0.009450	EEPFVFEKILMPE
9.8	1606.795105	0.009603	LGGQAPIDIPPDNPR
8.9	1606.799164	0.005544	GPPGSPGLQGFPGITPP
8.6	1606.795105	0.009603	LGGQAPIDIPPDNPR
8.6	1606.795105	0.009603	LGGQAPIDIPPDNPR
7.0	1606.799164	0.005544	GPPGSPGLQGFPGITPP
6.9	1606.813690	-0.008982	LGQASFEAMASIINR

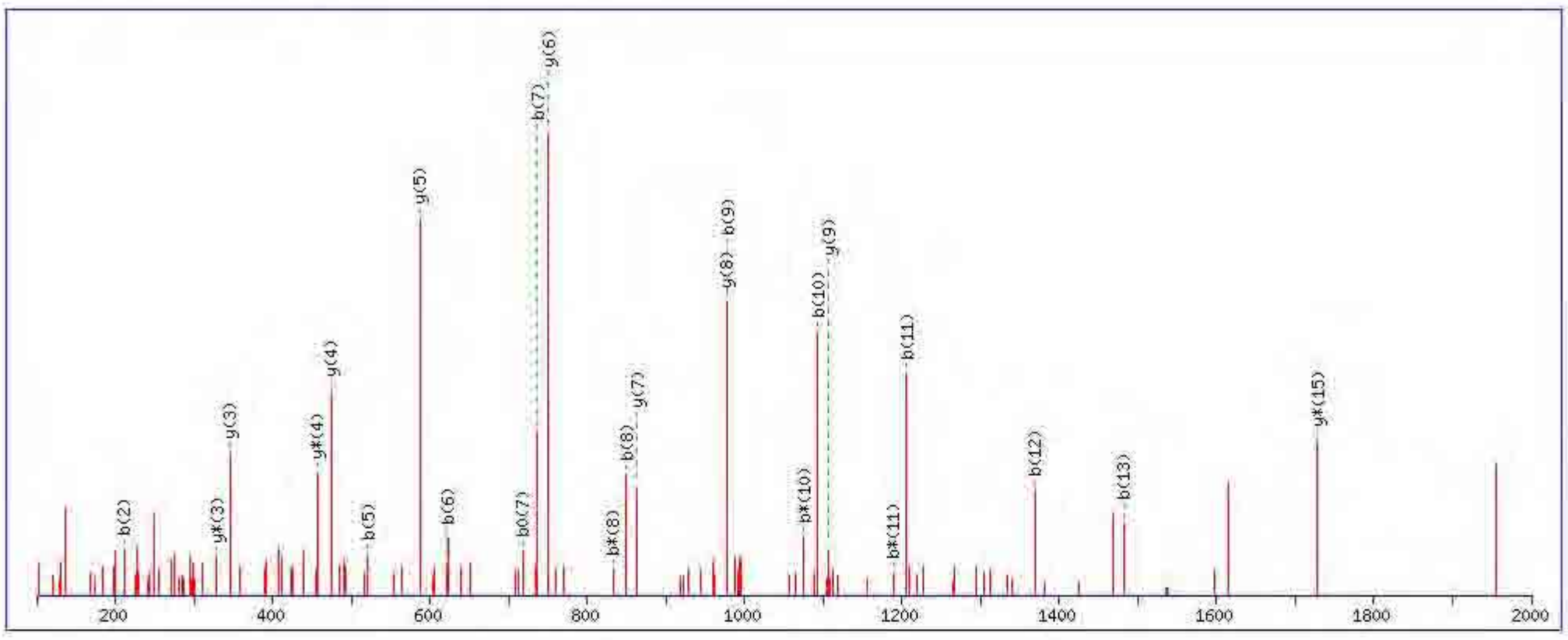
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPPVNTNLENLYLQGNR**
Found in **FMOD_HUMAN**, Fibromodulin OS=Homo sapiens GN=FMOD PE=1 SV=2

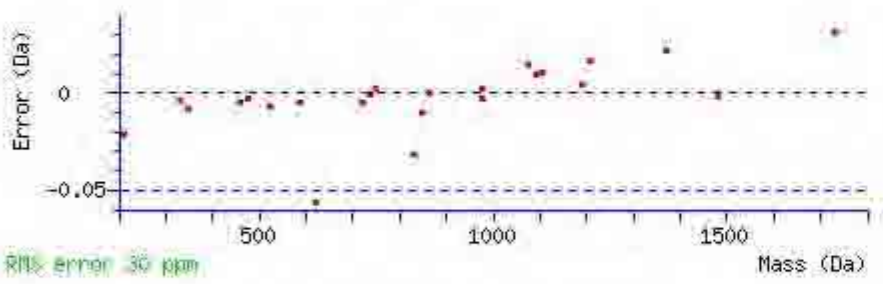
Match to Query 22194: 1954.018842 from(652.346890,3+) rtinseconds(2013) index(19349)
Title: Locus:1.1.1.1780.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

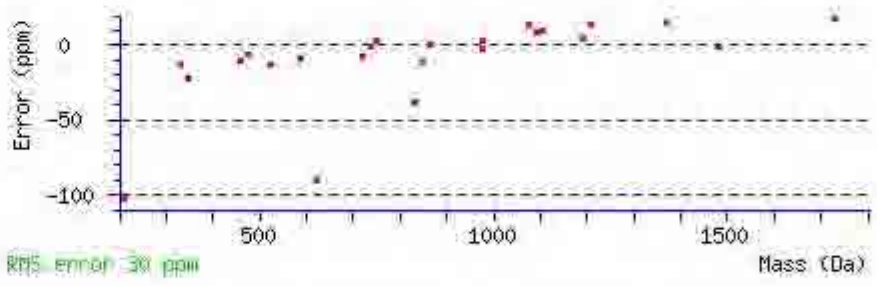
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1954.027191
Ions Score: 54 **Expect:** 3.6e-005
Matches : 24/158 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							17
2	*211.144104*	106.075690					P	1841.950437	921.478857	1824.923888	912.965582	1823.939872	912.473574	16
3	308.196868	154.602072					P	1744.897673	872.952474	1727.871124	864.439200	1726.887108	863.947192	15
4	407.265282	204.136279					V	1647.844909	824.426092	1630.818360	815.912818	1629.834344	815.420810	14
5	*521.308209*	261.157743	504.281660	252.644468			N	1548.776495	774.891885	1531.749946	766.378611	1530.765930	765.886603	13
6	*622.355888*	311.681582	605.329339	303.168308	604.345323	302.676300	T	1434.733568	717.870422	1417.707019	709.357148	1416.723003	708.865139	12
7	*736.398815*	368.703046	719.372266	360.189771	718.388250	359.697763	N	1333.685889	667.346582	1316.659340	658.833308	1315.675324	658.341300	11
8	*849.482879*	425.245078	832.456330	416.731803	831.472314	416.239795	L	1219.642962	610.325119	1202.616413	601.811845	1201.632397	601.319836	10
9	*978.525472*	489.766374	961.498923	481.253100	960.514907	480.761092	E	1106.558898	553.783087	1089.532349	545.269813	1088.548333	544.777805	9
10	*1092.568399*	546.787838	1075.541850	538.274563	1074.557834	537.782555	N	977.516305	489.261790	960.489756	480.748516			8
11	*1205.652463*	603.329869	1188.625914	594.816595	1187.641898	594.324587	L	863.473378	432.240327	846.446829	423.727052			7
12	*1368.715792*	684.861534	1351.689243	676.348260	1350.705227	675.856251	Y	750.389314	375.698295	733.362765	367.185021			6
13	*1481.799856*	741.403566	1464.773307	732.890291	1463.789291	732.398283	L	587.325985	294.166631	570.299436	285.653356			5
14	1609.858434	805.432855	1592.831885	796.919581	1591.847869	796.427573	Q	474.241921	237.624598	457.215372	229.111324			4
15	1666.879898	833.943587	1649.853349	825.430313	1648.869333	824.938304	G	346.183343	173.595309	329.156794	165.082035			3
16	1780.922825	890.965050	1763.896276	882.451776	1762.912260	881.959768	N	289.161879	145.084577	272.135330	136.571303			2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IPPVNTNLENLYLQGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1954.027191	-0.008349	IPPVNTNLENLYLQGNR
6.3	1954.034607	-0.015765	ARYLFLLTGGGALAVAAMGS
5.9	1954.004791	0.014051	PAGPVQAVPPPPPVPTEPK
5.7	1954.015961	0.002881	EAKQPAPEPPKPYSLVR
5.6	1954.023392	-0.004550	FTMLLGALPKTFQDGATK
5.6	1954.015961	0.002881	EAKQPAPEPPKPYSLVR
5.6	1954.015961	0.002881	EAKQPAPEPPKPYSLVR
5.5	1954.009445	0.009397	VMARPPLQWEKVAPER
4.3	1954.027176	-0.008334	NLKHENLQFLTAEER
1.8	1954.015961	0.002881	ALNLDGQHLFEITNLEK

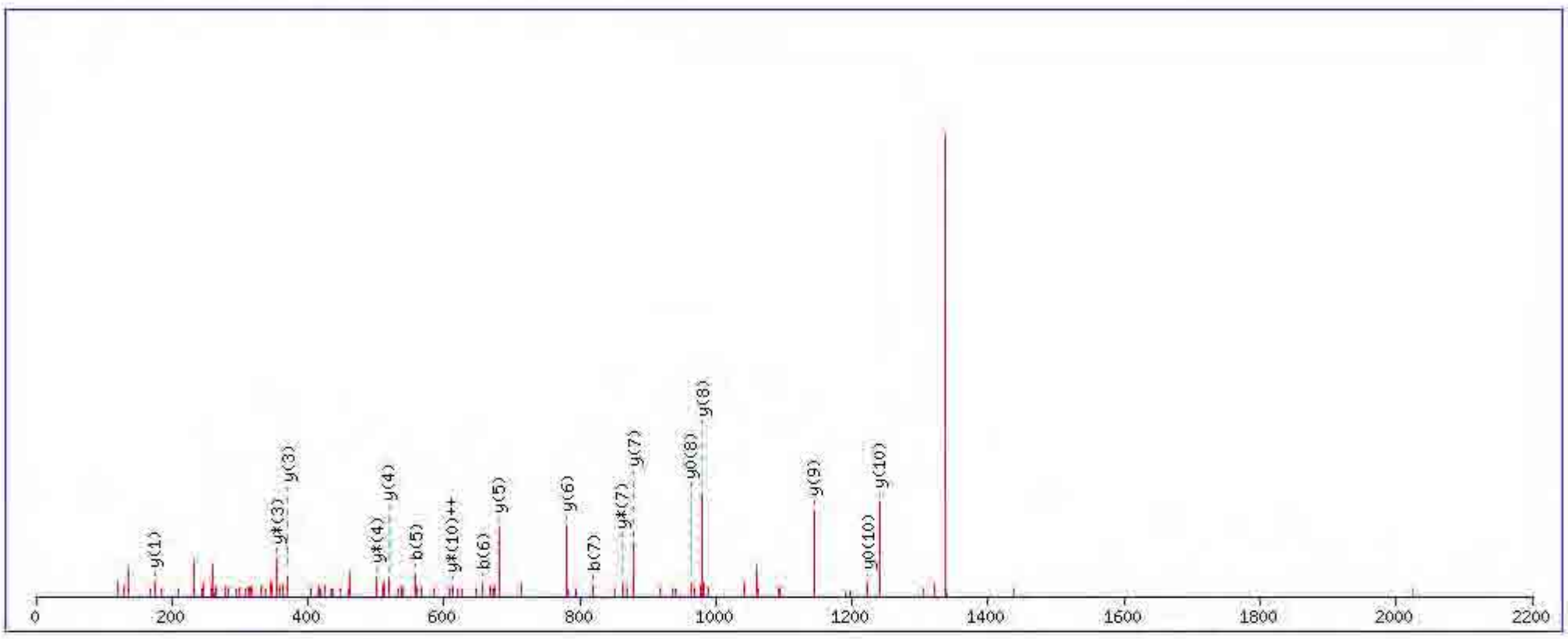
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PPYTVVYFPVR**
Found in **GSTP1_HUMAN**, Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2

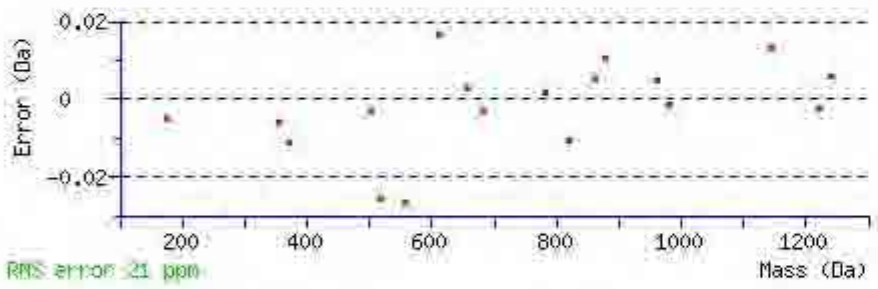
Match to Query 10616: 1336.723908 from(669.369230,2+) rtinseconds(2030) index(19576)
Title: Locus:1.1.1.1789.7
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

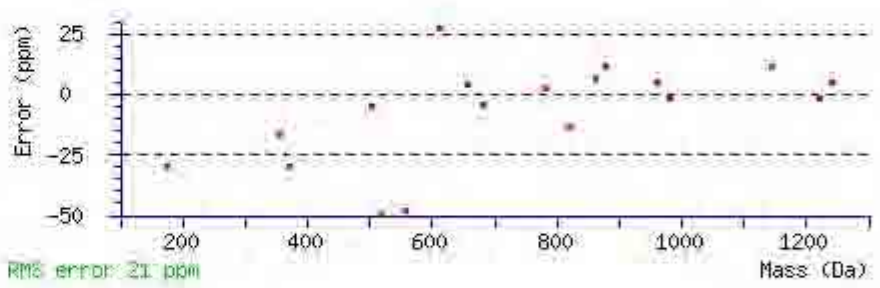
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1336.717972
Ions Score: 56 **Expect:** 2.3e-005
Matches : 18/80 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.060040	49.533658			P							11
2	195.112804	98.060040			P	*1240.672473*	620.839874	1223.645924	612.326600	1222.661908	611.834592	10
3	358.176133	179.591704			Y	*1143.619709*	572.313492	1126.593160	563.800218	1125.609144	563.308210	9
4	459.223812	230.115544	441.213247	221.110262	T	*980.556380*	490.781828	963.529831	482.268553	962.545815	481.776545	8
5	558.292226	279.649751	540.281661	270.644469	V	*879.508701*	440.257988	862.482152	431.744714			7
6	657.360640	329.183958	639.350075	320.178676	V	*780.440287*	390.723781	763.413738	382.210507			6
7	820.423969	410.715622	802.413404	401.710340	Y	*681.371873*	341.189574	664.345324	332.676300			5
8	967.492383	484.249829	949.481818	475.244547	F	*518.308544*	259.657910	501.281995	251.144635			4
9	1064.545147	532.776211	1046.534582	523.770929	P	*371.240130*	186.123703	354.213581	177.610428			3
10	1163.613561	582.310418	1145.602996	573.305136	V	274.187366	137.597321	257.160817	129.084047			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PPYTVVYFPVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	1336.717972	0.005936	PPYTVVYFPVR
6.1	1336.721329	0.002579	FIPMQFGIIQK
4.2	1336.712616	0.011292	DPIPLPVPSLLP
3.6	1336.721130	0.002778	PAELQQPVGRAR
3.3	1336.735046	-0.011138	KALSEHNVLVVE
3.2	1336.713943	0.009965	LFGLEPGRPPPTG
1.8	1336.721130	0.002778	PPSPSQVARLNR
1.5	1336.725174	-0.001266	PPFTHLRTPQK
1.2	1336.723816	0.000092	LLPENNVLSPLP
0.9	1336.723831	0.000077	EPNVQLTPLVID

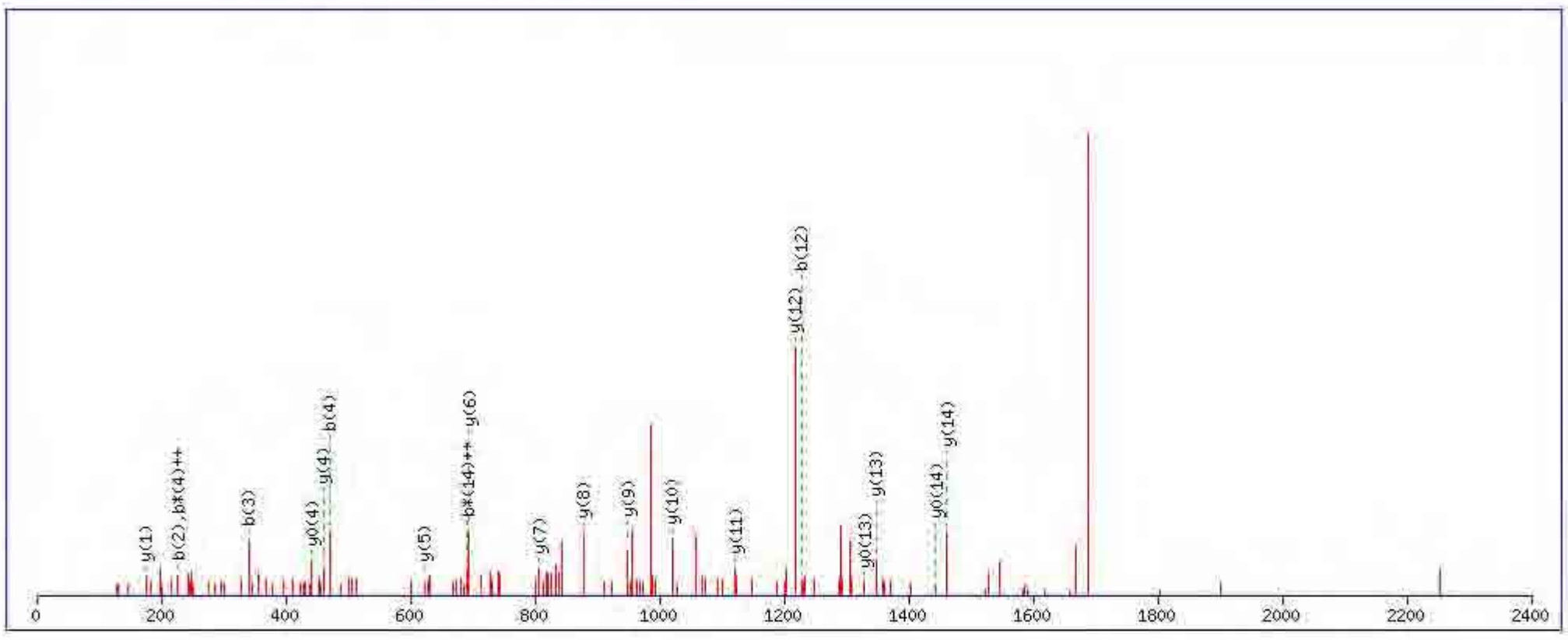
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IINEPTAAAIAYGLDR**
Found in **HSP71_HUMAN**, Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5

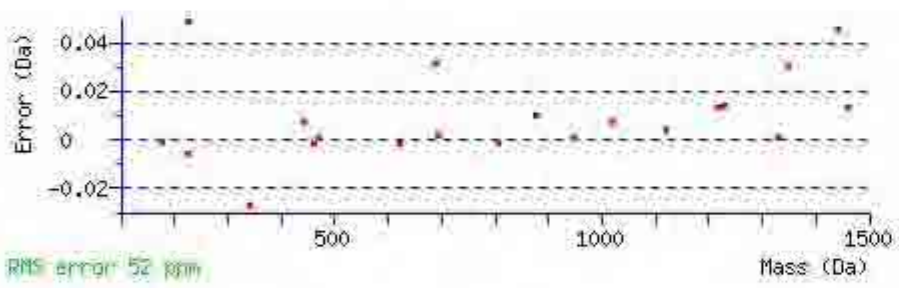
Match to Query 17843: 1686.908048 from(844.461300,2+) rtinseconds(2020) index(19441)
Title: Locus:1.1.1.1783.22
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

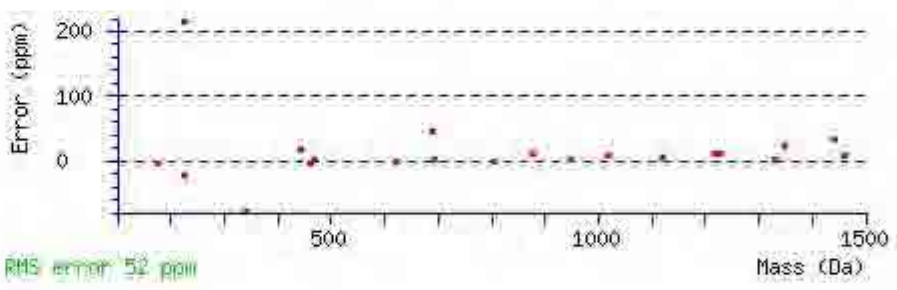
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1686.894043
Ions Score: 56 **Expect:** 2.3e-005
Matches : 21/168 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							16
2	227.175404	114.091340					I	1574.817299	787.912288	1557.790750	779.399013	1556.806734	778.907005	15
3	341.218331	171.112803	324.191782	162.599529			N	1461.733235	731.370255	1444.706686	722.856981	1443.722670	722.364973	14
4	470.260924	235.634100	453.234375	227.120826	452.250359	226.628818	E	1347.690308	674.348792	1330.663759	665.835518	1329.679743	665.343509	13
5	567.313688	284.160482	550.287139	275.647208	549.303123	275.155200	P	1218.647715	609.827495	1201.621166	601.314221	1200.637150	600.822213	12
6	668.361367	334.684322	651.334818	326.171047	650.350802	325.679039	T	1121.594951	561.301113	1104.568402	552.787839	1103.584386	552.295831	11
7	739.398481	370.202879	722.371932	361.689604	721.387916	361.197596	A	1020.547272	510.777274	1003.520723	502.263999	1002.536707	501.771991	10
8	810.435595	405.721436	793.409046	397.208161	792.425030	396.716153	A	949.510158	475.258717	932.483609	466.745442	931.499593	466.253434	9
9	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	A	878.473044	439.740160	861.446495	431.226885	860.462479	430.734877	8
10	994.556773	497.782025	977.530224	489.268750	976.546208	488.776742	I	807.435930	404.221603	790.409381	395.708328	789.425365	395.216320	7
11	1065.593887	533.300582	1048.567338	524.787307	1047.583322	524.295299	A	694.351866	347.679571	677.325317	339.166296	676.341301	338.674288	6
12	1228.657216	614.832246	1211.630667	606.318972	1210.646651	605.826964	Y	623.314752	312.161014	606.288203	303.647740	605.304187	303.155732	5
13	1285.678680	643.342978	1268.652131	634.829704	1267.668115	634.337696	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
14	1398.762744	699.885010	1381.736195	691.371736	1380.752179	690.879727	L	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
15	1513.789687	757.398482	1496.763138	748.885207	1495.779122	748.393199	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IINEPTAAAIAYGLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.2	1686.894043	0.014005	IINEPTAAAIAYGLDR
6.3	1686.898102	0.009946	LLNPFQPSPKSPFLS
5.7	1686.898102	0.009946	LPPPGALLWLQEPQP
5.7	1686.898102	0.009946	LPPPGALLWLQEPQP
5.3	1686.922592	-0.014544	SILQVSIKMTTEPPK
5.2	1686.919205	-0.011157	LENIQIPEAPPPIPK
4.3	1686.919205	-0.011157	LENIQIPEAPPPIPK
4.2	1686.897430	0.010618	IVKEPEINTTLQMR
3.6	1686.894089	0.013959	VVDVGNPEEVRLFSK
3.2	1686.904816	0.003232	MLAATDIALNTCILPK

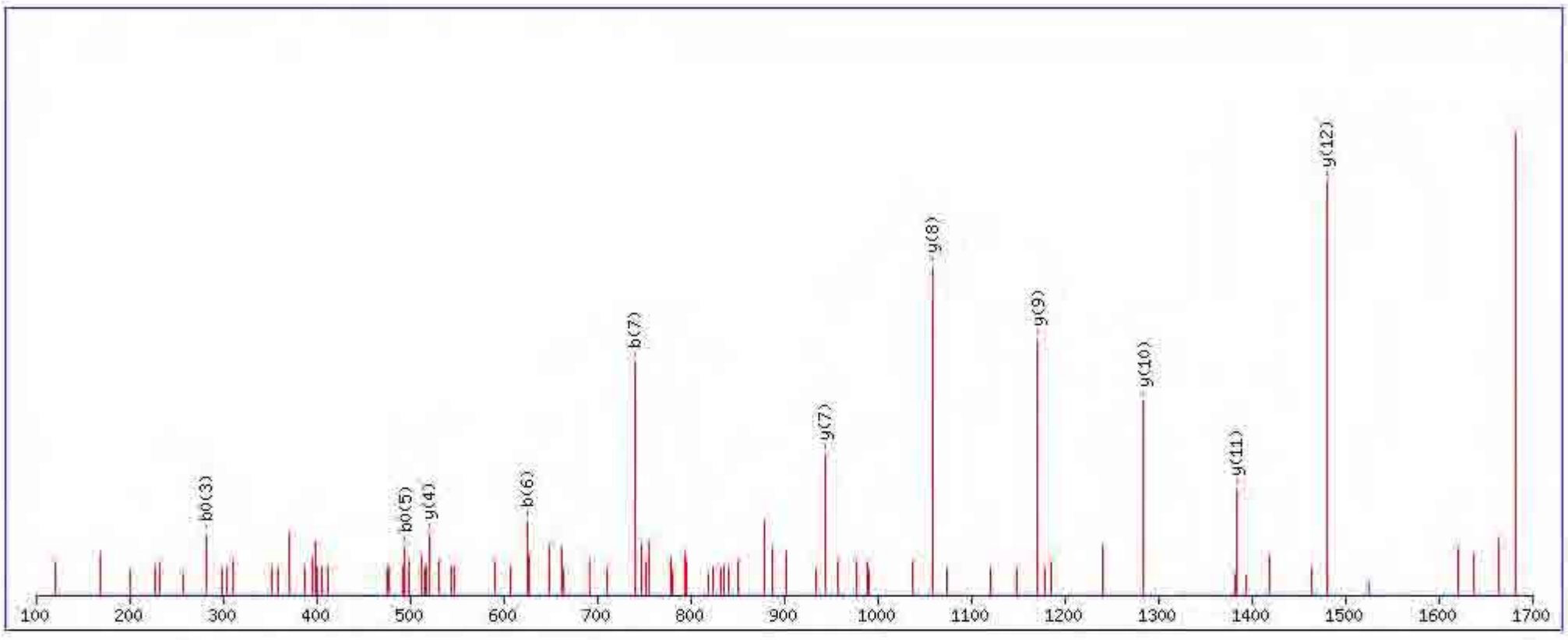
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSPVLIDFFEDTER**
Found in **HRG_HUMAN**, Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1

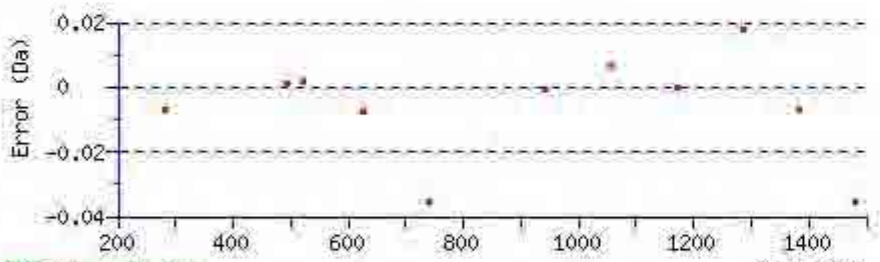
Match to Query 17763: 1681.799208 from(841.906880,2+) rtinseconds(2675) index(27934)
Title: Locus:1.1.1.2134.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

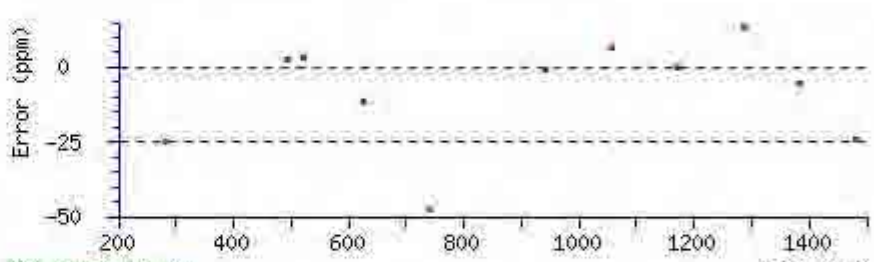
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1681.783539
Ions Score: 52 Expect: 6.4e-005
Matches : 11/128 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							14
2	203.066247	102.036761	185.055682	93.031479	S	1567.763865	784.385570	1550.737316	775.872296	1549.753300	775.380288	13
3	300.119011	150.563143	282.108446	141.557861	P	*1480.731837*	740.869557	1463.705288	732.356282	1462.721272	731.864274	12
4	399.187425	200.097350	381.176860	191.092068	V	*1383.679073*	692.343175	1366.652524	683.829900	1365.668508	683.337892	11
5	512.271489	256.639383	494.260924	247.634100	L	*1284.610659*	642.808967	1267.584110	634.295693	1266.600094	633.803685	10
6	625.355553	313.181415	607.344988	304.176132	I	*1171.526595*	586.266936	1154.500046	577.753661	1153.516030	577.261653	9
7	740.382496	370.694886	722.371931	361.689603	D	*1058.442531*	529.724903	1041.415982	521.211629	1040.431966	520.719621	8
8	887.450910	444.229093	869.440345	435.223810	F	*943.415588*	472.211432	926.389039	463.698158	925.405023	463.206150	7
9	1034.519324	517.763300	1016.508759	508.758017	F	796.347174	398.677225	779.320625	390.163951	778.336609	389.671943	6
10	1163.561917	582.284596	1145.551352	573.279314	E	649.278760	325.143018	632.252211	316.629744	631.268195	316.137736	5
11	1278.588860	639.798068	1260.578295	630.792785	D	*520.236167*	260.621722	503.209618	252.108447	502.225602	251.616439	4
12	1379.636539	690.321907	1361.625974	681.316625	T	405.209224	203.108250	388.182675	194.594976	387.198659	194.102968	3
13	1508.679132	754.843204	1490.668567	745.837921	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
14					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DSPVLIDFFEDTER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1681.783539	0.015669	DSPVLIDFFEDTER
6.7	1681.798843	0.000365	GPPFPPPPPPGTVFGASP
6.6	1681.806000	-0.006792	PVEPGPDPELRSWR
6.4	1681.806015	-0.006807	VTPDTDWARLLQDH
4.1	1681.806000	-0.006792	DSQRNSPFQIPPPSP
2.1	1681.798141	0.001067	TRPSFSLMSSPATTSP
2.1	1681.798141	0.001067	GESCPQAAQGPLLPPGL
2.1	1681.798141	0.001067	GESCPQAAQGPLLPPGL
2.0	1681.806015	-0.006807	PADVPRVSTDAFYGR
1.7	1681.813187	-0.013979	NAHSSKDEVQNAVQR

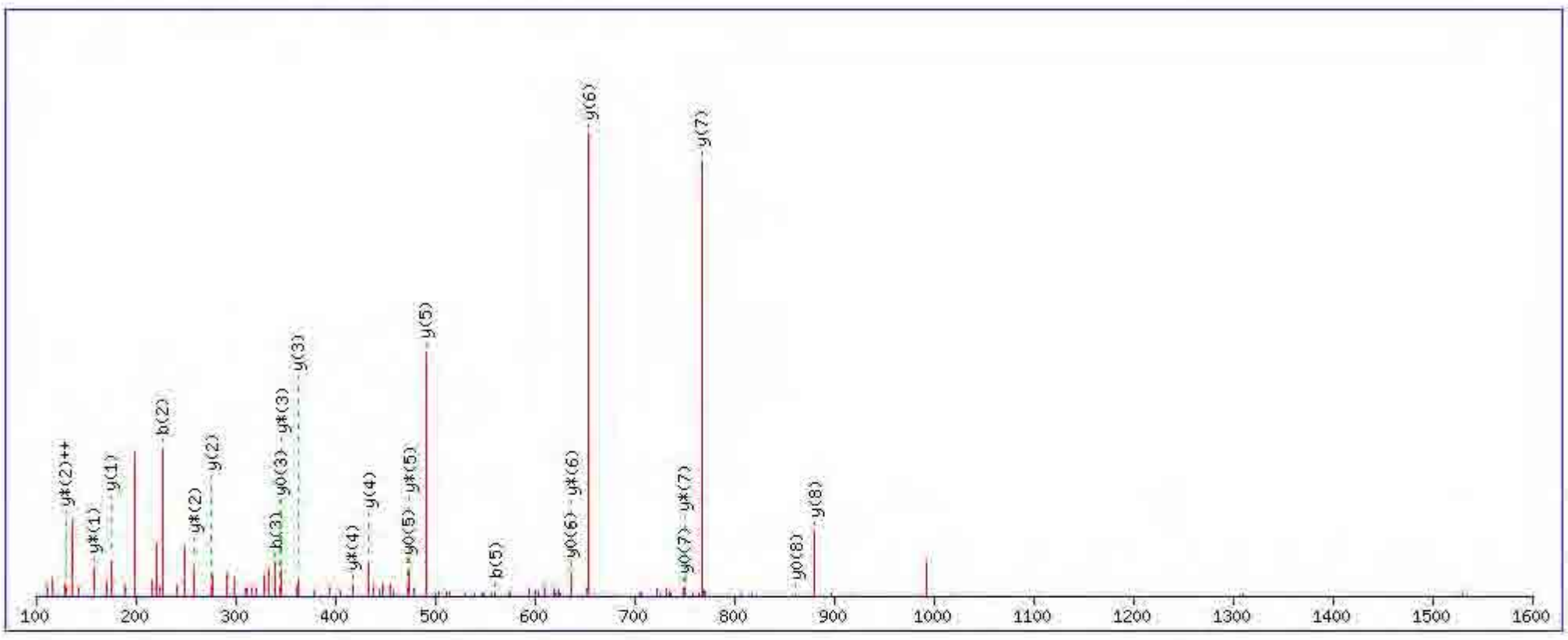
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

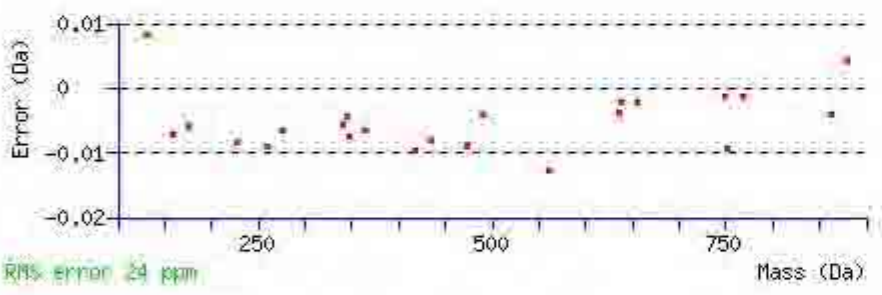
Match to Query 2966: 992.559428 from(497.286990,2+) rtinseconds(1349) index(10984)
Title: Locus:1.1.1.1416.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

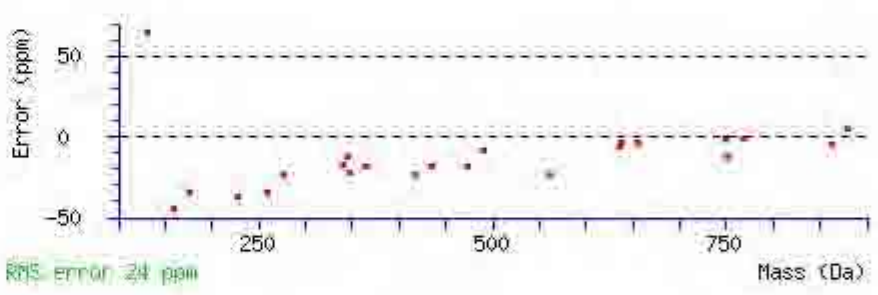
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 41 **Expect:** 0.0074
Matches : 24/66 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	*363.198659*	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	992.565460	-0.006032	LLIYGASTR
40.5	992.565460	-0.006032	LLIYGATSR
19.9	992.554245	0.005183	ILPPLSPPQ
18.3	992.565460	-0.006032	LIINSSPHL
17.8	992.554260	0.005168	LPPTPVGPAL
17.5	992.554245	0.005183	IPPPLPKPA
16.8	992.565475	-0.006047	PLLGPPDIR
16.7	992.555588	0.003840	IPLGWHVR
16.7	992.565460	-0.006032	LILGPHESK
16.7	992.565491	-0.006063	PLLGTVPHK

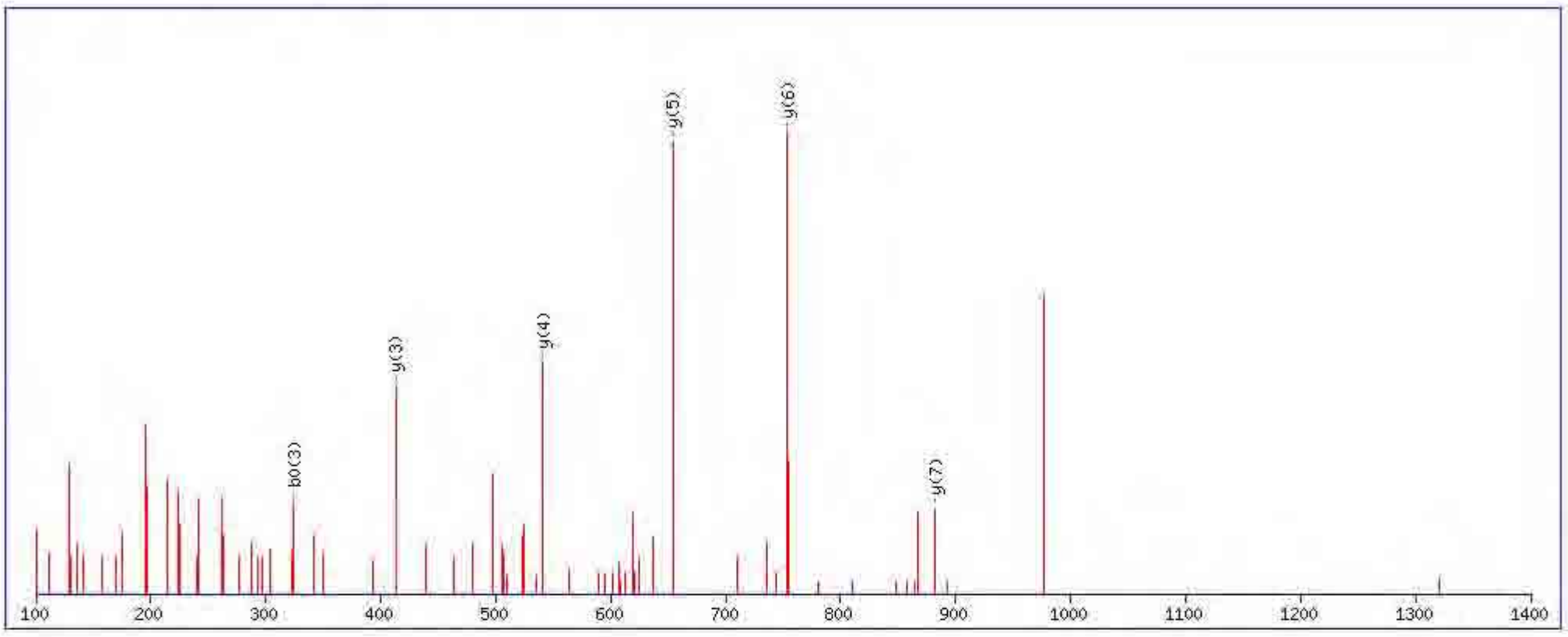
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEVLQQHE**
Found in **IMA3_HUMAN**, Importin subunit alpha-3 OS=Homo sapiens GN=KPNA3 PE=1 SV=2

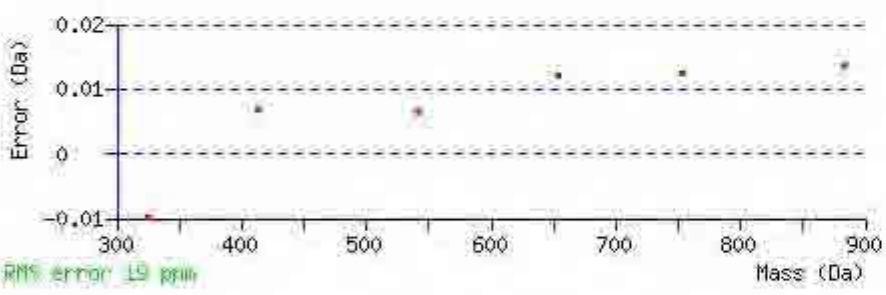
Match to Query 2994: 994.513648 from(498.264100,2+) rtinseconds(886) index(6139)
Title: Locus:1.1.1.1153.10
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

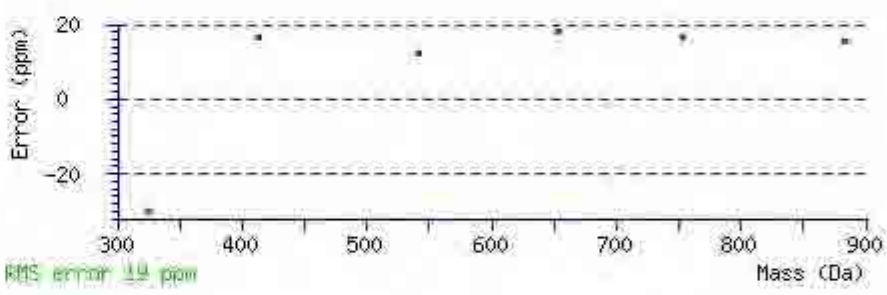
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 994.508347
Ions Score: 33 **Expect:** 0.0054
Matches : 6/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							8
2	243.133933	122.070605			225.123368	113.065322	E	*882.431573*	441.719425	865.405024	433.206150	864.421008	432.714142	7
3	342.202347	171.604812			324.191782	162.599529	V	*753.388980*	377.198128	736.362431	368.684854	735.378415	368.192846	6
4	455.286411	228.146844			437.275846	219.141561	L	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	5
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	Q	*541.236502*	271.121889	524.209953	262.608615	523.225937	262.116607	4
6	711.403567	356.205422	694.377018	347.692147	693.393002	347.200139	Q	*413.177924*	207.092600	396.151375	198.579325	395.167359	198.087317	3
7	848.462479	424.734878	831.435930	416.221603	830.451914	415.729595	H	285.119346	143.063311			267.108781	134.058028	2
8							E	148.060434	74.533855			130.049869	65.528572	1





NCBI **BLAST** search of IEVLQQHE
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.4	994.508347	0.005301	IEVLQQHE
8.7	994.519089	-0.005441	MELSKLMK
8.4	994.508362	0.005286	LEVGDNHLV
8.4	994.508377	0.005271	QLPPTTVSH
8.4	994.508377	0.005271	QLPPTTVSH
7.6	994.508362	0.005286	EPVPPGDLR
7.4	994.508362	0.005286	PEDPGIVPR
7.3	994.504517	0.009131	IDLLMDFL
7.3	994.504517	0.009131	LDLIYPMV
7.3	994.519592	-0.005944	LIDPHTQR

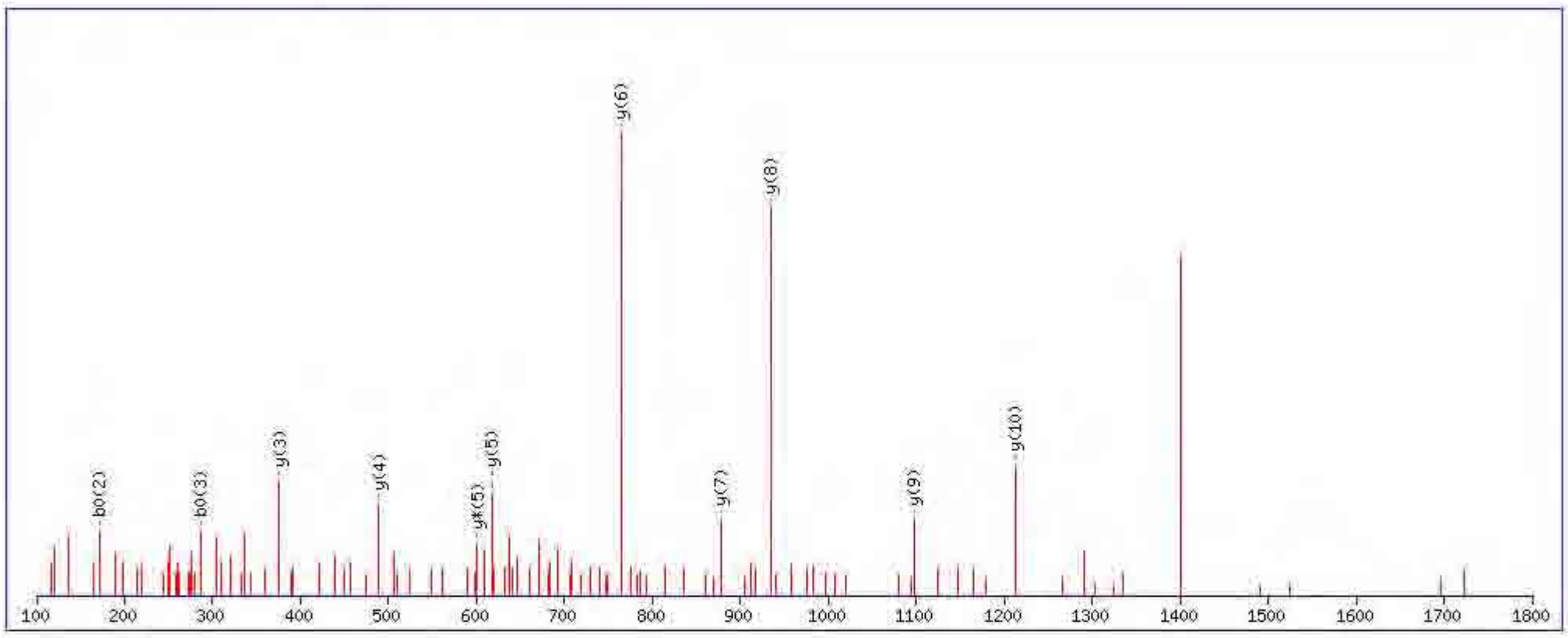
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STDYGIFQINSR**
Found in **LYSC_HUMAN**, Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1

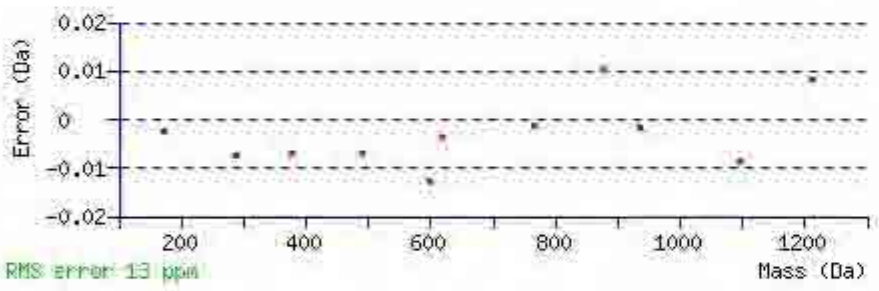
Match to Query 11931: 1399.680308 from(700.847430,2+) rtinseconds(1833) index(17003)
Title: Locus:1.1.1.1681.12
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

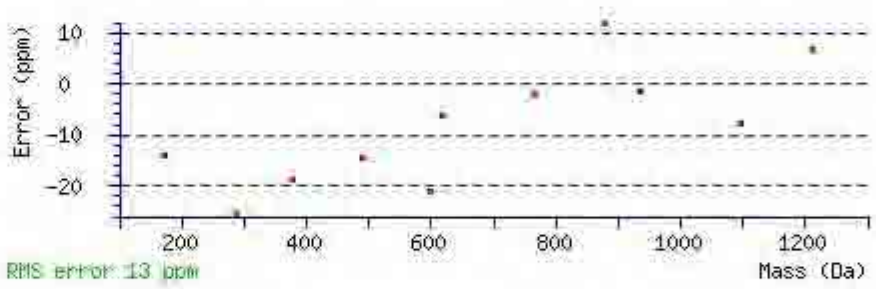
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1399.673187
Ions Score: 66 **Expect:** 5.9e-005
Matches : 11/116 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	189.086983	95.047129			171.076418	86.041847	T	1313.648442	657.327859	1296.621893	648.814585	1295.637877	648.322576	11
3	304.113926	152.560601			286.103361	143.555319	D	*1212.600763*	606.804020	1195.574214	598.290745	1194.590198	597.798737	10
4	467.177255	234.092266			449.166690	225.086983	Y	*1097.573820*	549.290548	1080.547271	540.777274	1079.563255	540.285266	9
5	524.198719	262.602998			506.188154	253.597715	G	*934.510491*	467.758884	917.483942	459.245609	916.499926	458.753601	8
6	637.282783	319.145030			619.272218	310.139747	I	*877.489027*	439.248152	860.462478	430.734877	859.478462	430.242869	7
7	784.351197	392.679237			766.340632	383.673954	F	*764.404963*	382.706120	747.378414	374.192845	746.394398	373.700837	6
8	912.409775	456.708526	895.383226	448.195251	894.399210	447.703243	Q	*617.336549*	309.171913	600.310000	300.658638	599.325984	300.166630	5
9	1025.493839	513.250558	1008.467290	504.737283	1007.483274	504.245275	I	*489.277971*	245.142623	472.251422	236.629349	471.267406	236.137341	4
10	1139.536766	570.272021	1122.510217	561.758747	1121.526201	561.266738	N	*376.193907*	188.600591	359.167358	180.087317	358.183342	179.595309	3
11	1226.568794	613.788035	1209.542245	605.274761	1208.558229	604.782753	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of STDYGIFQINSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.6	1399.673187	0.007121	STDYGIFQINSR
22.0	1399.684418	-0.004110	GPAGPAGYPGAKGER
13.7	1399.684418	-0.004110	GPAGPAGYPGAKGER
10.8	1399.676086	0.004222	GLMLSVMLASLMS
8.1	1399.687805	-0.007497	SHQNLCTKGQVVS
6.0	1399.683090	-0.002782	STDLLSLPNVNPD
4.4	1399.666672	0.013636	RLPGVNMFEQGH
3.7	1399.676529	0.003779	LATEMAASHLDNK
3.2	1399.687775	-0.007467	PSCGGSKLAPQAER
2.3	1399.687820	-0.007512	QPQPGTAGGMRVSV

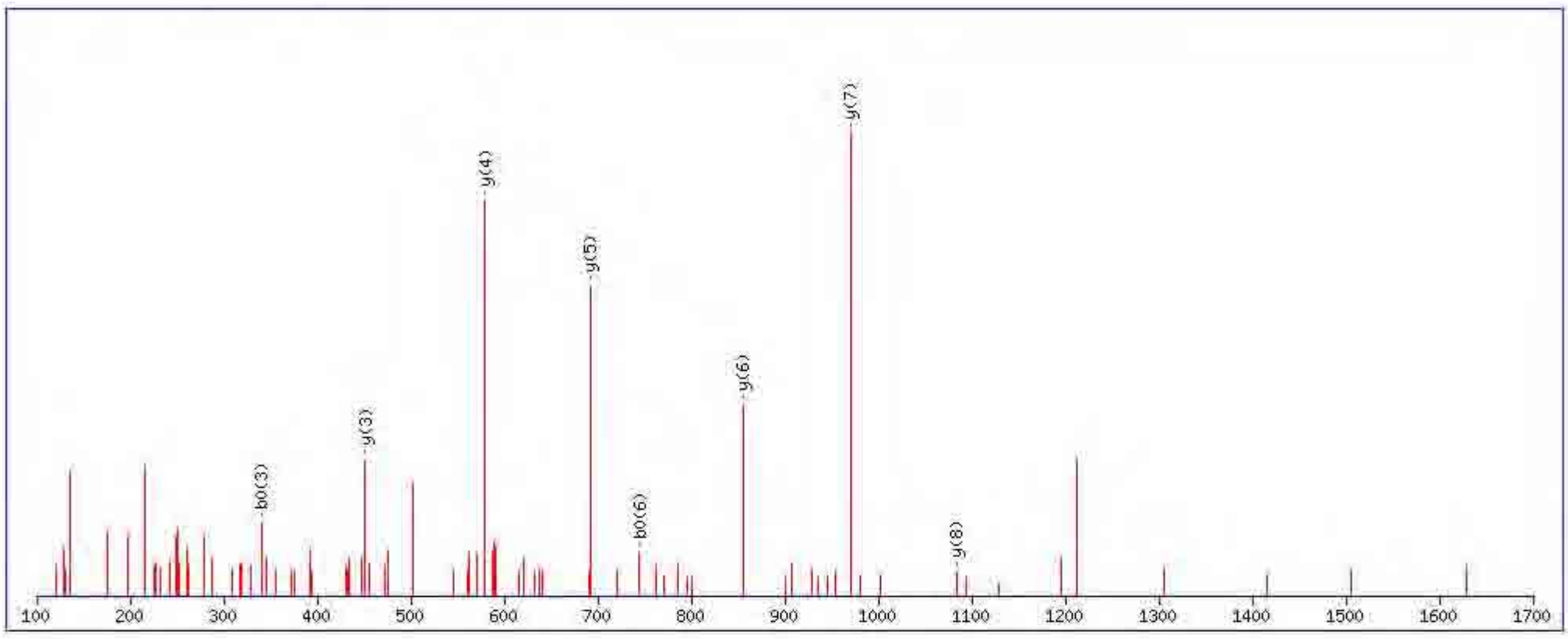
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIDYIQYLR**
Found in **OLFL1_HUMAN**, Olfactomedin-like protein 1 OS=Homo sapiens GN=OLFML1 PE=1 SV=2

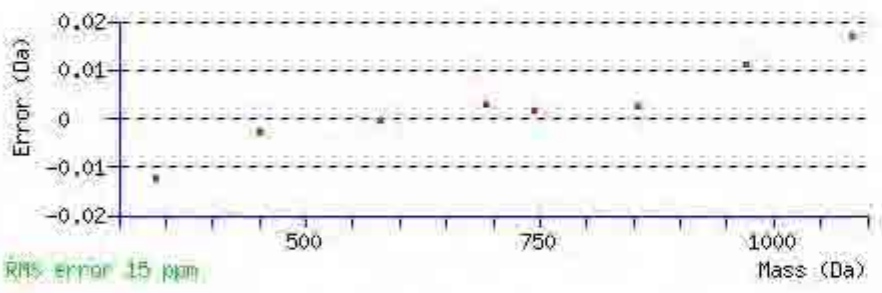
Match to Query 7384: 1211.615208 from(606.814880,2+) rtinseconds(2028) index(19548)
Title: Locus:1.1.1.1788.4
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

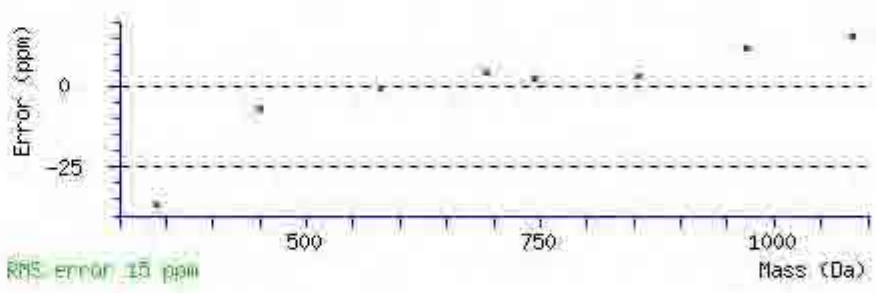
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1211.618607
Ions Score: 45 **Expect:** 0.00062
Matches : 8/74 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							9
2	243.133933	122.070605			225.123368	113.065322	I	*1083.583323*	542.295300	1066.556774	533.782025	1065.572758	533.290017	8
3	358.160876	179.584076			340.150311	170.578794	D	*970.499259*	485.753267	953.472710	477.239993	952.488694	476.747985	7
4	521.224205	261.115741			503.213640	252.110458	Y	*855.472316*	428.239796	838.445767	419.726521			6
5	634.308269	317.657773			616.297704	308.652490	I	*692.408987*	346.708131	675.382438	338.194857			5
6	762.366847	381.687062	745.340298	373.173787	744.356282	372.681779	Q	*579.324923*	290.166099	562.298374	281.652825			4
7	925.430176	463.218726	908.403627	454.705452	907.419611	454.213444	Y	*451.266345*	226.136810	434.239796	217.623536			3
8	1038.514240	519.760758	1021.487691	511.247483	1020.503675	510.755475	L	288.203016	144.605146	271.176467	136.091871			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIDYIQYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	1211.618607	-0.003399	EIDYIQYLR
9.7	1211.614609	0.000599	EPPPKPSRPK
9.4	1211.614609	0.000599	HLSIAVAATDQS
9.1	1211.603363	0.011845	ELDTPPNVEKA
7.8	1211.618637	-0.003429	ELIPKPDTFH
7.8	1211.625839	-0.010631	ELTPRAPGSPR
7.2	1211.603363	0.011845	ELDKVQESPAP
6.8	1211.625824	-0.010616	ELDELRPGQR
6.8	1211.607391	0.007817	ELDLIDYKFG
6.3	1211.618591	-0.003383	ELLLENYYR

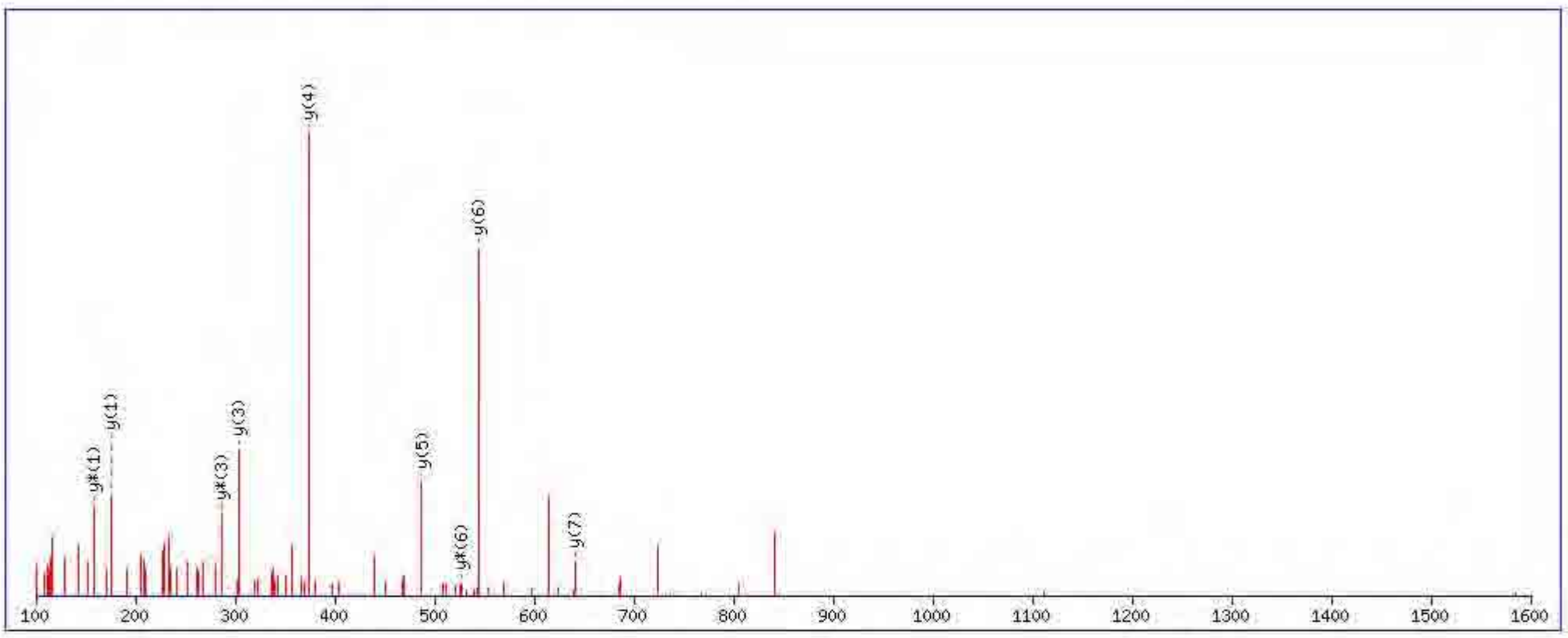
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PSPGPAAGR**
Found in **OTU7A_HUMAN**, OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=1 SV=1

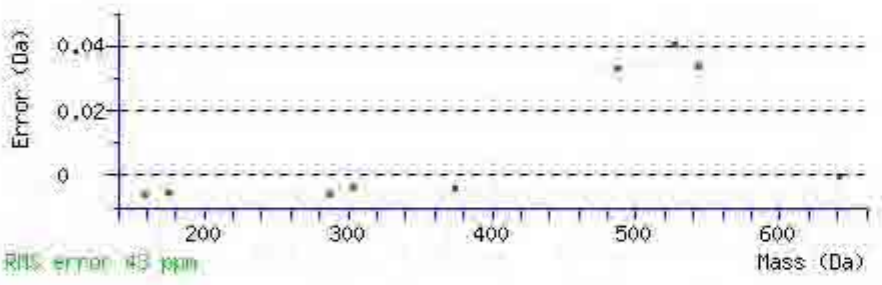
Match to Query 878: 840.414288 from(421.214420,2+) rtinseconds(388) index(464)
Title: Locus:1.1.1.873.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

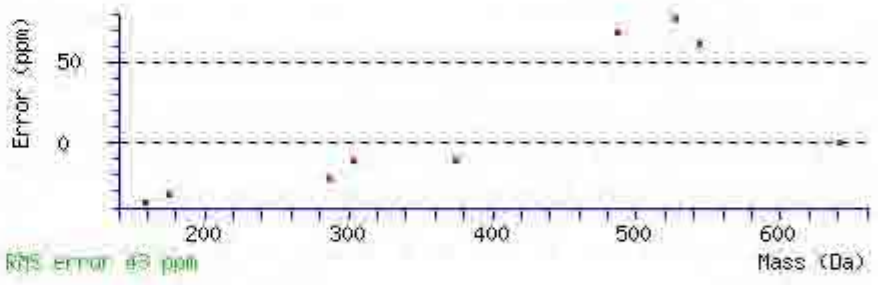
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 840.408981
Variable modifications:
P1 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 45 **Expect:** 0.0036
Matches : 9/64 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116			P							9
2	201.086983	101.047129	183.076418	92.041847	S	728.368579	364.687928	711.342030	356.174653	710.358014	355.682645	8
3	298.139747	149.573512	280.129182	140.568229	P	*641.336551*	321.171914	624.310002	312.658639			7
4	355.161211	178.084243	337.150646	169.078961	G	*544.283787*	272.645532	527.257238	264.132257			6
5	468.208890	234.608083	450.198325	225.602800	P	*487.262323*	244.134799	470.235774	235.621525			5
6	539.246004	270.126640	521.235439	261.121357	A	*374.214644*	187.610960	357.188095	179.097685			4
7	610.283118	305.645197	592.272553	296.639914	A	*303.177530*	152.092403	286.150981	143.579128			3
8	667.304582	334.155929	649.294017	325.150646	G	232.140416	116.573846	215.113867	108.060571			2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PSPGPAAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	840.408981	0.005307	PSPGPAAGR
33.3	840.408981	0.005307	PPAPGAQR
31.9	840.408966	0.005322	EPAGAPQR
31.8	840.408981	0.005307	PSPGPAAGR
30.4	840.408981	0.005307	PPAGSPAGR
28.3	840.408981	0.005307	PSGPPAGAR
21.6	840.408966	0.005322	PEASPGQR
19.3	840.408966	0.005322	EAPQPQR
19.3	840.408981	0.005307	SPPPQQR
18.6	840.408981	0.005307	PPAAPGAGR

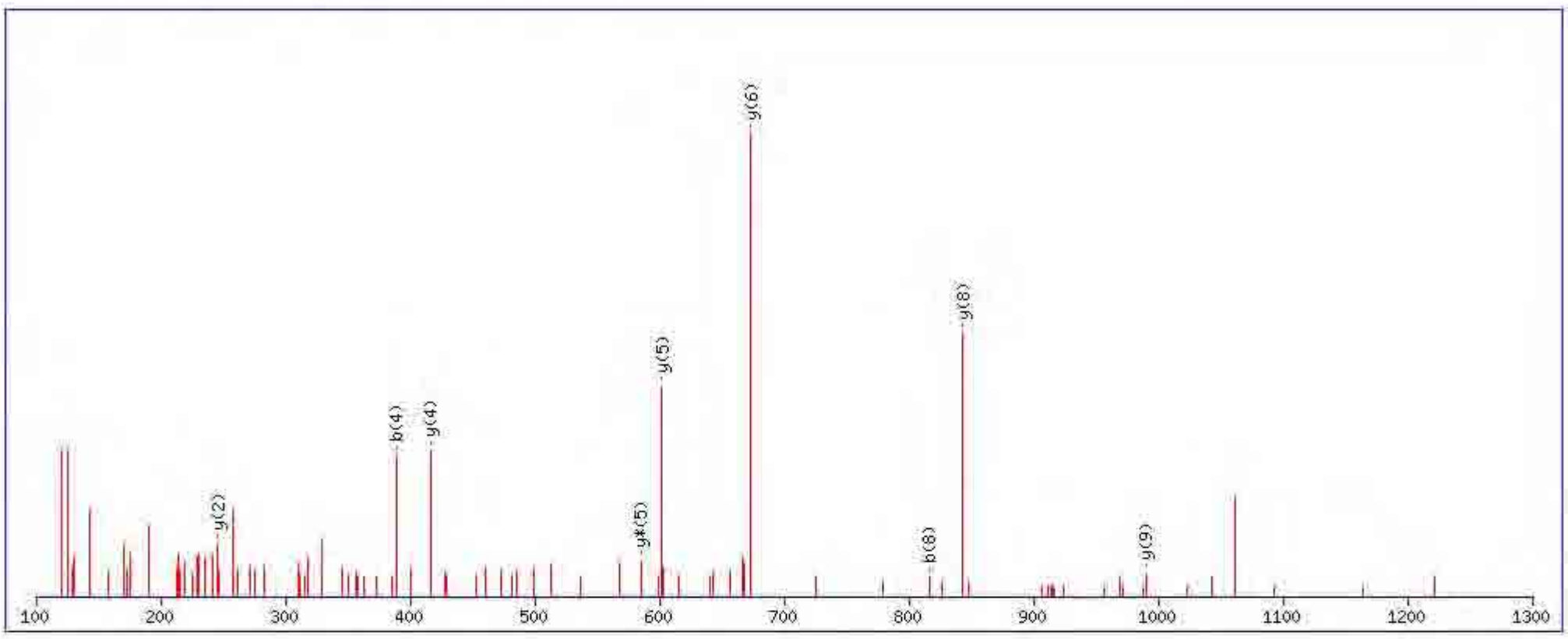
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFVAAWAVAR**
Found in **PTH2R_HUMAN**, Parathyroid hormone 2 receptor OS=Homo sapiens GN=PTH2R PE=1 SV=1

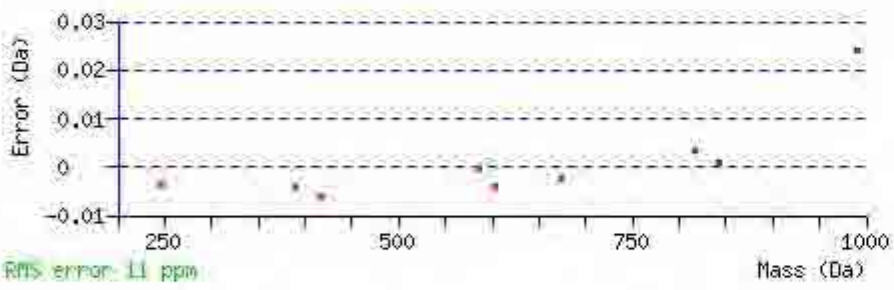
Match to Query 4092: 1060.573488 from(531.294020,2+) rtinseconds(1640) index(14410)
Title: Locus:1.1.1.1576.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

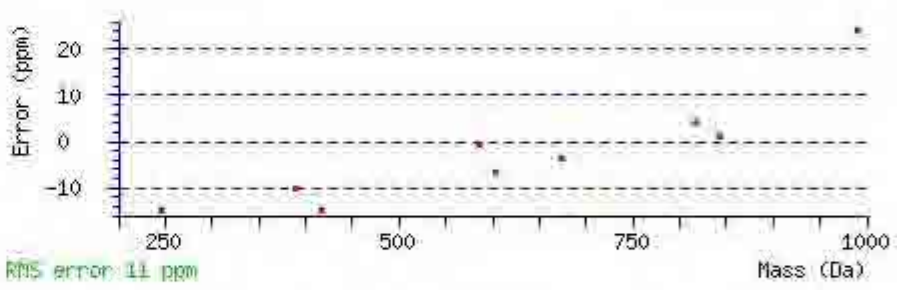
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1060.581787
Ions Score: 36 **Expect:** 0.0046
Matches : 9/54 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833	A					10
2	219.112804	110.060040	F	*990.551963*	495.779620	973.525414	487.266345	9
3	318.181218	159.594247	V	*843.483549*	422.245413	826.457000	413.732138	8
4	**389.218332**	195.112804	A	744.415135	372.711206	727.388586	364.197931	7
5	460.255446	230.631361	A	*673.378021*	337.192649	656.351472	328.679374	6
6	646.334759	323.671018	W	*602.340907*	301.674092	585.314358	293.160817	5
7	717.371873	359.189575	A	*416.261594*	208.634435	399.235045	200.121160	4
8	**816.440287**	408.723782	V	345.224480	173.115878	328.197931	164.602603	3
9	887.477401	444.242339	A	*246.156066*	123.581671	229.129517	115.068397	2
10			R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of AFVAAWAVAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1060.581787	-0.008299	AFVAAWAVAR
10.2	1060.566528	0.006960	AFAGLGPREK
9.8	1060.569901	0.003587	IMQAVSQIR
8.4	1060.569916	0.003572	AMTGRIVGGAL
7.7	1060.577759	-0.004271	QFPASRLAR
7.5	1060.569885	0.003603	AAISRCLLQS
7.2	1060.581787	-0.008299	AIGFAGAIWR
7.2	1060.577744	-0.004256	ALFGANANRK
7.0	1060.569916	0.003572	SPTCRTVAVK
6.2	1060.569901	0.003587	QICKLSGGQK

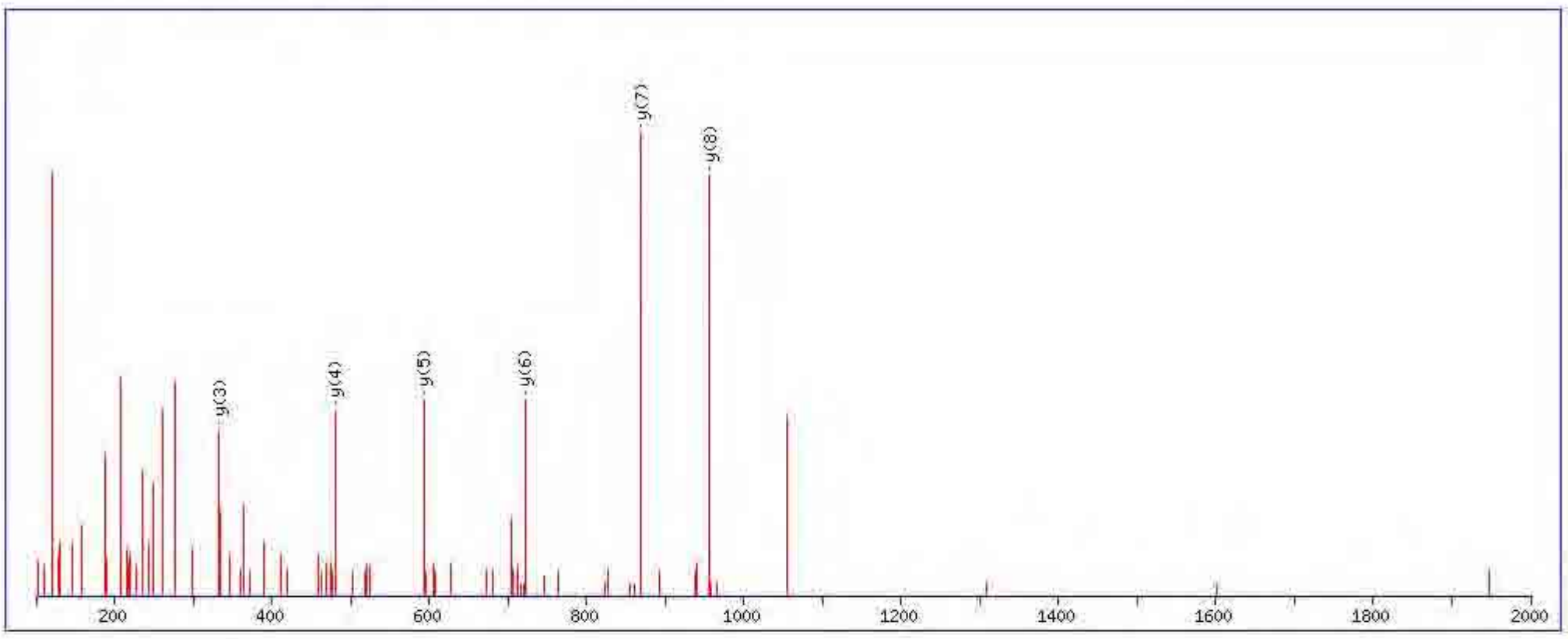
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSFELFADK**
Found in **PPIA_HUMAN**, Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2

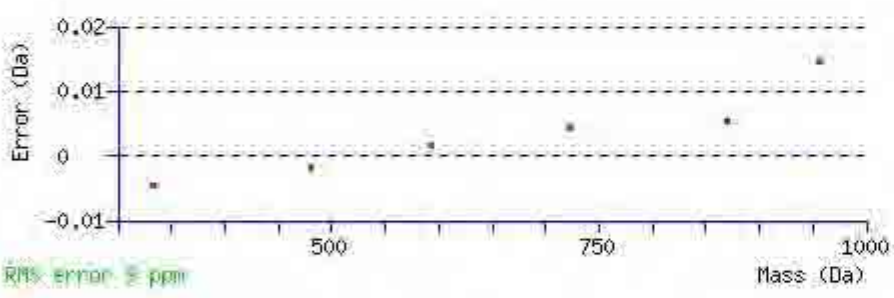
Match to Query 3982: 1054.535688 from(528.275120,2+) rtinseconds(1980) index(18899)
Title: Locus:1.1.1.1762.5
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

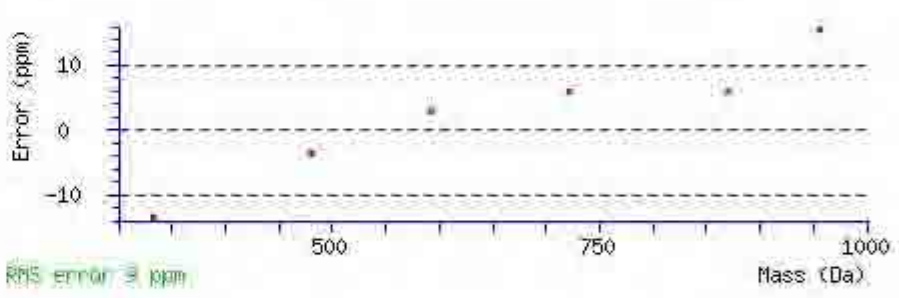
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1054.533508
Ions Score: 48 **Expect:** 0.0031
Matches : 6/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							9
2	187.107718	94.057497	169.097153	85.052214	S	*956.472374*	478.739825	939.445825	470.226551	938.461809	469.734543	8
3	334.176132	167.591704	316.165567	158.586422	F	*869.440346*	435.223811	852.413797	426.710537	851.429781	426.218529	7
4	463.218725	232.113001	445.208160	223.107718	E	*722.371932*	361.689604	705.345383	353.176330	704.361367	352.684322	6
5	576.302789	288.655033	558.292224	279.649750	L	*593.329339*	297.168308	576.302790	288.655033	575.318774	288.163025	5
6	723.371203	362.189240	705.360638	353.183957	F	*480.245275*	240.626275	463.218726	232.113001	462.234710	231.620993	4
7	794.408317	397.707797	776.397752	388.702514	A	*333.176861*	167.092068	316.150312	158.578794	315.166296	158.086786	3
8	909.435260	455.221268	891.424695	446.215985	D	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VSFELFADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	1054.533508	0.002180	VSFELFADK
20.4	1054.533508	0.002180	VYSLLFADQ
10.8	1054.544754	-0.009066	VSFTYVPSR
10.4	1054.536880	-0.001192	VSMLSFISAT
9.2	1054.529495	0.006193	VSPKSPPTDQ
8.3	1054.536880	-0.001192	VAAISLMFST
8.3	1054.540710	-0.005022	VSSPHKSEGK
7.7	1054.529495	0.006193	VSLEHPTSAV
7.7	1054.544739	-0.009051	VSQNGYKFL
7.7	1054.526993	0.008695	MAIPFFTGR

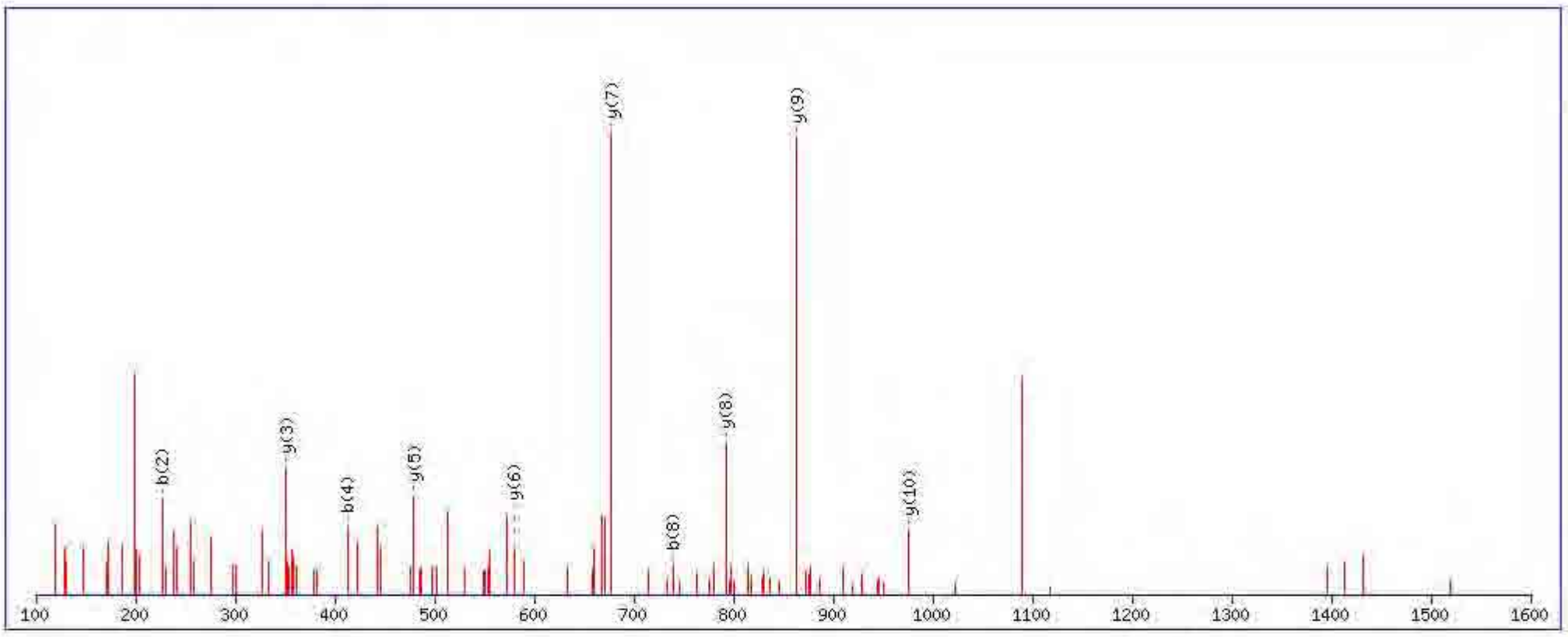
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLADPTGAFGK**
Found in **PRDX5_HUMAN**, Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4

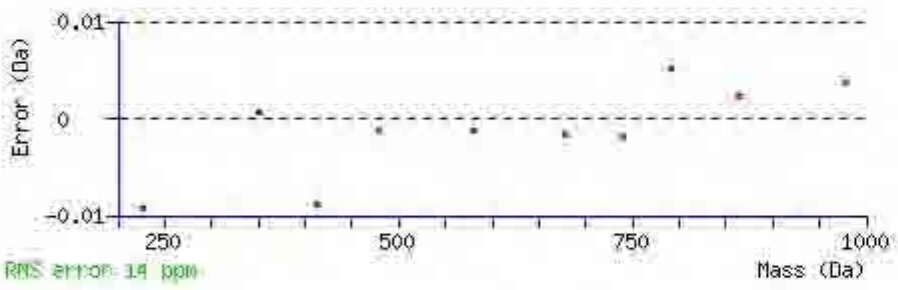
Match to Query 4638: 1088.588028 from(545.301290,2+) rtinseconds(1564) index(13363)
Title: Locus:1.1.1.1534.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

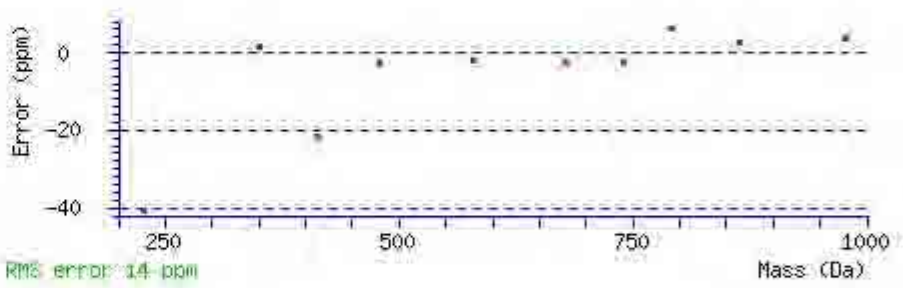
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1088.586609
Ions Score: 46 Expect: 0.0041
Matches : 10/84 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	227.175404	114.091340			L	976.509824	488.758550	959.483275	480.245276	958.499259	479.753268	10
3	298.212518	149.609897			A	863.425760	432.216518	846.399211	423.703244	845.415195	423.211236	9
4	413.239461	207.123369	395.228896	198.118086	D	792.388646	396.697961	775.362097	388.184687	774.378081	387.692679	8
5	510.292225	255.649750	492.281660	246.644468	P	677.361703	339.184490	660.335154	330.671215	659.351138	330.179207	7
6	611.339904	306.173590	593.329339	297.168308	T	580.308939	290.658108	563.282390	282.144833	562.298374	281.652825	6
7	668.361368	334.684322	650.350803	325.679040	G	479.261260	240.134268	462.234711	231.620994			5
8	739.398482	370.202879	721.387917	361.197597	A	422.239796	211.623536	405.213247	203.110261			4
9	886.466896	443.737086	868.456331	434.731804	F	351.202682	176.104979	334.176133	167.591704			3
10	943.488360	472.247818	925.477795	463.242536	G	204.134268	102.570772	187.107719	94.057498			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLADPTGAFGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	1088.586609	0.001419	LLADPTGAFGK
19.0	1088.580078	0.007950	RPPKTPPCPP
10.7	1088.589951	-0.001923	LLAALGEMQK
9.6	1088.589951	-0.001923	LPAVEAAMKK
8.7	1088.589966	-0.001938	PLCGLDLSKK
7.8	1088.578735	0.009293	ILGELAMVLD
7.8	1088.580750	0.007278	LLWHQVFF
7.8	1088.586594	0.001434	LPDAERFLI
6.9	1088.597855	-0.009827	LLGPPPPPRGG
6.9	1088.597855	-0.009827	LLGPPPPPRGG

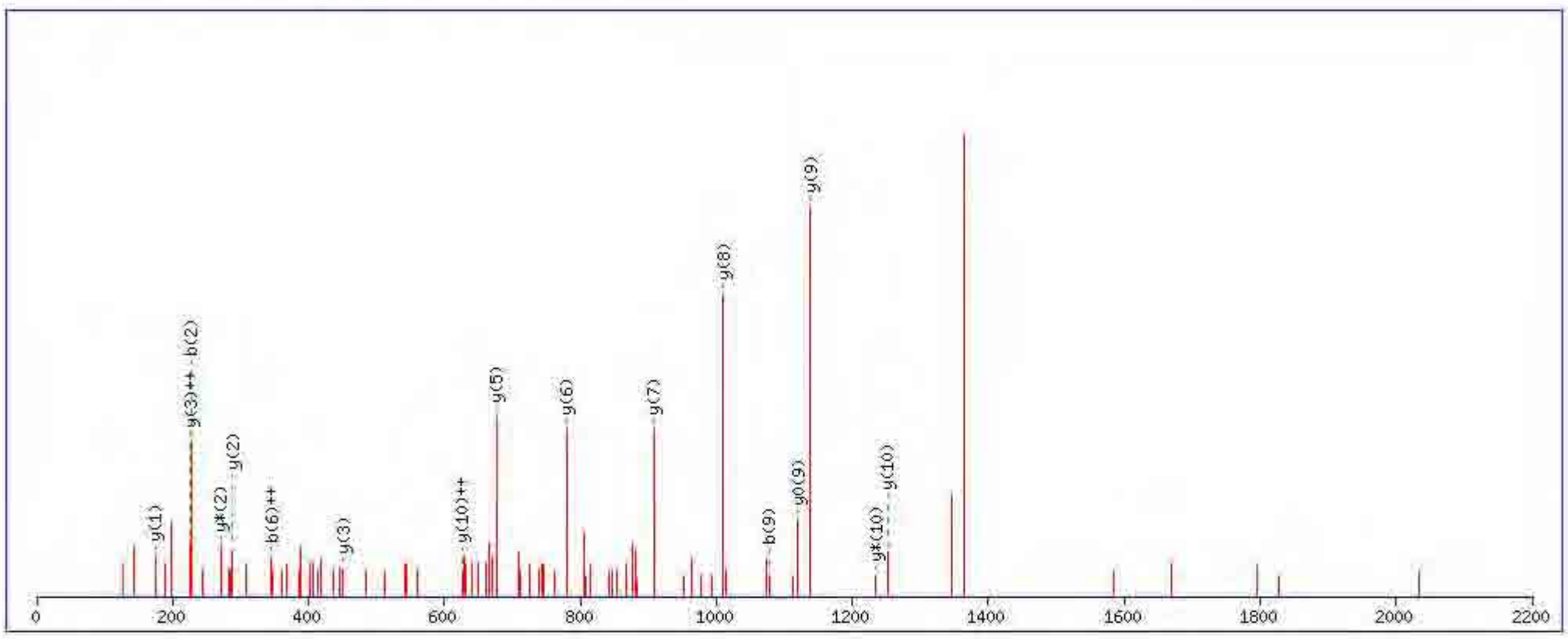
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **S10A8_HUMAN**, Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1

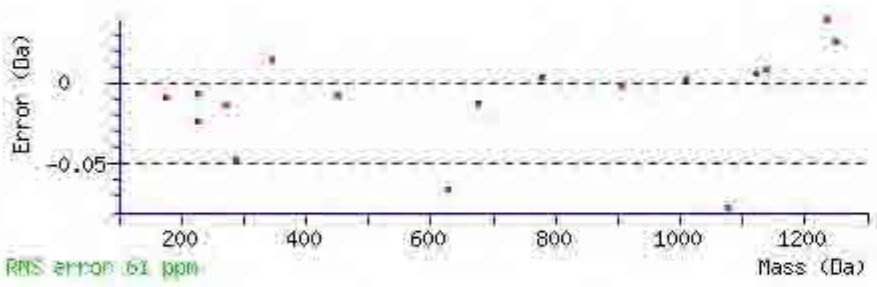
Match to Query 11300: 1363.672468 from(682.843510,2+) rtinseconds(1617) index(14101)
Title: Locus:1.1.1.1563.19
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

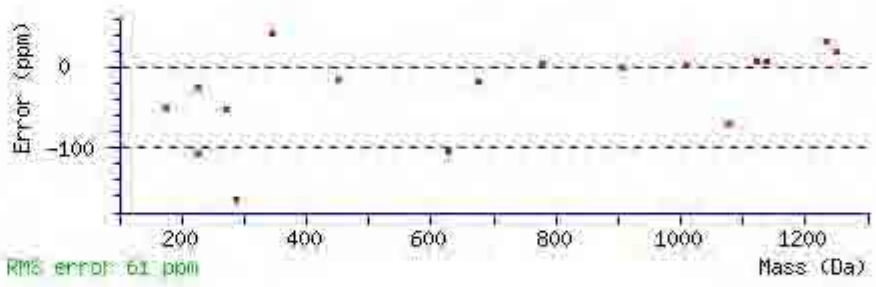
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1363.680557
Ions Score: 46 **Expect:** 0.0057
Matches : 17/90 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	227.175404	114.091340					L	1251.603801	626.305539	1234.577252	617.792264	1233.593236	617.300256	10
3	356.217997	178.612637			338.207432	169.607354	E	1138.519737	569.763507	1121.493188	561.250232	1120.509172	560.758224	9
4	457.265676	229.136476			439.255111	220.131194	T	1009.477144	505.242210	992.450595	496.728936	991.466579	496.236928	8
5	586.308269	293.657773			568.297704	284.652490	E	908.429465	454.718371	891.402916	446.205096	890.418900	445.713088	7
6	689.317454	345.162365			671.306889	336.157083	C	779.386872	390.197074	762.360323	381.683800			6
7	786.370218	393.688747			768.359653	384.683465	P	676.377687	338.692482	659.351138	330.179207			5
8	914.428796	457.718036	897.402247	449.204762	896.418231	448.712754	Q	579.324923	290.166100	562.298374	281.652825			4
9	1077.492125	539.249701	1060.465576	530.736426	1059.481560	530.244418	Y	451.266345	226.136810	434.239796	217.623536			3
10	1190.576189	595.791733	1173.549640	587.278458	1172.565624	586.786450	I	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLETECPQYIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	1363.680557	-0.008089	LLETECPQYIR
27.4	1363.661926	0.010542	LPETEKNYNLQ
20.4	1363.661957	0.010511	ILETSTSSFDHK
17.7	1363.677200	-0.004732	PIEADFSWQKK
16.1	1363.661942	0.010526	PIEPHPKEEPK
16.0	1363.671844	0.000624	IPTEETTISTEK
12.7	1363.673203	-0.000735	LPERPGPSNPPVG
12.7	1363.673203	-0.000735	LPERPGPSNPPVG
11.9	1363.673203	-0.000735	LPERPGPSNPPVG
11.9	1363.673203	-0.000735	LPERPGPSNPPVG

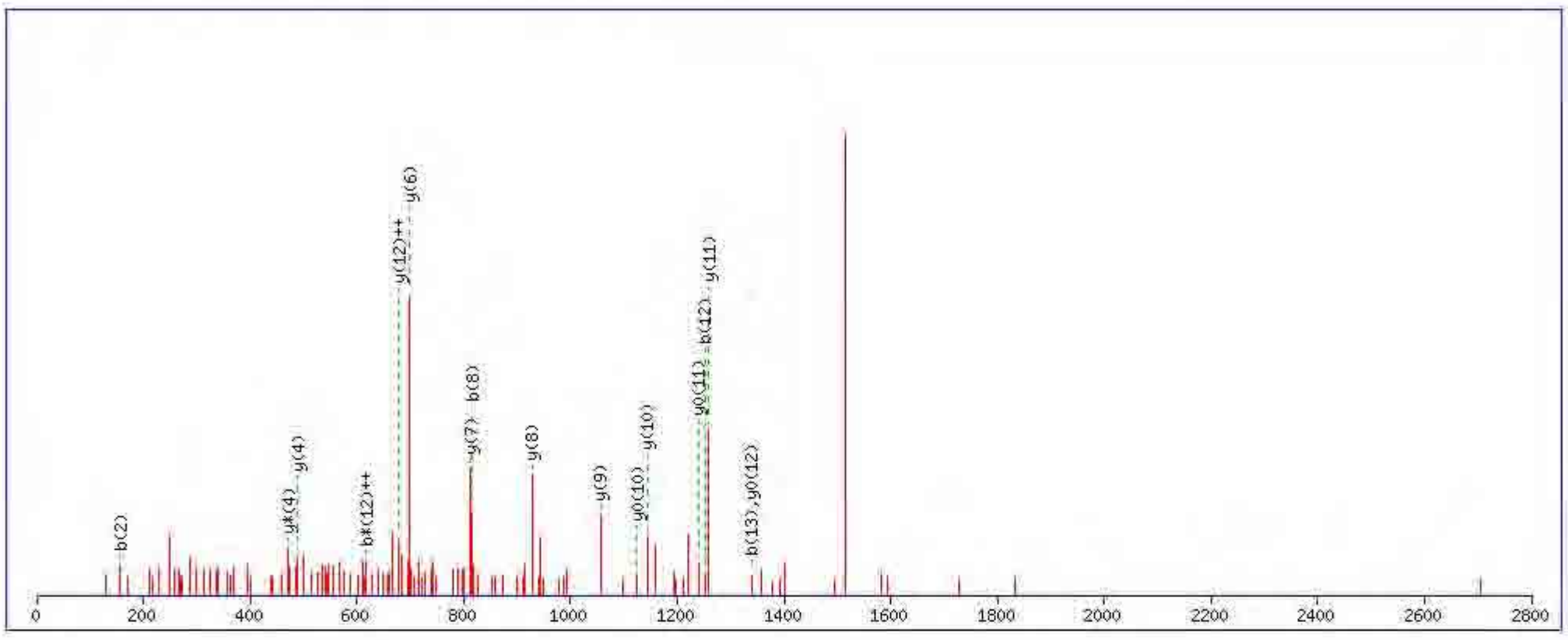
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVVDSEDIPLNLSR**
Found in **TRAP1_HUMAN**, Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3

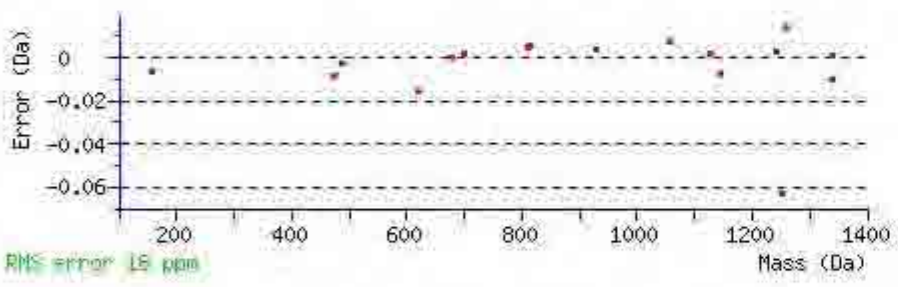
Match to Query 14273: 1512.783728 from(757.399140,2+) rtinseconds(1841) index(17107)
Title: Locus:1.1.1.1685.16
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

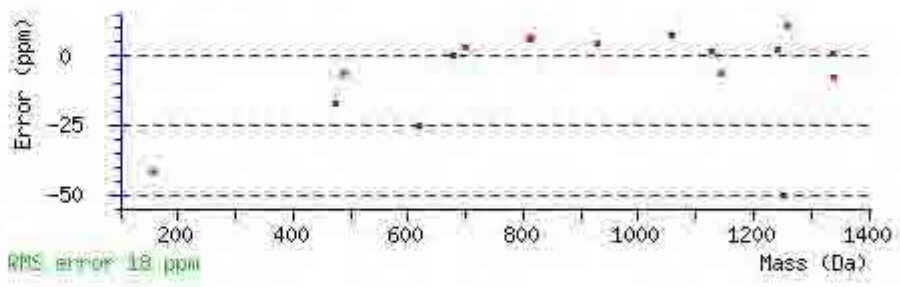
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1512.778381
Ions Score: 32 **Expect:** 0.004
Matches : 17/128 fragment ions using 40 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							14
2	*157.097154*	79.052215					V	1456.764198	728.885737	1439.737649	720.372463	1438.753633	719.880455	13
3	256.165568	128.586422					V	1357.695784	679.351530	1340.669235	670.838256	1339.685219	670.346248	12
4	371.192511	186.099894			353.181946	177.094611	D	*1258.627370*	629.817323	1241.600821	621.304049	1240.616805	620.812040	11
5	458.224539	229.615907			440.213974	220.610625	S	*1143.600427*	572.303852	1126.573878	563.790577	1125.589862	563.298569	10
6	587.267132	294.137204			569.256567	285.131922	E	*1056.568399*	528.787838	1039.541850	520.274563	1038.557834	519.782555	9
7	702.294075	351.650676			684.283510	342.645393	D	*927.525806*	464.266541	910.499257	455.753267	909.515241	455.261259	8
8	*815.378139*	408.192708			797.367574	399.187425	I	*812.498863*	406.753070	795.472314	398.239795	794.488298	397.747787	7
9	912.430903	456.719090			894.420338	447.713807	P	*699.414799*	350.211038	682.388250	341.697763	681.404234	341.205755	6
10	1025.514967	513.261122			1007.504402	504.255839	L	602.362035	301.684656	585.335486	293.171381	584.351470	292.679373	5
11	1139.557894	570.282585	1122.531345	561.769311	1121.547329	561.277303	N	*489.277971*	245.142623	472.251422	236.629349	471.267406	236.137341	4
12	*1252.641958*	626.824617	1235.615409	618.311343	1234.631393	617.819334	L	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	*1339.673986*	670.340631	1322.647437	661.827357	1321.663421	661.335349	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
14							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GVVDSEDIPLNLSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	1512.778381	0.005347	GVVDSEDIPLNLSR
31.8	1512.778381	0.005347	GVVDSEDLPLNISR
5.9	1512.778366	0.005362	EKLTNIPSDQQPK
4.7	1512.779709	0.004019	SAPVHEPPSPRSPR
4.6	1512.789627	-0.005899	RDPSLTPSIGPVSR
4.5	1512.793640	-0.009912	PGSPSLLLPAATWR
3.7	1512.797653	-0.013925	LEPPVYVPPPSYR
2.0	1512.778366	0.005362	RAALPTPALSPEDK
1.9	1512.797012	-0.013284	RPMEVVNTEVKPV
1.1	1512.778381	0.005347	ETEVKDLPGAGPLR

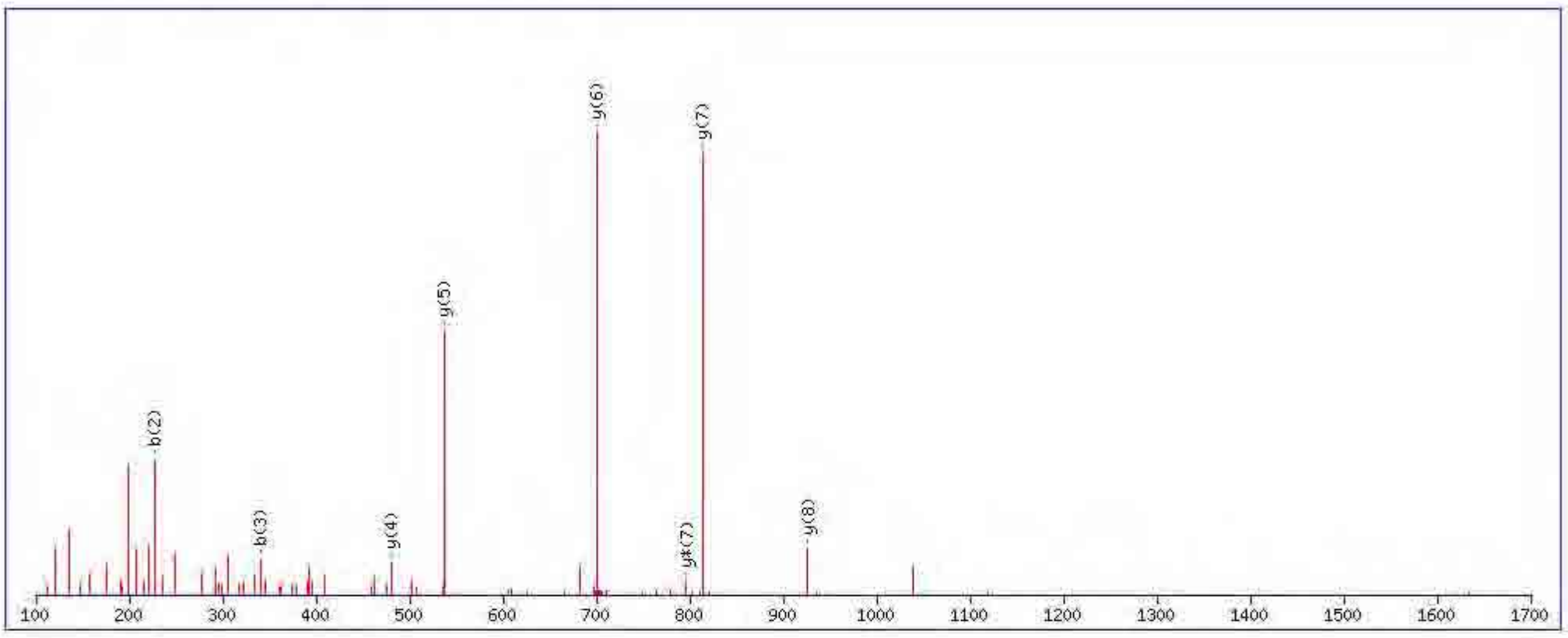
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILIYGNISF**
Found in **RMI1_HUMAN**, RecQ-mediated genome instability protein 1 OS=Homo sapiens GN=RMI1 PE=1 SV=3

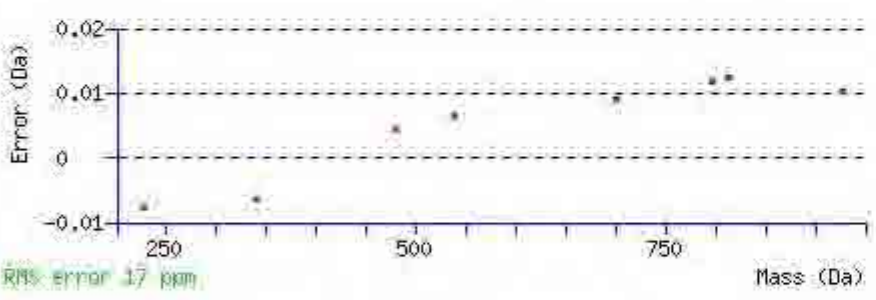
Match to Query 3712: 1038.583428 from(520.298990,2+) rtinseconds(1847) index(17194)
Title: Locus:1.1.1.1689.3
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

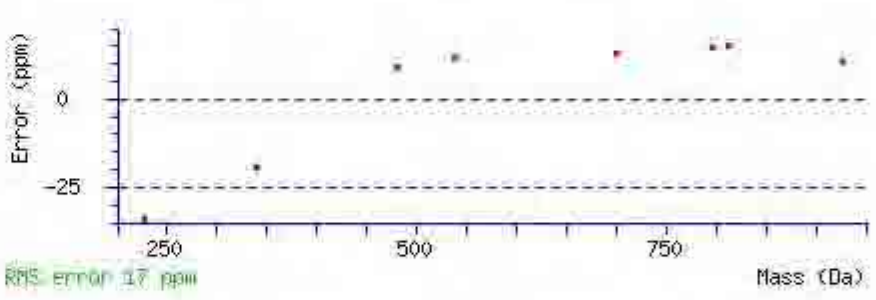
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1038.574966
Ions Score: 46 **Expect:** 0.0023
Matches : 8/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							9
2	227.175404	114.091340					L	926.498195	463.752736	909.471646	455.239461	908.487630	454.747453	8
3	340.259468	170.633372					I	813.414131	407.210704	796.387582	398.697429	795.403566	398.205421	7
4	503.322797	252.165036					Y	700.330067	350.668672	683.303518	342.155397	682.319502	341.663389	6
5	560.344261	280.675769					G	537.266738	269.137007	520.240189	260.623733	519.256173	260.131725	5
6	674.387188	337.697232	657.360639	329.183958			N	480.245274	240.626275	463.218725	232.113000	462.234709	231.620992	4
7	787.471252	394.239264	770.444703	385.725990			I	366.202347	183.604811			348.191782	174.599529	3
8	874.503280	437.755278	857.476731	429.242004	856.492715	428.749996	S	253.118283	127.062779			235.107718	118.057497	2
9							F	166.086255	83.546765					1





NCBI **BLAST** search of ILIYGNISF
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	1038.574966	0.008462	ILIYGNISF
23.5	1038.593414	-0.009986	LPLASGPGRR
20.5	1038.578339	0.005089	LLLGTYMTK
18.1	1038.582184	0.001244	PLPGATPAKR
17.7	1038.582184	0.001244	IPLQNGRLP
17.7	1038.586227	-0.002799	LIPHVQVFA
17.7	1038.582153	0.001275	LLLNAENPR
17.7	1038.586197	-0.002769	LLPAQPAWK
17.7	1038.589584	-0.006156	PILVCPPLR
17.7	1038.589584	-0.006156	PILVCPPLR

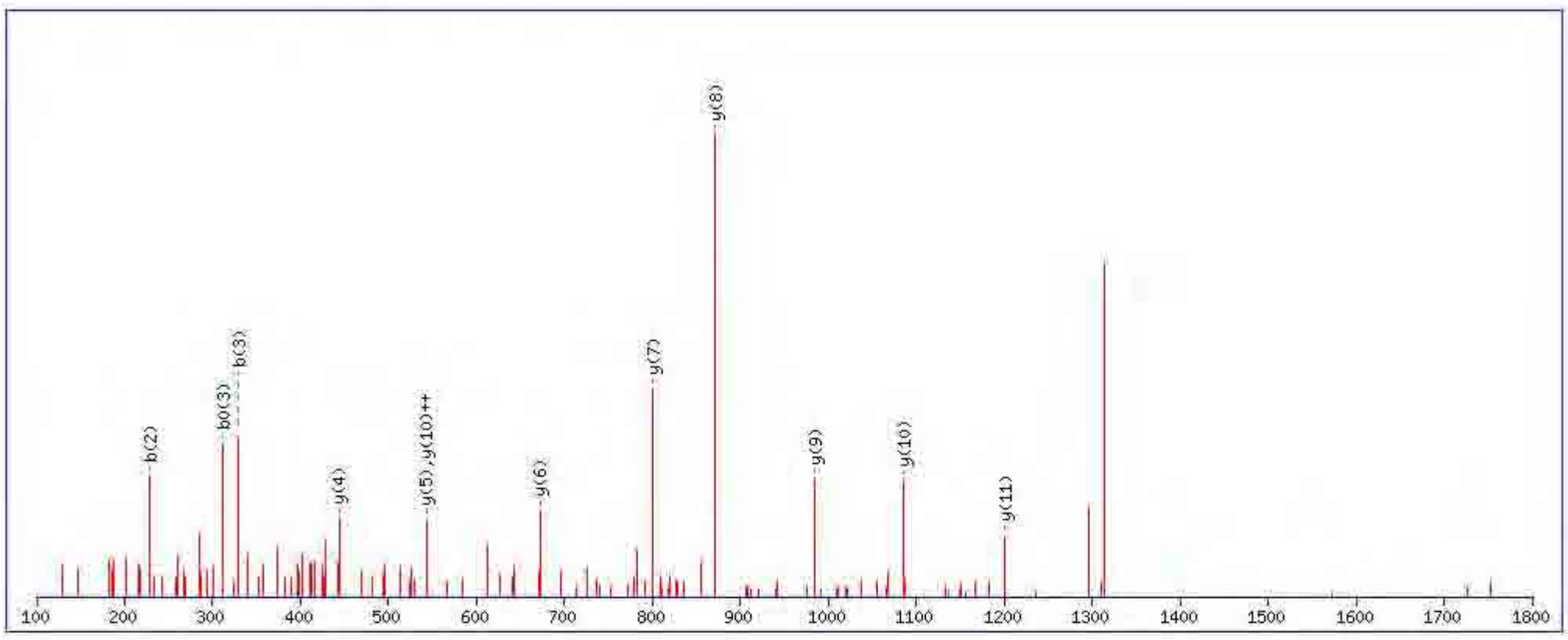
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

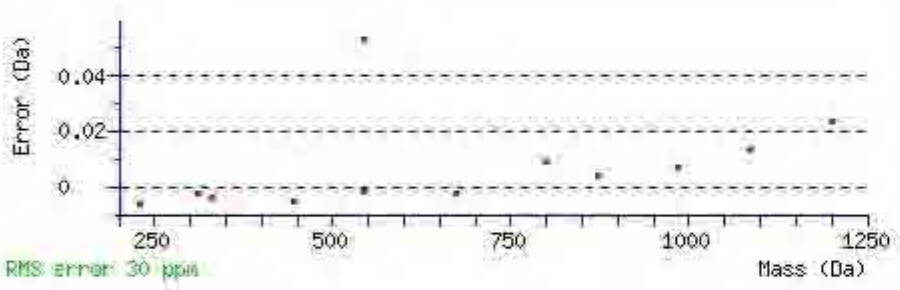
Match to Query 9926: 1312.769588 from(657.392070,2+) rtinseconds(2202) index(21829)
Title: Locus:1.1.1.1882.6
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

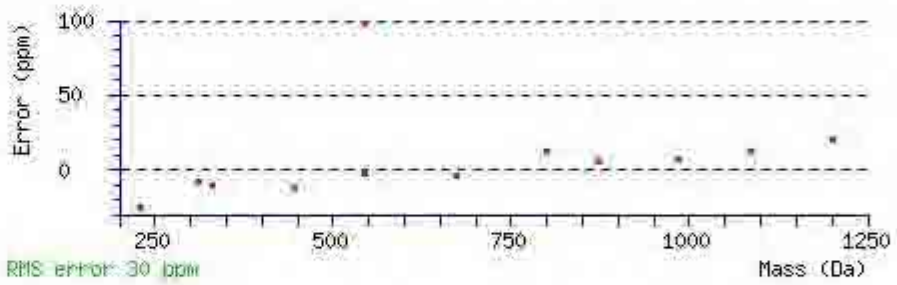
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1312.760193
Ions Score: 87 **Expect:** 8.8e-008
Matches : 12/110 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	229.118283	115.062779			211.107718	106.057497	D	*1200.683431*	600.845353	1183.656882	592.332079	1182.672866	591.840071	11
3	330.165962	165.586619			312.155397	156.581336	T	*1085.656488*	543.331882	1068.629939	534.818607	1067.645923	534.326599	10
4	443.250026	222.128651			425.239461	213.123369	L	*984.608809*	492.808042	967.582260	484.294768	966.598244	483.802760	9
5	514.287140	257.647208			496.276575	248.641926	A	*871.524745*	436.266010	854.498196	427.752736	853.514180	427.260728	8
6	642.345718	321.676497	625.319169	313.163223	624.335153	312.671215	Q	*800.487631*	400.747453	783.461082	392.234179	782.477066	391.742171	7
7	771.388311	386.197794	754.361762	377.684519	753.377746	377.192511	E	*672.429053*	336.718164	655.402504	328.204890	654.418488	327.712882	6
8	870.456725	435.732001	853.430176	427.218726	852.446160	426.726718	V	*543.386460*	272.196868	526.359911	263.683593			5
9	941.493839	471.250558	924.467290	462.737283	923.483274	462.245275	A	*444.318046*	222.662661	427.291497	214.149386			4
10	1054.577903	527.792589	1037.551354	519.279315	1036.567338	518.787307	L	373.280932	187.144104	356.254383	178.630829			3
11	1167.661967	584.334621	1150.635418	575.821347	1149.651402	575.329339	L	260.196868	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDTLAQEVALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.4	1312.760193	0.009395	LDTLAQEVALLK
23.1	1312.760193	0.009395	ITSAAPLISSPLK
18.4	1312.761551	0.008037	LDRFGVRPLPK
17.5	1312.771408	-0.001820	ILSNKNISAIIQ
16.3	1312.760193	0.009395	ITSAAPLISSPLK
15.5	1312.771439	-0.001851	IDLTVLQRDLK
13.3	1312.771408	-0.001820	ASIELLARSLPK
12.9	1312.771408	-0.001820	SNEIVEKLLLR
11.9	1312.771423	-0.001835	LSQGQVLKLEAK
10.7	1312.771454	-0.001866	VTVKPSQSQVLK

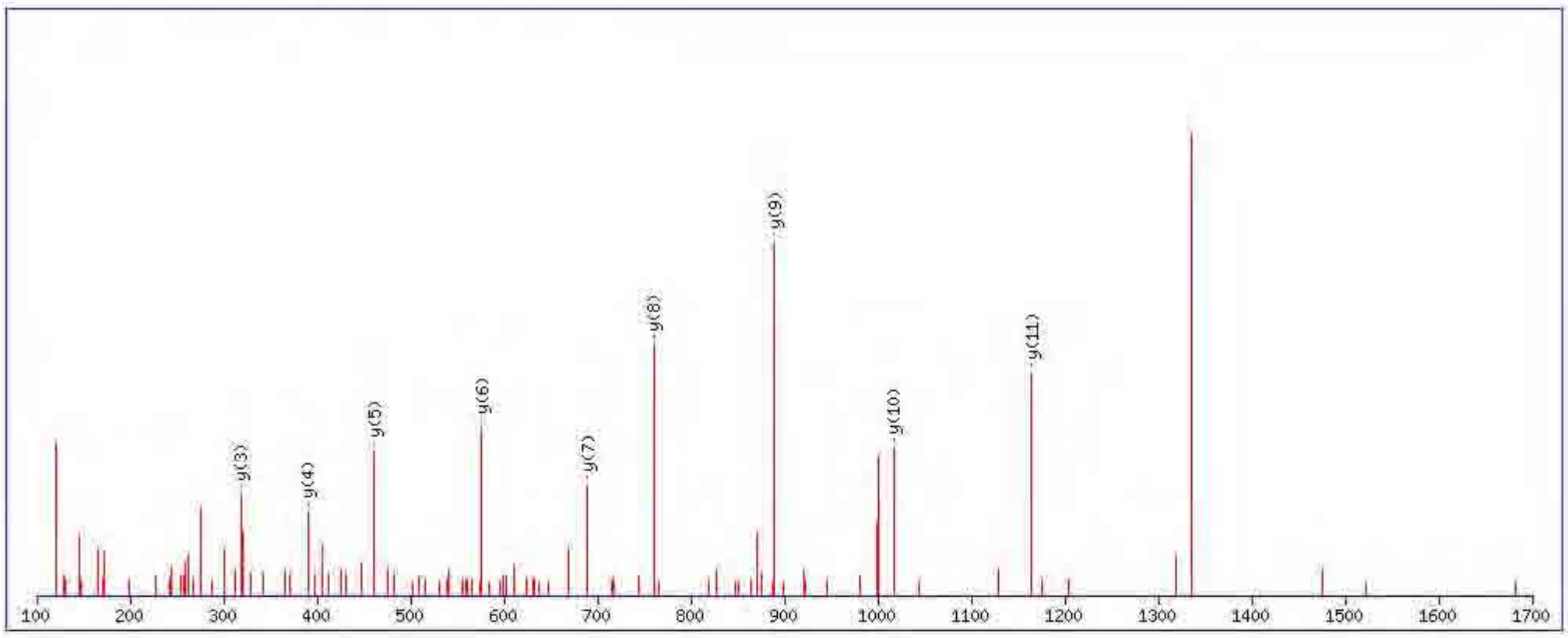
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

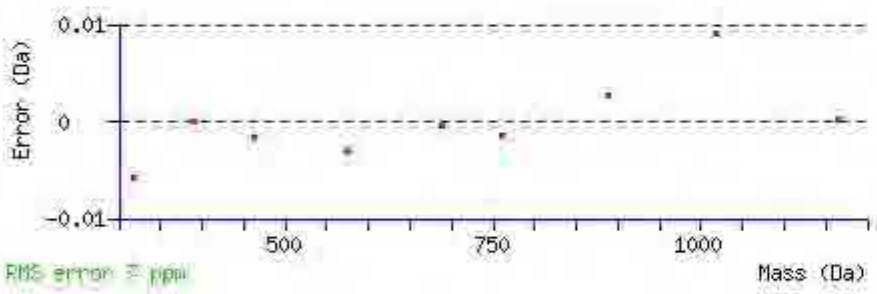
Match to Query 10586: 1335.640028 from(668.827290,2+) rtinseconds(1650) index(14547)
Title: Locus:1.1.1.1581.15
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

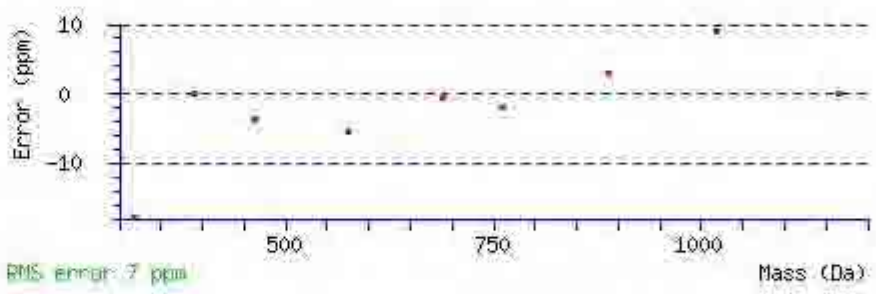
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 87 **Expect:** 3.8e-007
Matches : 9/136 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	1235.590259	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	*319.161211*	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.3	1335.630646	0.009382	TAFQEALDAAGDK
17.7	1335.651794	-0.011766	TSTSALSPGSKPST
16.1	1335.649277	-0.009249	QGFQDIAVAMEK
14.7	1335.638031	0.001997	FIDISPAEMANL
13.7	1335.651794	-0.011766	TSTSALSPGSKPST
8.0	1335.649277	-0.009249	GMASTKLSPWDK
7.7	1335.652634	-0.012606	VRKPEEMMSLT
7.7	1335.652634	-0.012606	VRKPEEMMSLT
6.1	1335.649277	-0.009249	LHSPPEVEGAMAV
6.1	1335.645233	-0.005205	STMQELNSRLAS

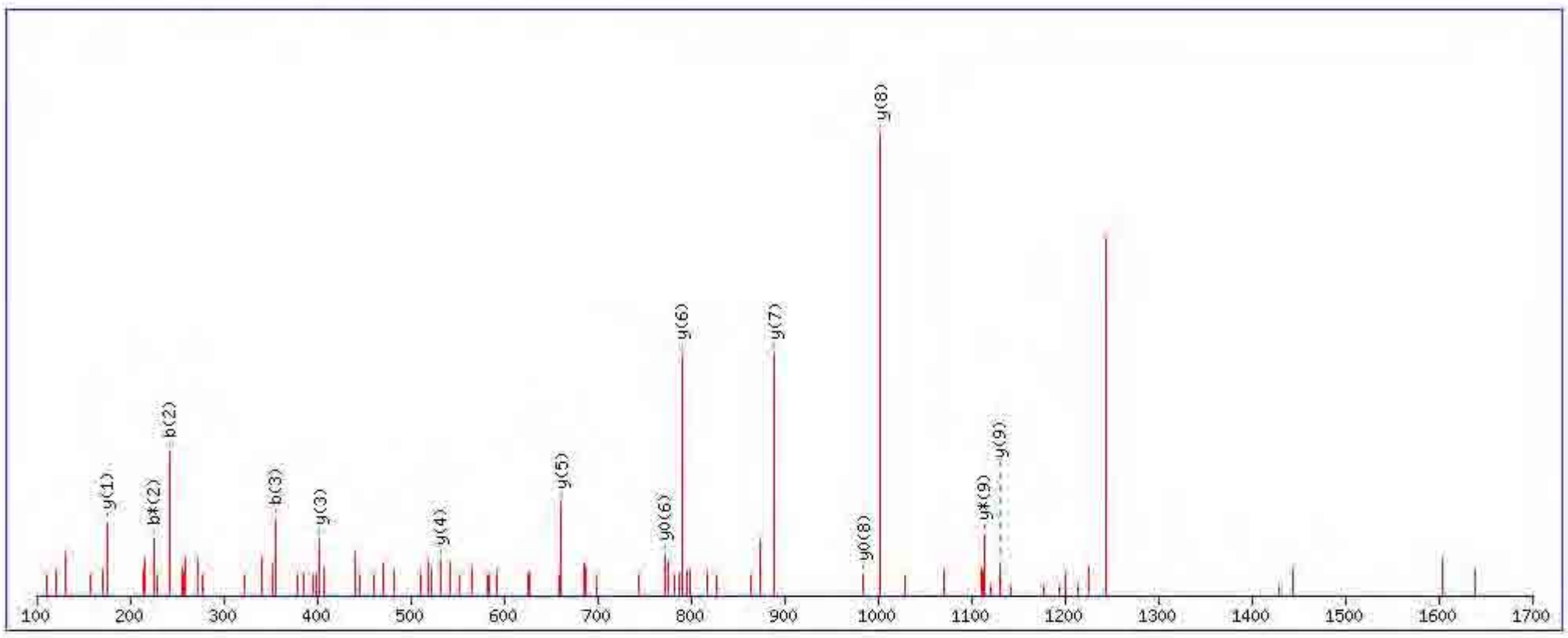
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQLVEEELDR**
Found in **TPM1_HUMAN**, Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2

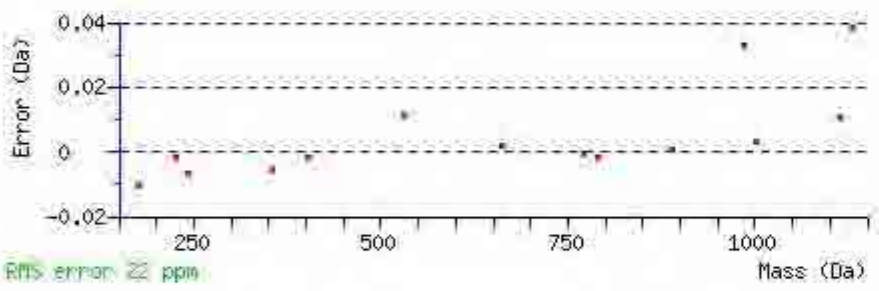
Match to Query 8186: 1242.649308 from(622.331930,2+) rtinseconds(1617) index(14096)
Title: Locus:1.1.1.1563.14
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

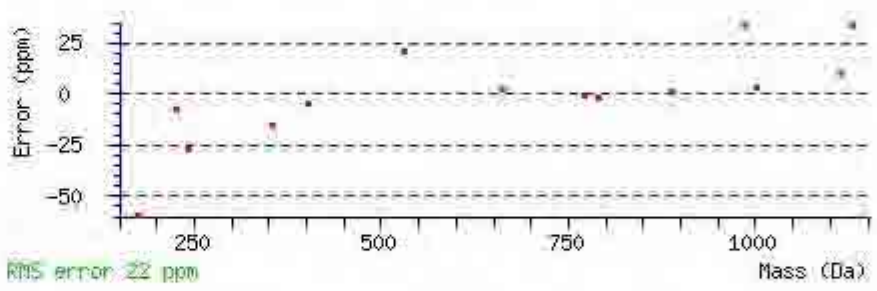
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1242.645554
Ions Score: 59 **Expect:** 0.00026
Matches : 14/96 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							10
2	**242.149918**	121.578597	225.123369	113.065323			Q	*1130.568794*	565.788035	1113.542245	557.274761	1112.558229	556.782753	9
3	**355.233982**	178.120629	338.207433	169.607355			L	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	8
4	454.302396	227.654836	437.275847	219.141562			V	*889.426152*	445.216714	872.399603	436.703440	871.415587	436.211432	7
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	E	*790.357738*	395.682507	773.331189	387.169233	772.347173	386.677225	6
6	712.387582	356.697429	695.361033	348.184155	694.377017	347.692147	E	*661.315145*	331.161211	644.288596	322.647936	643.304580	322.155928	5
7	841.430175	421.218726	824.403626	412.705451	823.419610	412.213443	E	*532.272552*	266.639914	515.246003	258.126640	514.261987	257.634632	4
8	954.514239	477.760758	937.487690	469.247483	936.503674	468.755475	L	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	1069.541182	535.274229	1052.514633	526.760955	1051.530617	526.268947	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQLVEEELDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	1242.645554	0.003754	IQLVEEELDR
21.2	1242.660858	-0.011550	QIPVHPVPDPL
20.8	1242.646912	0.002396	KPLDIPDHHR
15.1	1242.656799	-0.007491	LQPTSAAPISAR
12.9	1242.650284	-0.000976	PQPSIQRMVR
12.8	1242.645554	0.003754	PKLLEDQQEK
12.7	1242.656784	-0.007476	IVKQNEELDR
12.6	1242.656799	-0.007491	IGALLQSSGPER
12.6	1242.656784	-0.007476	PGALSAAEVEKR
12.4	1242.650284	-0.000976	IQLGLQCAGGAGR

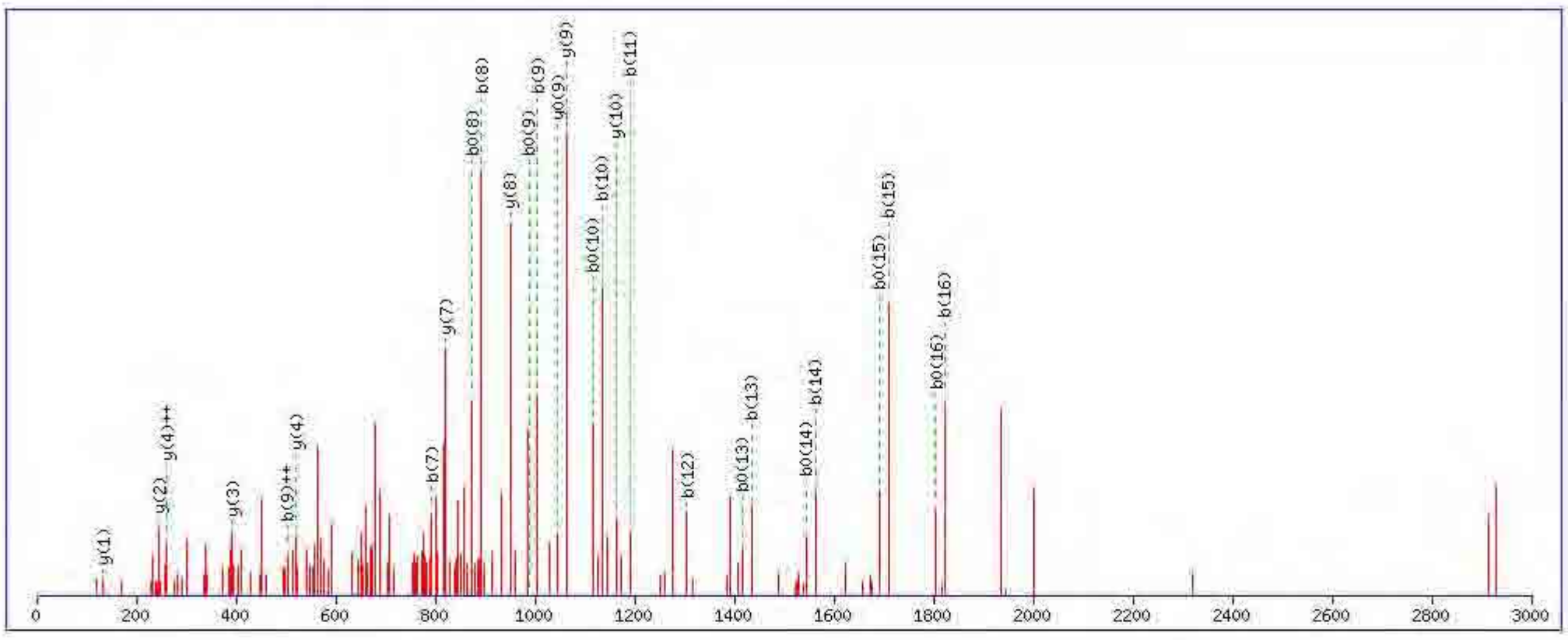
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGEHNIEVLEGNEQFIN**
Found in **TRY1_HUMAN**, Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1

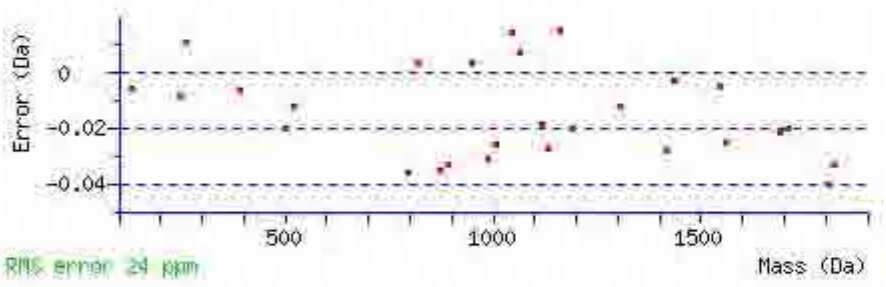
Match to Query 22189: 1953.930308 from(977.972430,2+) rtinseconds(2260) index(22621)
Title: Locus:1.1.1.1913.23
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

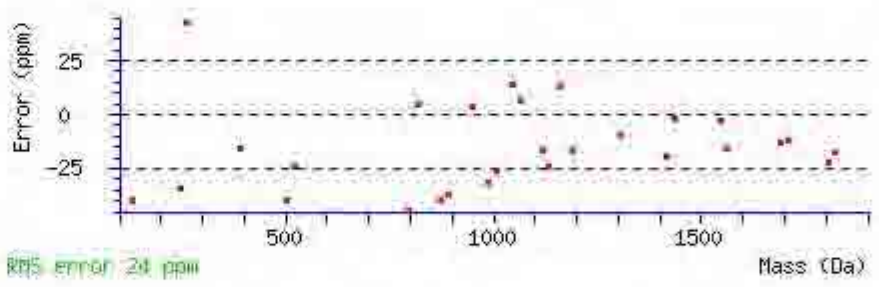
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1953.943192
Ions Score: 52 **Expect:** 0.00013
Matches : 28/172 fragment ions using 53 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							17
2	171.112804	86.060040					G	1841.866432	921.436854	1824.839883	912.923580	1823.855867	912.431572	16
3	300.155397	150.581336			282.144832	141.576054	E	1784.844968	892.926122	1767.818419	884.412848	1766.834403	883.920840	15
4	437.214309	219.110793			419.203744	210.105510	H	1655.802375	828.404826	1638.775826	819.891551	1637.791810	819.399543	14
5	551.257236	276.132256	534.230687	267.618982	533.246671	267.126974	N	1518.743463	759.875370	1501.716914	751.362095	1500.732898	750.870087	13
6	664.341300	332.674288	647.314751	324.161014	646.330735	323.669006	I	1404.700536	702.853906	1387.673987	694.340632	1386.689971	693.848624	12
7	*793.383893*	397.195585	776.357344	388.682310	775.373328	388.190302	E	1291.616472	646.311874	1274.589923	637.798600	1273.605907	637.306592	11
8	*892.452307*	446.729792	875.425758	438.216517	874.441742	437.724509	V	**1162.573879**	581.790578	1145.547330	573.277303	1144.563314	572.785295	10
9	*1005.536371*	503.271824	988.509822	494.758549	987.525806	494.266541	L	**1063.505465**	532.256371	1046.478916	523.743096	1045.494900	523.251088	9
10	*1134.578964*	567.793120	1117.552415	559.279846	1116.568399	558.787838	E	**950.421401**	475.714339	933.394852	467.201064	932.410836	466.709056	8
11	*1191.600428*	596.303852	1174.573879	587.790578	1173.589863	587.298569	G	**821.378808**	411.193042	804.352259	402.679768	803.368243	402.187760	7
12	*1305.643355*	653.325315	1288.616806	644.812041	1287.632790	644.320033	N	764.357344	382.682310	747.330795	374.169036	746.346779	373.677028	6
13	*1434.685948*	717.846612	1417.659399	709.333338	1416.675383	708.841330	E	650.314417	325.660847	633.287868	317.147572	632.303852	316.655564	5
14	*1562.744526*	781.875901	1545.717977	773.362627	1544.733961	772.870619	Q	**521.271824**	261.139550	504.245275	252.626276			4
15	*1709.812940*	855.410108	1692.786391	846.896834	1691.802375	846.404826	F	**393.213246**	197.110261	376.186697	188.596986			3
16	*1822.897004*	911.952140	1805.870455	903.438866	1804.886439	902.946858	I	**246.144832**	123.576054	229.118283	115.062779			2
17							N	**133.060768**	67.034022	116.034219	58.520747			1





NCBI **BLAST** search of LGEHNIEVLEGNEQFIN
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	1953.943192	-0.012884	LGEHNIEVLEGNEQFIN
9.6	1953.932663	-0.002355	SIHPPRDMPAAGSLGSSSR
7.4	1953.915558	0.014750	SSYLVHHGYCATATAFAR
5.2	1953.932663	-0.002355	SIHPPRDMPAAGSLGSSSR
4.6	1953.946609	-0.016301	SKSSPTSPTSCTPPPRPPV
3.5	1953.946579	-0.016271	STLNSVSKAVFGNQNEMI
2.9	1953.914230	0.016078	QIASQFPPPPTPPAMESQ
2.4	1953.947922	-0.017614	QELFDIQMPGHAPGRAR
2.0	1953.932663	-0.002355	SIHPPRDMPAAGSLGSSSR
1.9	1953.924988	0.005320	ISCSDTWVIEQMVILMA

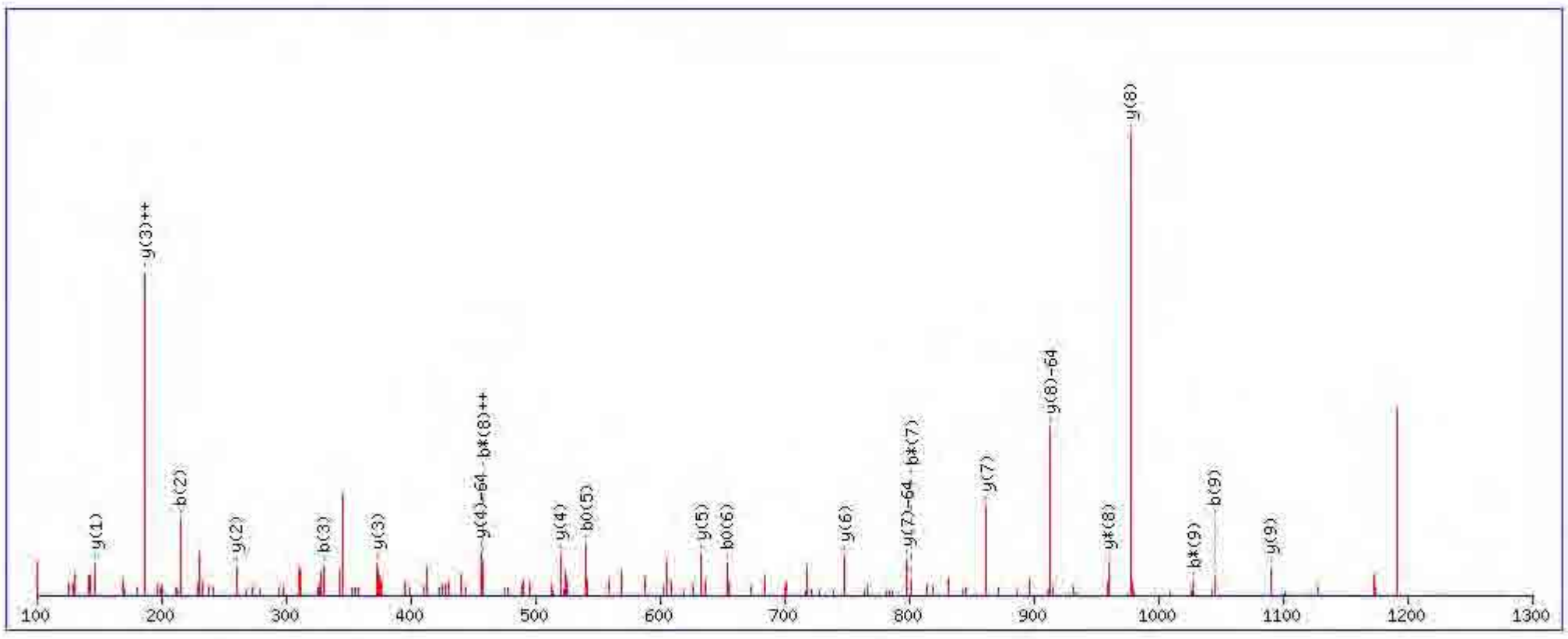
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLDNDIMLIK**
Found in **TRY3_HUMAN**, Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2

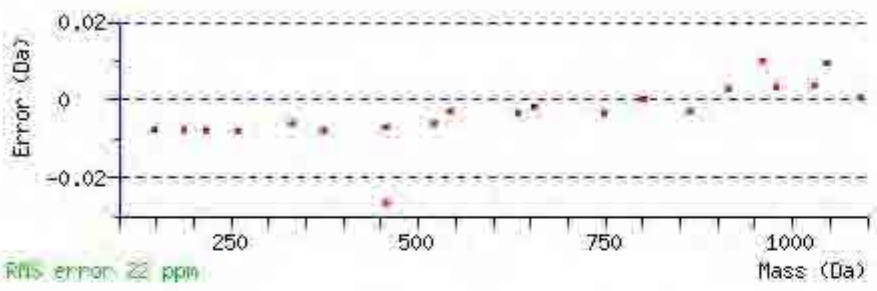
Match to Query 6868: 1190.618648 from(596.316600,2+) rtinseconds(1693) index(15102)
Title: Locus:1.1.1.1605.8
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

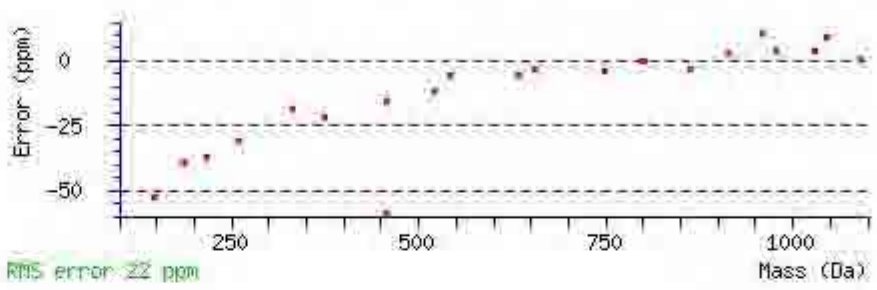
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1190.621658
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 77 **Expect:** 3.8e-006
Matches : 22/142 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	215.139019	108.073147			197.128454	99.067865	L	1090.581273	545.794275	1073.554724	537.281000	1072.570708	536.788992	9
3	330.165962	165.586619			312.155397	156.581336	D	977.497209	489.252243	960.470660	480.738968	959.486644	480.246960	8
4	444.208889	222.608082	427.182340	214.094808	426.198324	213.602800	N	862.470266	431.738771	845.443717	423.225497	844.459701	422.733489	7
5	559.235832	280.121554	542.209283	271.608280	541.225267	271.116272	D	748.427339	374.717308	731.400790	366.204033	730.416774	365.712025	6
6	672.319896	336.663586	655.293347	328.150312	654.309331	327.658304	I	633.400396	317.203836	616.373847	308.690562			5
7	819.355296	410.181286	802.328747	401.668012	801.344731	401.176004	M	520.316332	260.661804	503.289783	252.148530			4
8	932.439360	466.723318	915.412811	458.210044	914.428795	457.718036	L	373.280932	187.144104	356.254383	178.630829			3
9	1045.523424	523.265350	1028.496875	514.752076	1027.512859	514.260067	I	260.196868	130.602072	243.170319	122.088797			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TLDNDIMLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.4	1190.621658	-0.003010	TLDNDIMLIK
18.8	1190.621674	-0.003026	VDAGLLTDIMK
18.5	1190.621689	-0.003041	DVATSMPVVIK
18.4	1190.618332	0.000316	TPPPPPVPPTK
17.7	1190.618332	0.000316	TPPPPPVPPTK
16.8	1190.615128	0.003520	EMPMGRTILK
16.1	1190.629532	-0.010884	RYLGDLTPLQ
16.0	1190.615128	0.003520	EMPMGRTILK
14.7	1190.614258	0.004390	TLSGEAASLTNK
13.8	1190.618317	0.000331	TPAGTPVPEPLP

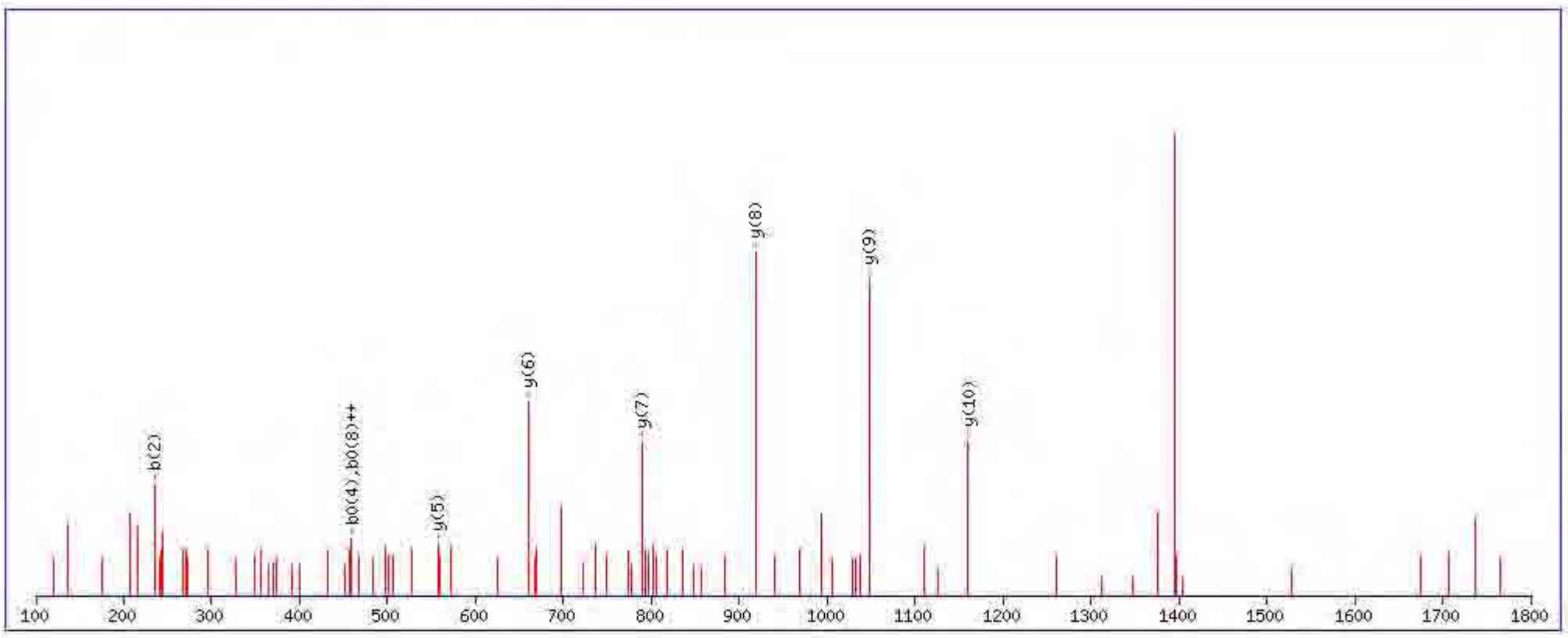
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYLEEECPATLR**
Found in **ZA2G_HUMAN**, Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2

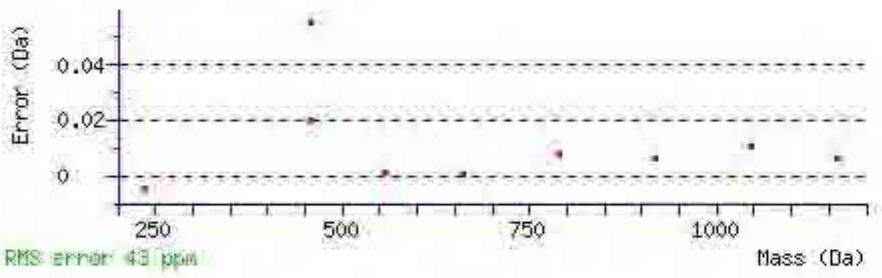
Match to Query 11822: 1393.655428 from(697.834990,2+) rtinseconds(1592) index(13744)
Title: Locus:1.1.1.1549.12
Data file \\192.168.1.20\MS\ETP - Ebbe Toftgaard Poulsen\Cornea\June, 2012 - Sibling cases\120612_ETP_StromaControl_6.mgf

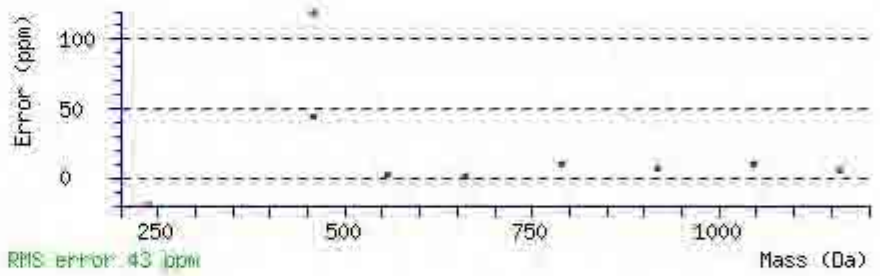
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1393.654724
Ions Score: 36 **Expect:** 0.0031
Matches : 9/100 fragment ions using 13 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833			A							12
2	235.107719	118.057498			Y	1323.624930	662.316103	1306.598381	653.802829	1305.614365	653.310820	11
3	348.191783	174.599529			L	*1160.561601*	580.784438	1143.535052	572.271164	1142.551036	571.779156	10
4	477.234376	239.120826	459.223811	230.115544	E	*1047.477537*	524.242407	1030.450988	515.729132	1029.466972	515.237124	9
5	606.276969	303.642123	588.266404	294.636840	E	*918.434944*	459.721110	901.408395	451.207835	900.424379	450.715827	8
6	735.319562	368.163419	717.308997	359.158137	E	*789.392351*	395.199814	772.365802	386.686539	771.381786	386.194531	7
7	838.328747	419.668012	820.318182	410.662729	C	*660.349758*	330.678517	643.323209	322.165242	642.339193	321.673234	6
8	935.381511	468.194394	917.370946	459.189111	P	*557.340573*	279.173925	540.314024	270.660650	539.330008	270.168642	5
9	1006.418625	503.712951	988.408060	494.707668	A	460.287809	230.647542	443.261260	222.134268	442.277244	221.642260	4
10	1107.466304	554.236790	1089.455739	545.231508	T	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	3
11	1220.550368	610.778822	1202.539803	601.773539	L	288.203016	144.605146	271.176467	136.091871			2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AYLEEECPATLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1393.654724	0.000704	AYLEEECPATLR
9.2	1393.662628	-0.007200	SFLELHSPHSPQ
3.1	1393.662628	-0.007200	SFLELHSPHSPQ
2.7	1393.663498	-0.008070	HPPYTMCFRVK
2.6	1393.643524	0.011904	YALDEMPTTLPQ
2.1	1393.661285	-0.005857	FLSEEDDIVPSK
2.1	1393.658096	-0.002668	MTDEEIMEKLR
2.0	1393.651382	0.004046	LVPYGNHSYLES
1.9	1393.658112	-0.002684	MISEAIKTNAPTC
1.7	1393.654770	0.000658	LGPETPLAMDRF

Sibling 1 – technical replicate # 1

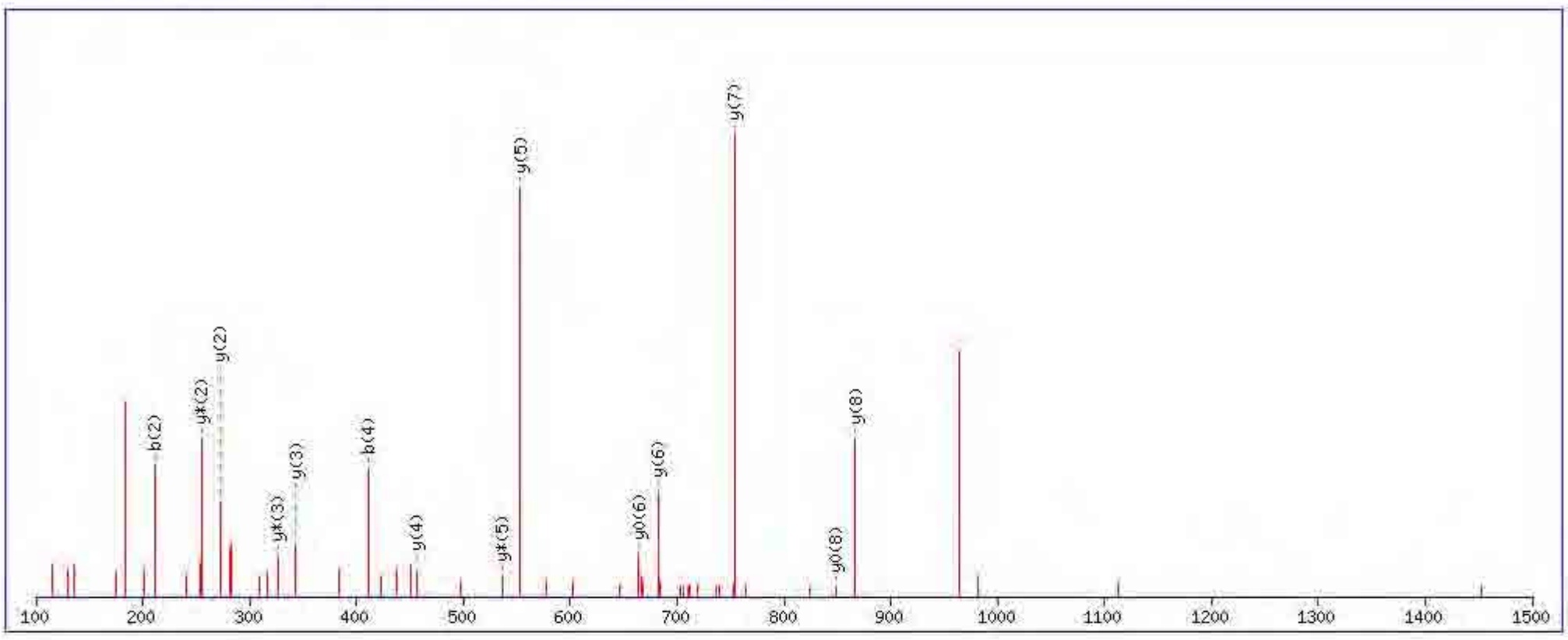
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLAEPLAPR**
Found in **LFNG_HUMAN**, Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2

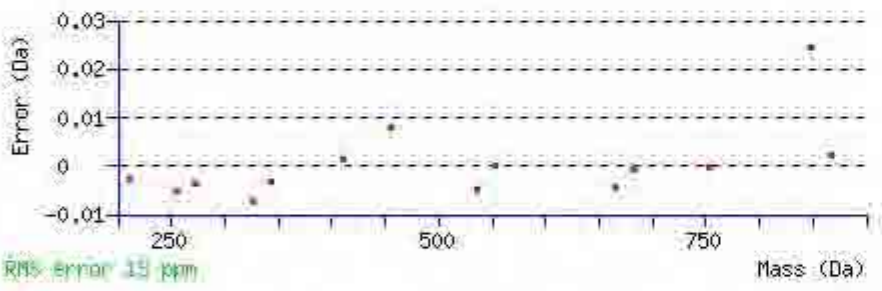
Match to Query 4589: 962.553448 from(482.284000,2+) rtinseconds(1127) index(6018)
Title: Locus:1.1.1.1405.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

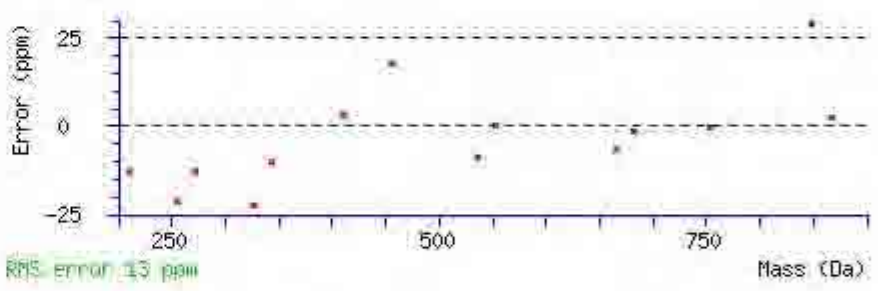
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 962.554886
Ions Score: 53 **Expect:** 0.00028
Matches : 14/64 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.060040	49.533658			P							9
2	211.144104	106.075690			L	*866.509429*	433.758353	849.482880	425.245078	848.498864	424.753070	8
3	282.181218	141.594247			A	*753.425365*	377.216321	736.398816	368.703046	735.414800	368.211038	7
4	411.223811	206.115544	393.213246	197.110261	E	*682.388251*	341.697764	665.361702	333.184489	664.377686	332.692481	6
5	508.276575	254.641926	490.266010	245.636643	P	*553.345658*	277.176467	536.319109	268.663193			5
6	621.360639	311.183958	603.350074	302.178675	L	*456.292894*	228.650085	439.266345	220.136811			4
7	692.397753	346.702515	674.387188	337.697232	A	*343.208830*	172.108053	326.182281	163.594779			3
8	789.450517	395.228897	771.439952	386.223614	P	*272.171716*	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PLAEPLAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	962.554886	-0.001438	PLAEPLAPR
22.3	962.554901	-0.001453	PPLSLPPAR
20.5	962.554901	-0.001453	PLALPSPPR
18.6	962.554916	-0.001468	PPALTPVPR
16.8	962.554901	-0.001453	PLALPSPPR
14.5	962.554901	-0.001453	PPLSLPPAR
12.5	962.547028	0.006420	VMKELSLK
10.8	962.554901	-0.001453	PLALPSPPR
10.3	962.554901	-0.001453	PLIPPASPR
9.8	962.554901	-0.001453	PPPIAPLAR

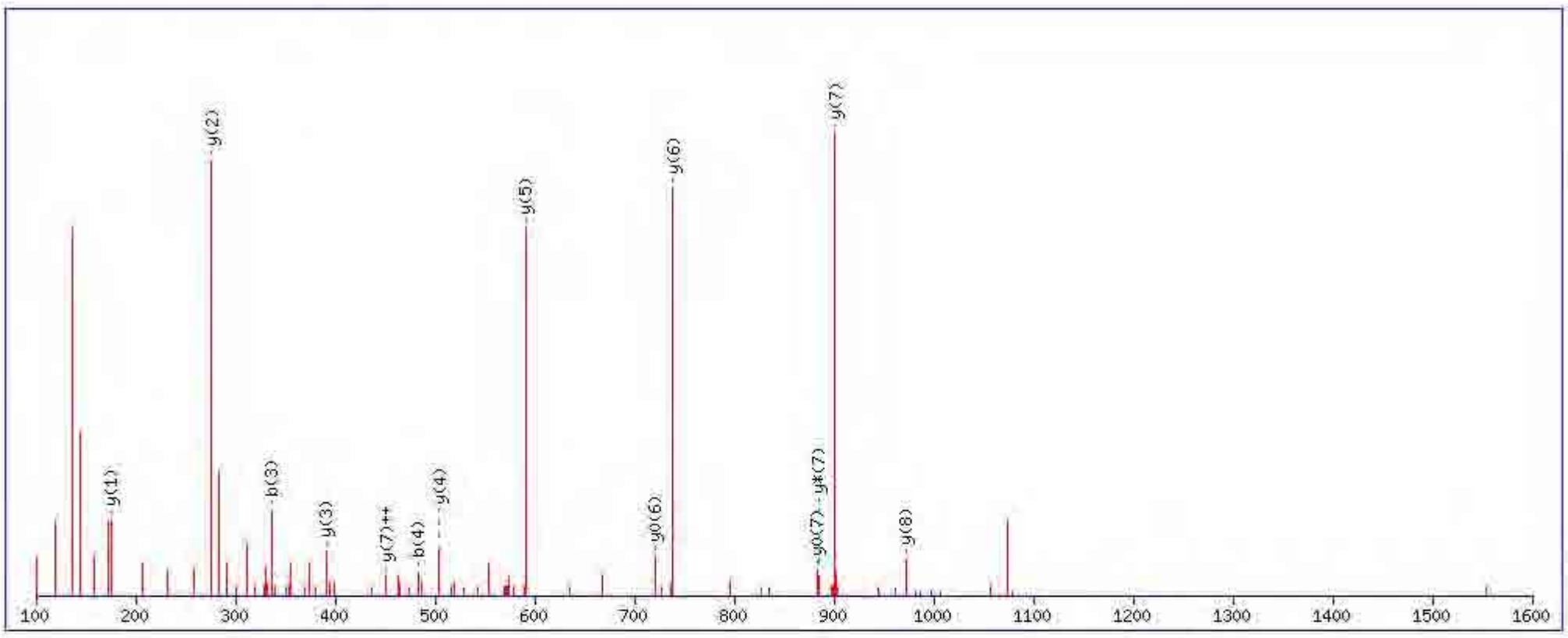
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAYFSLDTR**
Found in **CADH1_HUMAN**, Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3

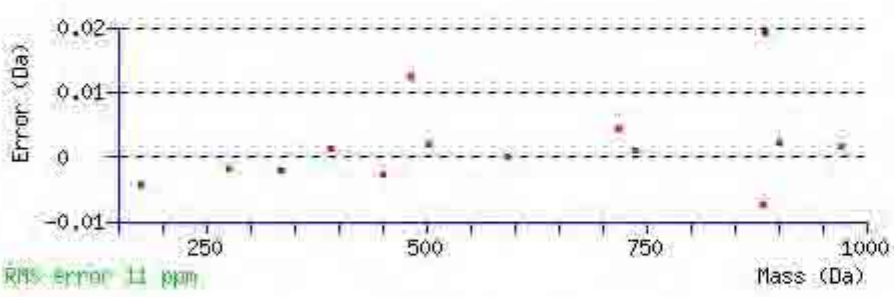
Match to Query 7036: 1072.521808 from(537.268180,2+) rtinseconds(1502) index(10506)
Title: Locus:1.1.1.1613.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

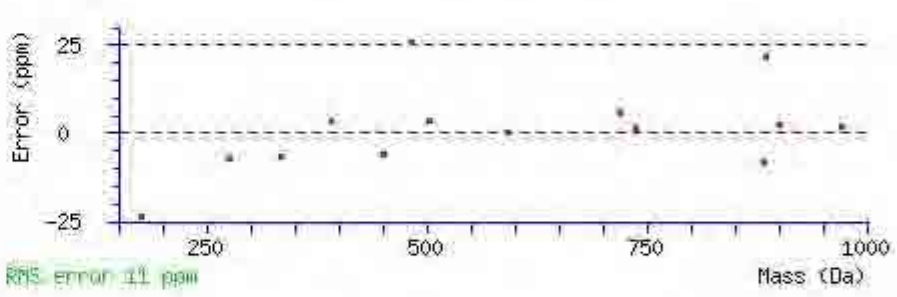
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1072.518921
Ions Score: 56 **Expect:** 4.6e-005
Matches : 14/78 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	173.092069	87.049672	155.081504	78.044390	A	*972.478523*	486.742900	955.451974	478.229625	954.467958	477.737617	8
3	**336.155398**	168.581337	318.144833	159.576055	Y	*901.441409*	451.224343	884.414860	442.711068	883.430844	442.219060	7
4	**483.223812**	242.115544	465.213247	233.110262	F	*738.378080*	369.692678	721.351531	361.179403	720.367515	360.687395	6
5	570.255840	285.631558	552.245275	276.626276	S	*591.309666*	296.158471	574.283117	287.645197	573.299101	287.153189	5
6	683.339904	342.173590	665.329339	333.168308	L	*504.277638*	252.642457	487.251089	244.129182	486.267073	243.637174	4
7	798.366847	399.687062	780.356282	390.681779	D	*391.193574*	196.100425	374.167025	187.587150	373.183009	187.095142	3
8	899.414526	450.210901	881.403961	441.205619	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TAYFSLDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	1072.518921	0.002887	TAYFSLDTR
8.7	1072.522308	-0.000500	TANVPQTVPM
8.7	1072.522308	-0.000500	TANVPQTVPM
7.5	1072.519791	0.002017	TAFFLCCLR
7.0	1072.522278	-0.000470	QLAGPLAMEQ
6.0	1072.518936	0.002872	TPHDLFSSGL
5.7	1072.514908	0.006900	TALPPGASDGR
4.2	1072.512375	0.009433	ATYERMFR
3.1	1072.530182	-0.008374	HVVFNGDGTK
3.1	1072.519806	0.002002	VTRMCFAVF

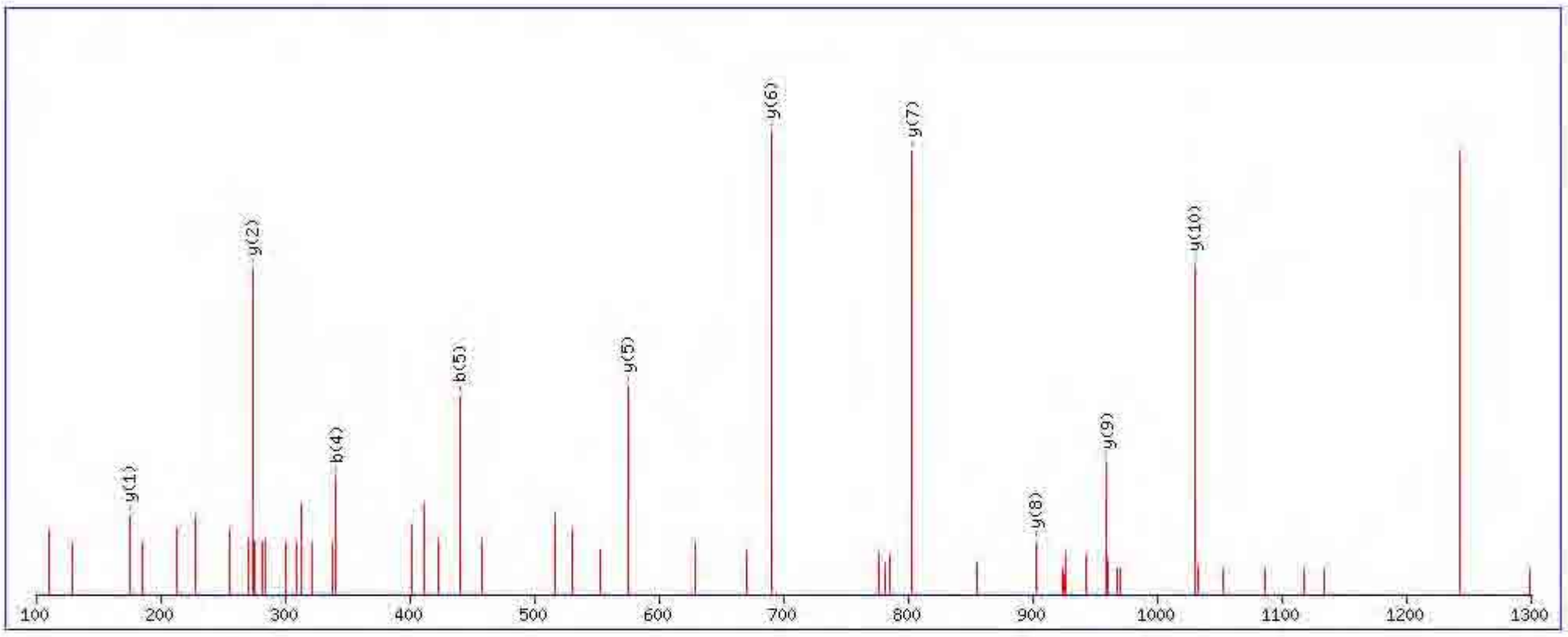
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLAGVLDSVDVR**
Found in **CHSTE_HUMAN**, Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14 PE=1 SV=2

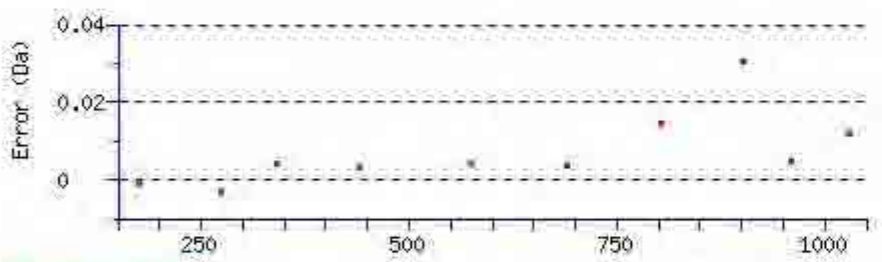
Match to Query 11604: 1241.699288 from(621.856920,2+) rtinseconds(1673) index(12616)
Title: Locus:1.1.1.1707.16
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

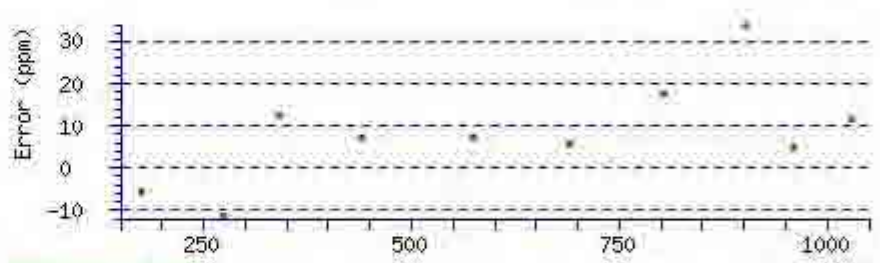
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1241.697968
Ions Score: 82 Expect: 6.8e-007
Matches : 10/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	213.159754	107.083515			L	1143.636814	572.322045	1126.610265	563.808770	1125.626249	563.316762	11
3	284.196868	142.602072			A	*1030.552750*	515.780013	1013.526201	507.266738	1012.542185	506.774730	10
4	**341.218332**	171.112804			G	*959.515636*	480.261456	942.489087	471.748181	941.505071	471.256173	9
5	**440.286746**	220.647011			V	*902.494172*	451.750724	885.467623	443.237449	884.483607	442.745441	8
6	553.370810	277.189043			L	*803.425758*	402.216517	786.399209	393.703242	785.415193	393.211234	7
7	668.397753	334.702515	650.387188	325.697232	D	*690.341694*	345.674485	673.315145	337.161210	672.331129	336.669202	6
8	755.429781	378.218528	737.419216	369.213246	S	*575.314751*	288.161013	558.288202	279.647739	557.304186	279.155731	5
9	854.498195	427.752735	836.487630	418.747453	V	488.282723	244.644999	471.256174	236.131725	470.272158	235.639717	4
10	969.525138	485.266207	951.514573	476.260924	D	389.214309	195.110792	372.187760	186.597518	371.203744	186.105510	3
11	1068.593552	534.800414	1050.582987	525.795131	V	*274.187366*	137.597321	257.160817	129.084046			2
12					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VLAGVLDSVDVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.8	1241.697968	0.001320	VLAGVLDSVDVR
24.6	1241.699265	0.000023	LLNHPDIKHR
19.8	1241.709167	-0.009879	GLAVVLETERR
19.4	1241.697952	0.001336	LVKVDDEVVAR
18.1	1241.695465	0.003823	LVVQLHCKFGV
15.1	1241.697952	0.001336	VLAVGLALTGNGAS
12.8	1241.697952	0.001336	GIPPLSSLTSVR
12.0	1241.688065	0.011223	VPAHRPLPGAVP
11.7	1241.699265	0.000023	LRGLSYIHQR
10.2	1241.697952	0.001336	VPSTDLILNVR

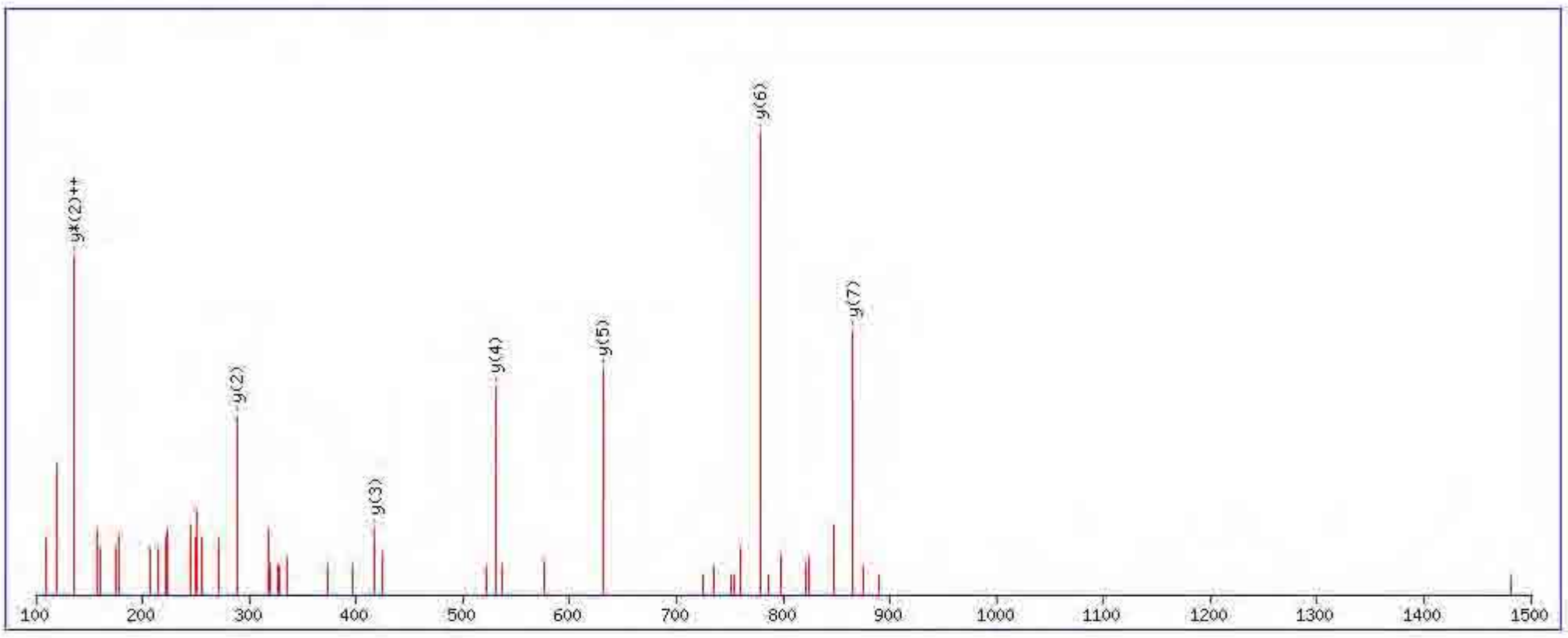
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFTIELR**
Found in **CBPB2_HUMAN**, Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

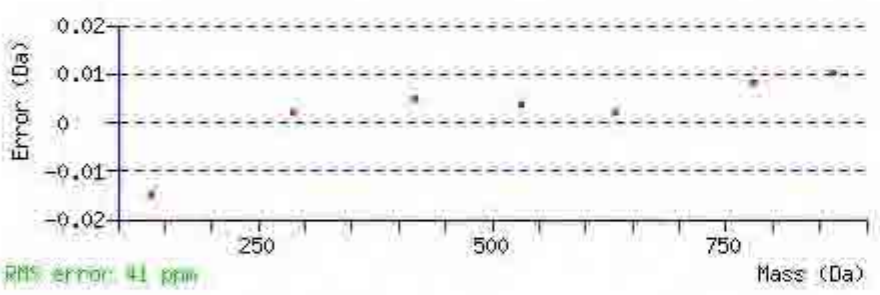
Match to Query 5959: 1027.535408 from(514.774980,2+) rtinseconds(1821) index(14332)
Title: Locus:1.1.1.1787.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

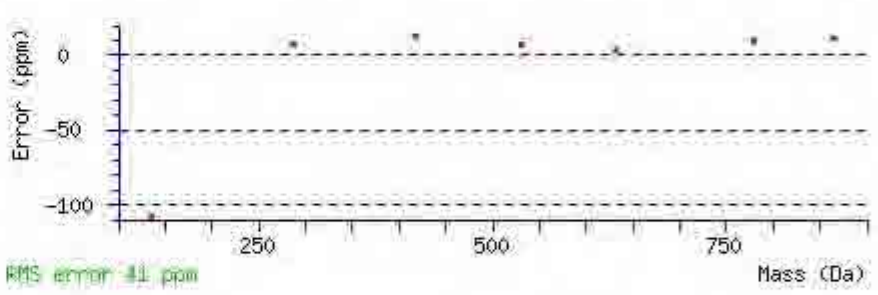
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1027.533829
Ions Score: 58 **Expect:** 0.00033
Matches : 7/64 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							8
2	251.102633	126.054954	233.092068	117.049672	S	*865.477794*	433.242535	848.451245	424.729261	847.467229	424.237253	7
3	398.171047	199.589161	380.160482	190.583879	F	*778.445766*	389.726521	761.419217	381.213247	760.435201	380.721239	6
4	499.218726	250.113001	481.208161	241.107719	T	*631.377352*	316.192314	614.350803	307.679040	613.366787	307.187032	5
5	612.302790	306.655033	594.292225	297.649751	I	*530.329673*	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	741.345383	371.176330	723.334818	362.171047	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
7	854.429447	427.718362	836.418882	418.713079	L	*288.203016*	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YSFTIELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.8	1027.533829	0.001579	YSFTIELR
24.5	1027.529800	0.005608	DNAPTIEIR
13.1	1027.531143	0.004265	LHSHHELR
11.9	1027.529800	0.005608	AEAGGLPELR
11.9	1027.529800	0.005608	AQLGEPELR
11.9	1027.541031	-0.005623	NLRDPELR
11.9	1027.541031	-0.005623	RIASAPEPR
11.9	1027.541031	-0.005623	RNLDIERP
11.9	1027.545059	-0.009651	WKPAPEIR
11.7	1027.541031	-0.005623	KSSNLTNHK

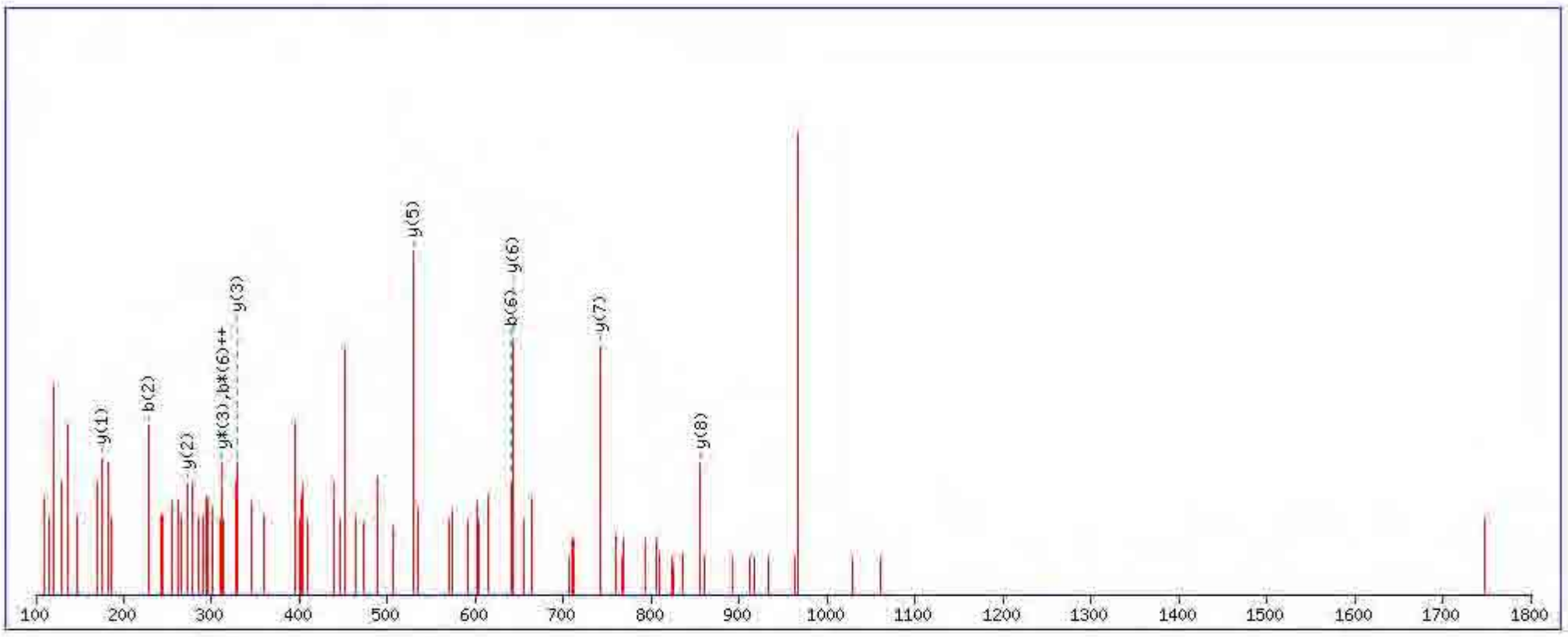
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNVITVGPR**
Found in **CATA_HUMAN**, Catalase OS=Homo sapiens GN=CAT PE=1 SV=3

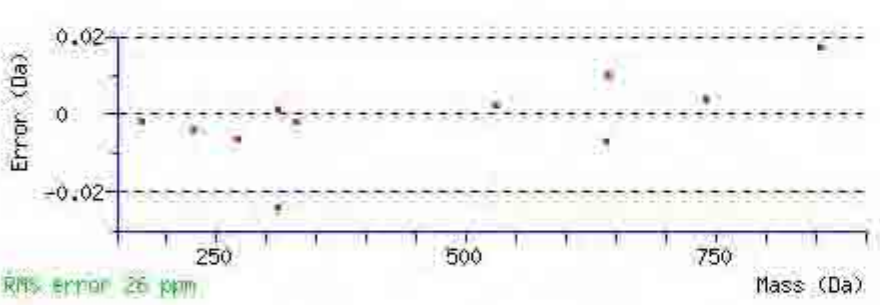
Match to Query 4689: 967.587388 from(484.800970,2+) rtinseconds(1327) index(8230)
Title: Locus:1.1.1.1518.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

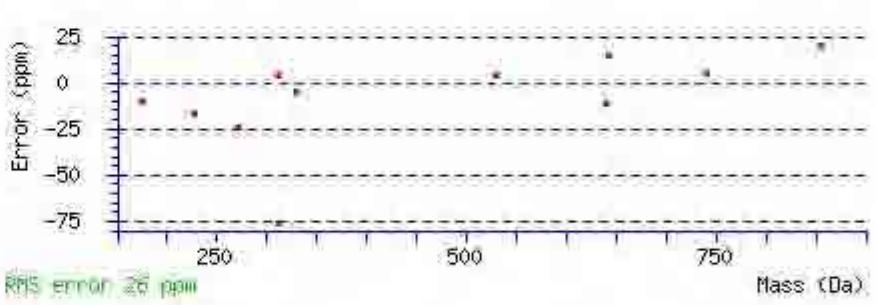
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 967.581467
Ions Score: 37 **Expect:** 0.0031
Matches : 11/78 fragment ions using 27 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							9
2	**228.134267**	114.570771	211.107718	106.057497			N	*855.504678*	428.255977	838.478129	419.742703	837.494113	419.250695	8
3	327.202681	164.104978	310.176132	155.591704			V	*741.461751*	371.234514	724.435202	362.721239	723.451186	362.229231	7
4	440.286745	220.647010	423.260196	212.133736			I	*642.393337*	321.700307	625.366788	313.187032	624.382772	312.695024	6
5	541.334424	271.170850	524.307875	262.657576	523.323859	262.165568	T	*529.309273*	265.158275	512.282724	256.645000	511.298708	256.152992	5
6	**640.402838**	320.705057	623.376289	**312.191782**	622.392273	311.699774	V	428.261594	214.634435	411.235045	206.121161			4
7	697.424302	349.215789	680.397753	340.702515	679.413737	340.210507	G	*329.193180*	165.100228	**312.166631**	156.586954			3
8	794.477066	397.742171	777.450517	389.228897	776.466501	388.736889	P	*272.171716*	136.589496	255.145167	128.076222			2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LNVITVGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	967.581467	0.005921	LNVITVGPR
9.4	967.592682	-0.005294	ARVILGSPR
7.9	967.581482	0.005906	KVVLGGPGGGK
6.8	967.592667	-0.005279	RAVLERPK
6.2	967.581436	0.005952	LNPDLIRK
6.2	967.581467	0.005921	LNTPLGVVR
5.8	967.581451	0.005937	LNVAIVRPS
5.3	967.581467	0.005921	LRGLPGQLV
4.3	967.581451	0.005937	GTAPLKLPR
2.9	967.592682	-0.005294	GRLLQPIR

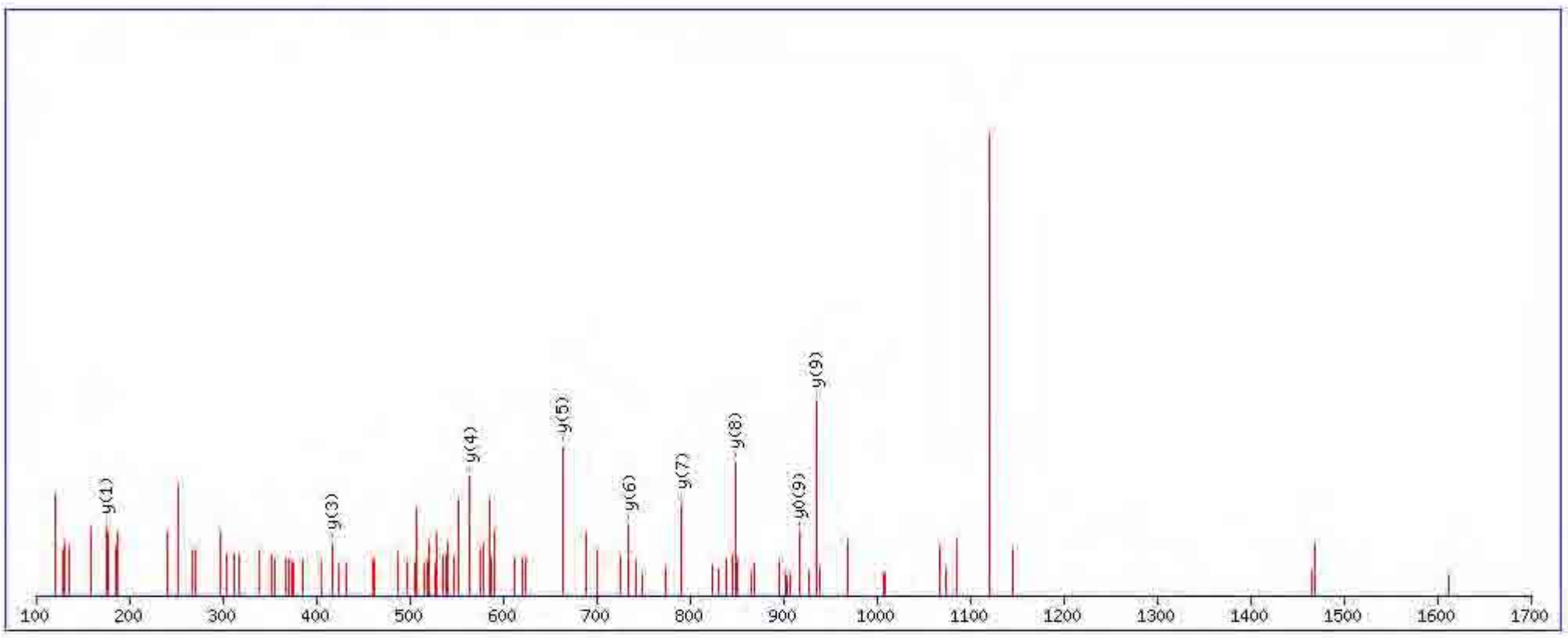
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GESGGAVFLER**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

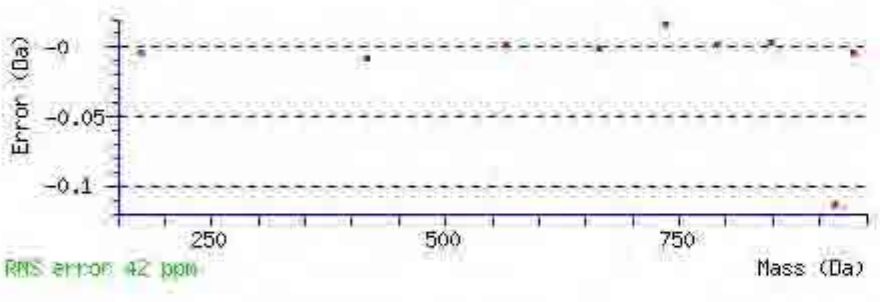
Match to Query 8177: 1120.552848 from(561.283700,2+) rtinseconds(1254) index(7445)
Title: Locus:1.1.1.1476.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

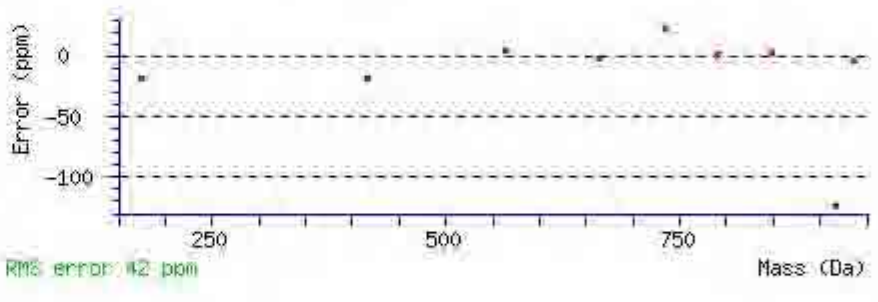
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1120.551285
Ions Score: 53 **Expect:** 0.00035
Matches : 9/96 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	187.071333	94.039305	169.060768	85.034022	E	1064.537100	532.772188	1047.510551	524.258914	1046.526535	523.766906	10
3	274.103361	137.555319	256.092796	128.550036	S	*935.494507*	468.250891	918.467958	459.737617	917.483942	459.245609	9
4	331.124825	166.066050	313.114260	157.060768	G	*848.462479*	424.734877	831.435930	416.221603	830.451914	415.729595	8
5	388.146289	194.576782	370.135724	185.571500	G	*791.441015*	396.224145	774.414466	387.710871	773.430450	387.218863	7
6	459.183403	230.095339	441.172838	221.090057	A	*734.419551*	367.713414	717.393002	359.200139	716.408986	358.708131	6
7	558.251817	279.629547	540.241252	270.624264	V	*663.382437*	332.194857	646.355888	323.681582	645.371872	323.189574	5
8	705.320231	353.163753	687.309666	344.158471	F	*564.314023*	282.660650	547.287474	274.147375	546.303458	273.655367	4
9	818.404295	409.705785	800.393730	400.700503	L	*417.245609*	209.126442	400.219060	200.613168	399.235044	200.121160	3
10	947.446888	474.227082	929.436323	465.221799	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GESGGAVFLER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	1120.551285	0.001563	GESGGAVFLER
15.4	1120.551300	0.001548	VSLEPHQGPGT
8.1	1120.551300	0.001548	SVSGFSEPVGR
7.7	1120.551270	0.001578	VSSNLNLNNF
7.6	1120.562515	-0.009667	FSPSEVQRR
5.6	1120.548615	0.004233	SGQHPGPGGRR
5.5	1120.551300	0.001548	VGPYTEQGVR
4.4	1120.547226	0.005622	NTASSAASKER
4.1	1120.551270	0.001578	VSPASYENVR
3.3	1120.554626	-0.001778	LIASNSTMER

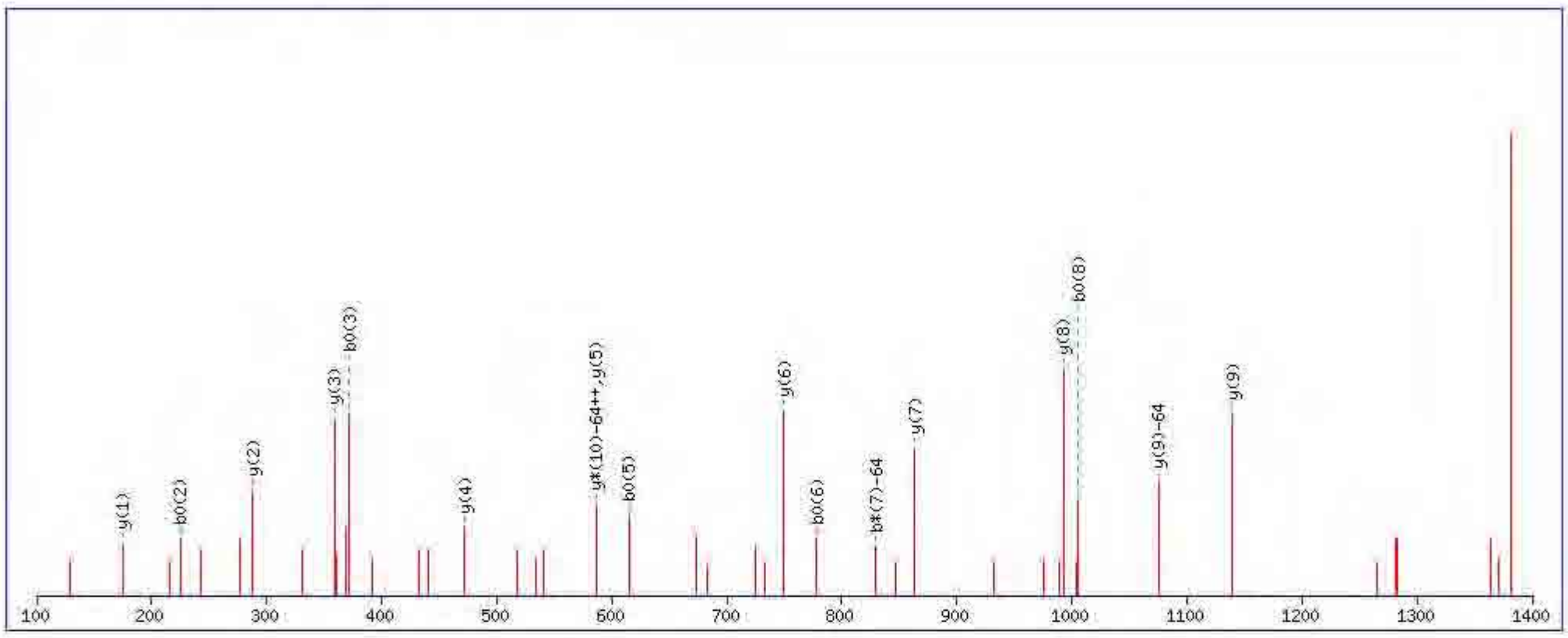
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

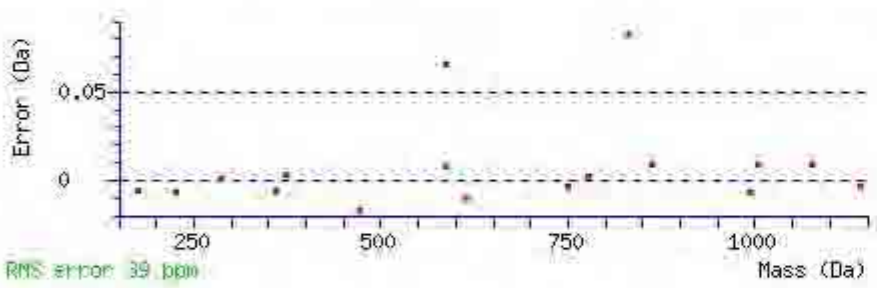
Match to Query 14471: 1380.671008 from(691.342780,2+) rtinseconds(1455) index(9917)
Title: Locus:1.1.1.1587.25
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

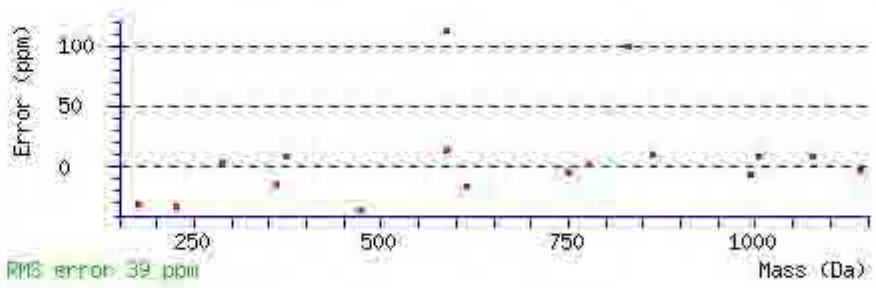
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 58 **Expect:** 0.0001
Matches : 17/154 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1252.635434	626.821355	1235.608885	618.308081	1234.624869	617.816073	10
3	390.169333	195.588304			372.158768	186.583022	M	*1139.551370*	570.279323	1122.524821	561.766049	1121.540805	561.274040	9
4	519.211926	260.109601			501.201361	251.104319	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	633.254853	317.131065	616.228304	308.617790	615.244288	308.125782	N	*863.473377*	432.240326	846.446828	423.727052			7
6	796.318182	398.662729	779.291633	390.149454	778.307617	389.657446	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	910.361109	455.684192	893.334560	447.170918	892.350544	446.678910	N	*586.367121*	293.687199	569.340572	285.173924			5
8	1023.445173	512.226224	1006.418624	503.712950	1005.434608	503.220942	I	*472.324194*	236.665735	455.297645	228.152460			4
9	1094.482287	547.744782	1077.455738	539.231507	1076.471722	538.739499	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1207.566351	604.286813	1190.539802	595.773539	1189.555786	595.281531	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	1380.670700	0.000308	EIMENYNIALR
14.3	1380.659500	0.011508	MELENYKQPVV
7.4	1380.667374	0.003634	QNVPFEDYTRL
6.8	1380.670731	0.000277	EIEKDCAVYVGR
5.9	1380.663361	0.007647	GPGPEGQSPAPALR
5.9	1380.663361	0.007647	GPGPEGQSPAPALR
5.8	1380.663361	0.007647	QPAQDTAPTPAPR
5.5	1380.681961	-0.010953	EDLMPSRPPSPR
5.4	1380.670715	0.000293	LEEFLSAMQSAR
5.1	1380.678604	-0.007596	ELESFPGSFRGR

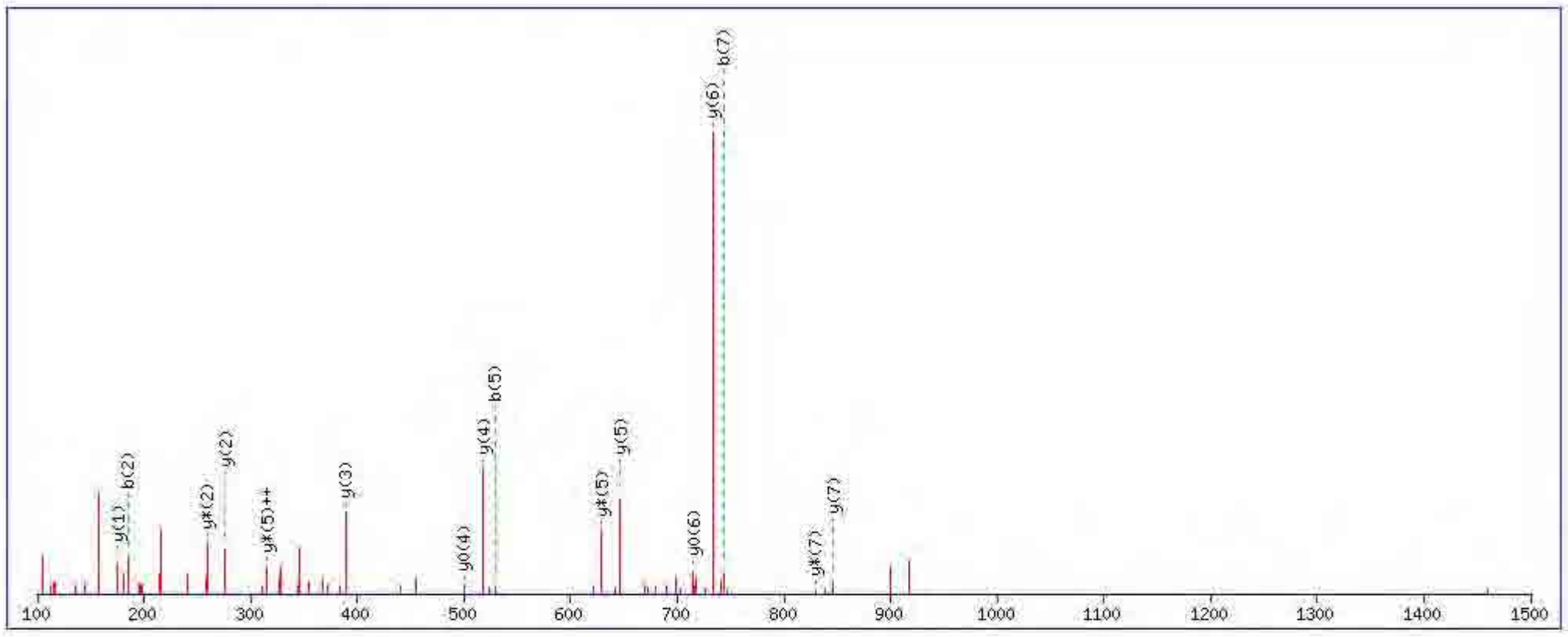
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALSQEITR**
Found in **CYTL1_HUMAN**, Cytokine-like protein 1 OS=Homo sapiens GN=CYTL1 PE=1 SV=1

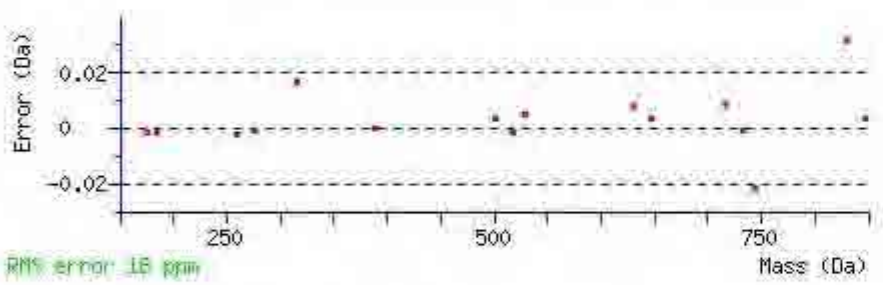
Match to Query 3611: 916.494268 from(459.254410,2+) rtinseconds(776) index(2867)
Title: Locus:1.1.1.1203.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

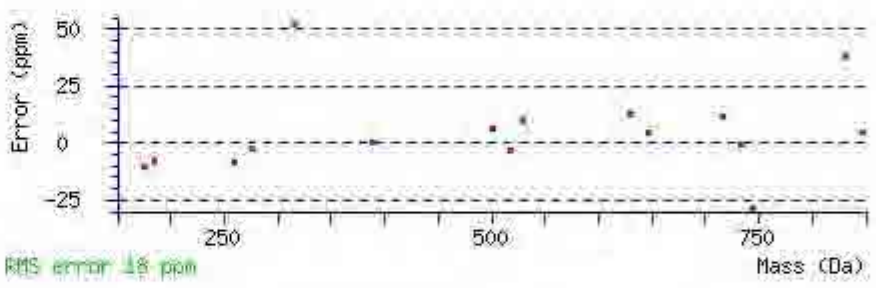
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 916.497772
Ions Score: 50 **Expect:** 0.0024
Matches : 16/72 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							8
2	**185.128454**	93.067865					L	***846.467958***	423.737617	829.441409	415.224343	828.457393	414.732335	7
3	272.160482	136.583879			254.149917	127.578596	S	***733.383894***	367.195585	716.357345	358.682311	715.373329	358.190303	6
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	Q	***646.351866***	323.679571	629.325317	315.166297	628.341301	314.674289	5
5	**529.261653**	265.134465	512.235104	256.621190	511.251088	256.129182	E	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	I	***389.250695***	195.128986	372.224146	186.615711	371.240130	186.123703	3
7	**743.393396**	372.200336	726.366847	363.687062	725.382831	363.195054	T	***276.166631***	138.586954	259.140082	130.073679	258.156066	129.581671	2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALSQEITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	916.497772	-0.003504	ALSQEITR
32.4	916.486526	0.007742	ALSKEELQ
27.4	916.497757	-0.003489	AEKAEITR
27.2	916.486526	0.007742	ALNTEIEK
23.3	916.497772	-0.003504	ALSLQETR
21.8	916.497772	-0.003504	AINTLETR
20.6	916.497787	-0.003519	ALSKGQNVT
20.6	916.486557	0.007711	APSKVTDAL
19.8	916.497787	-0.003519	ALSAGNGVTK
18.3	916.497772	-0.003504	LSAKEDVR

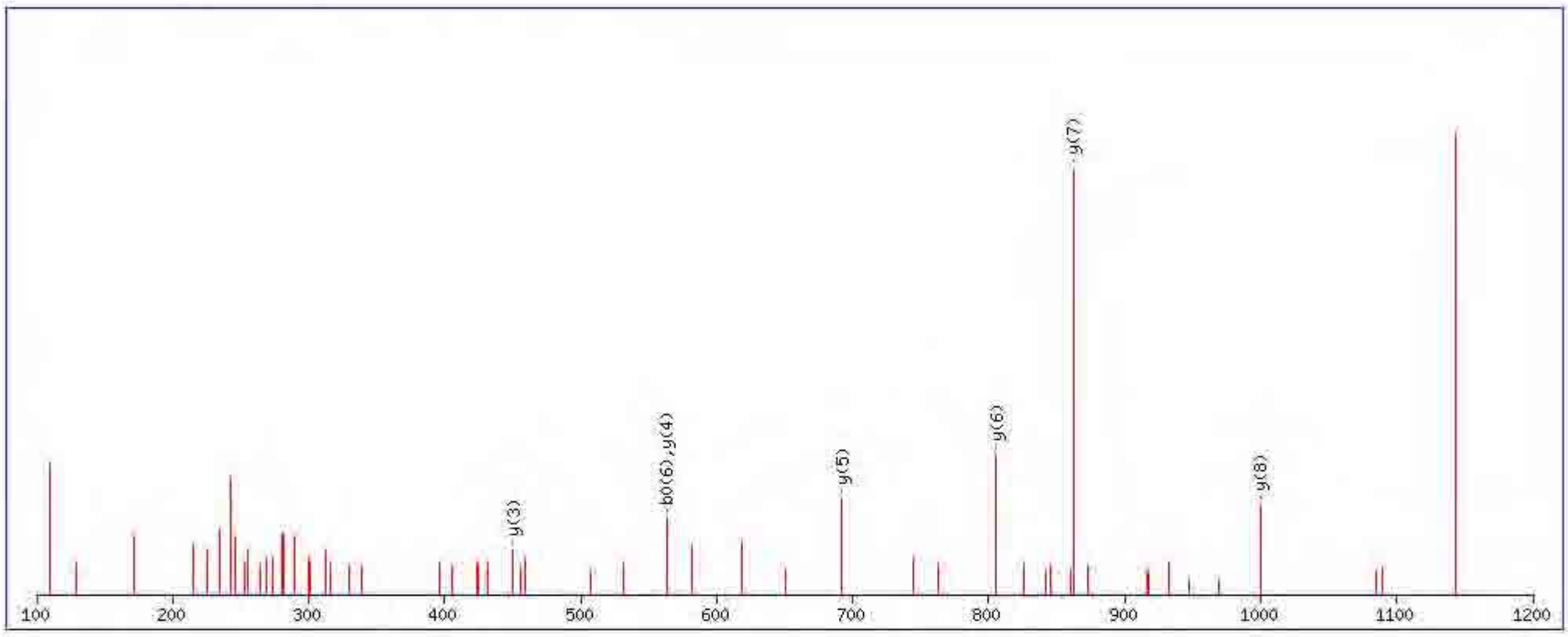
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSHGLEIFQR**
Found in **DKK1_HUMAN**, Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1

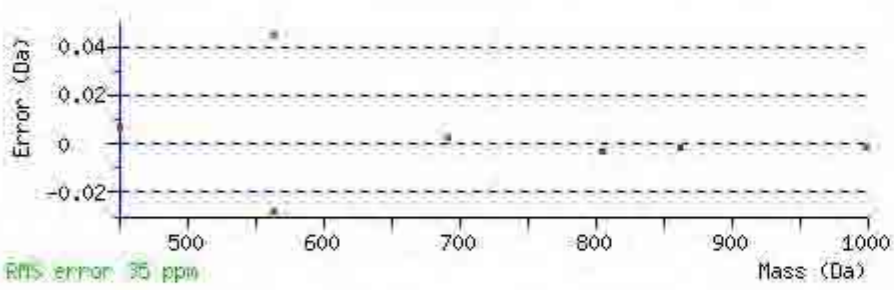
Match to Query 8703: 1142.585308 from(572.299930,2+) rtinseconds(1231) index(7228)
Title: Locus:1.1.1.1463.12
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

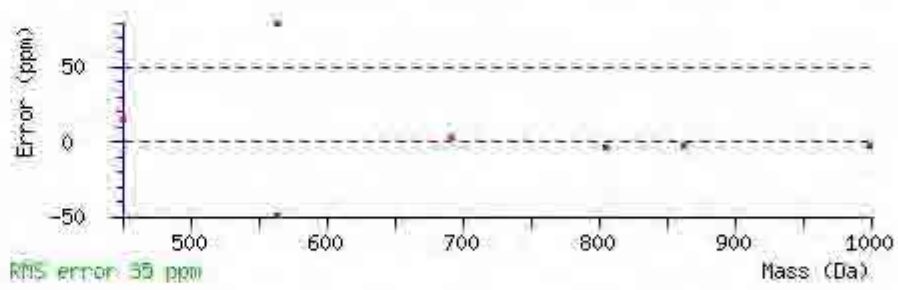
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1142.583252
Ions Score: 43 **Expect:** 0.00037
Matches : 7/82 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							10
2	145.060768	73.034022			127.050203	64.028740	S	1086.569069	543.788173	1069.542520	535.274898	1068.558504	534.782890	9
3	282.119680	141.563478			264.109115	132.558195	H	*999.537041*	500.272159	982.510492	491.758884	981.526476	491.266876	8
4	339.141144	170.074210			321.130579	161.068927	G	*862.478129*	431.742703	845.451580	423.229428	844.467564	422.737420	7
5	452.225208	226.616242			434.214643	217.610959	L	*805.456665*	403.231971	788.430116	394.718696	787.446100	394.226688	6
6	581.267801	291.137539			563.257236	282.132256	E	*692.372601*	346.689939	675.346052	338.176664	674.362036	337.684656	5
7	694.351865	347.679571			676.341300	338.674288	I	*563.330008*	282.168642	546.303459	273.655368			4
8	841.420279	421.213777			823.409714	412.208495	F	*450.245944*	225.626610	433.219395	217.113336			3
9	969.478857	485.243067	952.452308	476.729792	951.468292	476.237784	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GSHGLEIFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1142.583252	0.002056	GSHGLEIFQR
5.9	1142.579224	0.006084	QVARGEPGSAR
5.8	1142.583420	0.001888	MAWFALYLL
4.4	1142.581909	0.003399	LPGPIAPESSK
1.3	1142.586609	-0.001301	PEGMKGKPGAR
0.5	1142.581924	0.003384	LTPGPVPSESK
0.1	1142.581894	0.003414	AIPPDSEKSIS

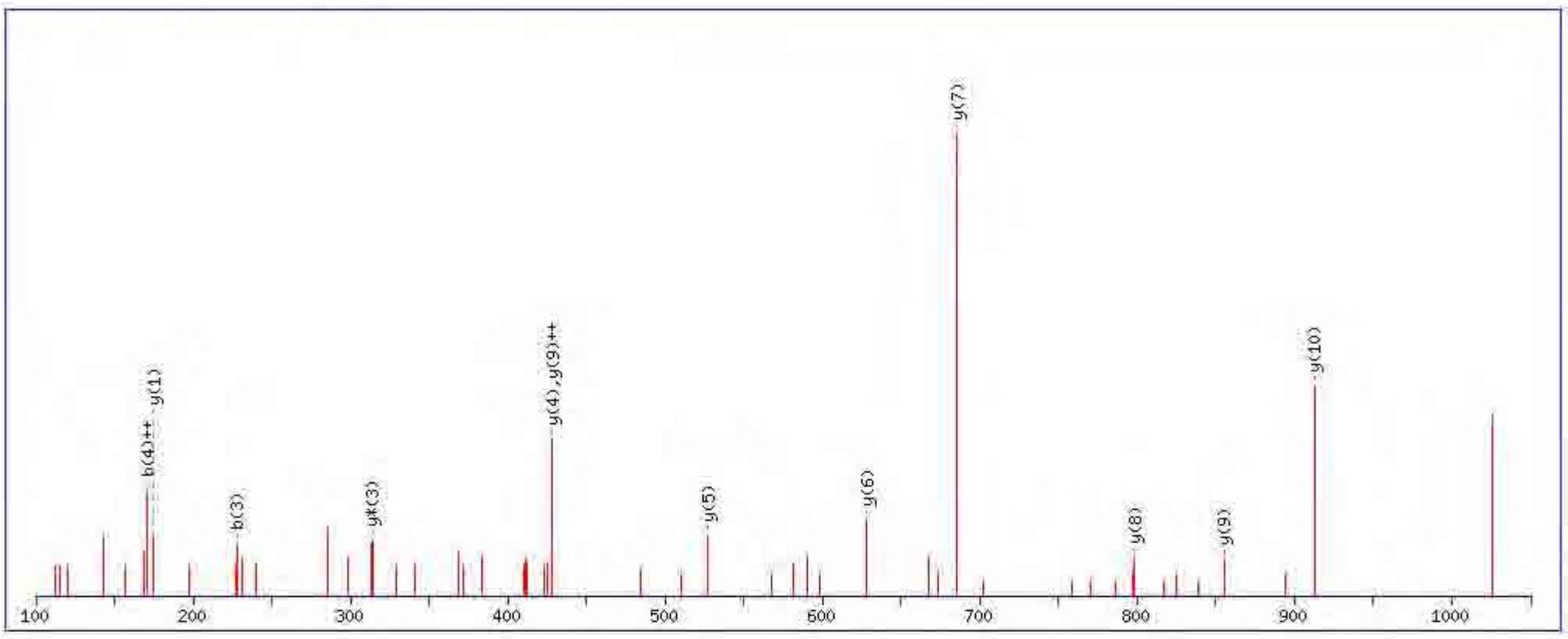
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

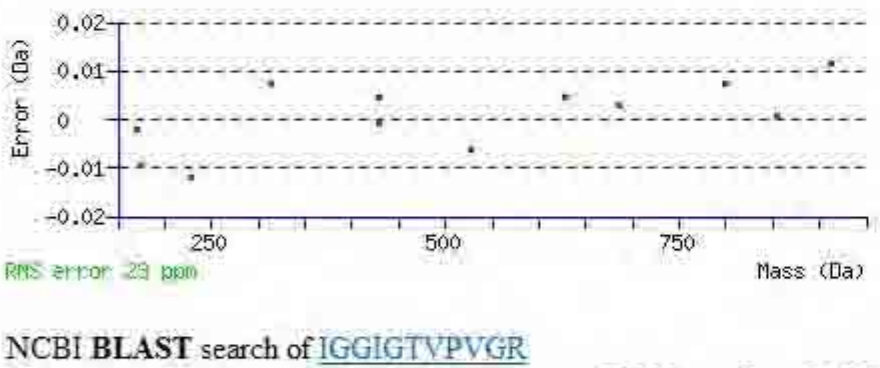
Match to Query 5894: 1024.601708 from(513.308130,2+) rtinseconds(1264) index(7518)
Title: Locus:1.1.1.1482.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

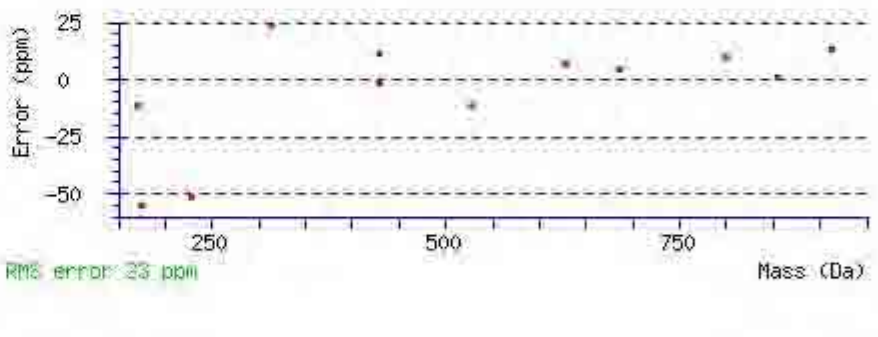
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 66 Expect: 1.7e-005
Matches : 13/80 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	912.526143	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	228.134268	114.570772			G	855.504679	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	341.218332	171.112804			I	798.483215	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	685.399151	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	628.377687	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	527.330008	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	428.261594	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	232.140416	116.573846	215.113867	108.060572			2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	1024.602951	-0.001243	IGGIGTVPVGR
39.5	1024.591690	0.010018	LGGPSALPKGL
26.6	1024.591690	0.010018	LGGINNILVP
16.2	1024.602905	-0.001197	PGAVAAAAILR
14.4	1024.602890	-0.001182	ARALDAAKPL
11.9	1024.591690	0.010018	VQLISGPPAK
11.8	1024.591705	0.010003	VQLGGLGTAPL
11.0	1024.602905	-0.001197	LNLPEGKVR
9.9	1024.602905	-0.001197	INLKRPPTA
9.9	1024.602905	-0.001197	INLKRPPTA

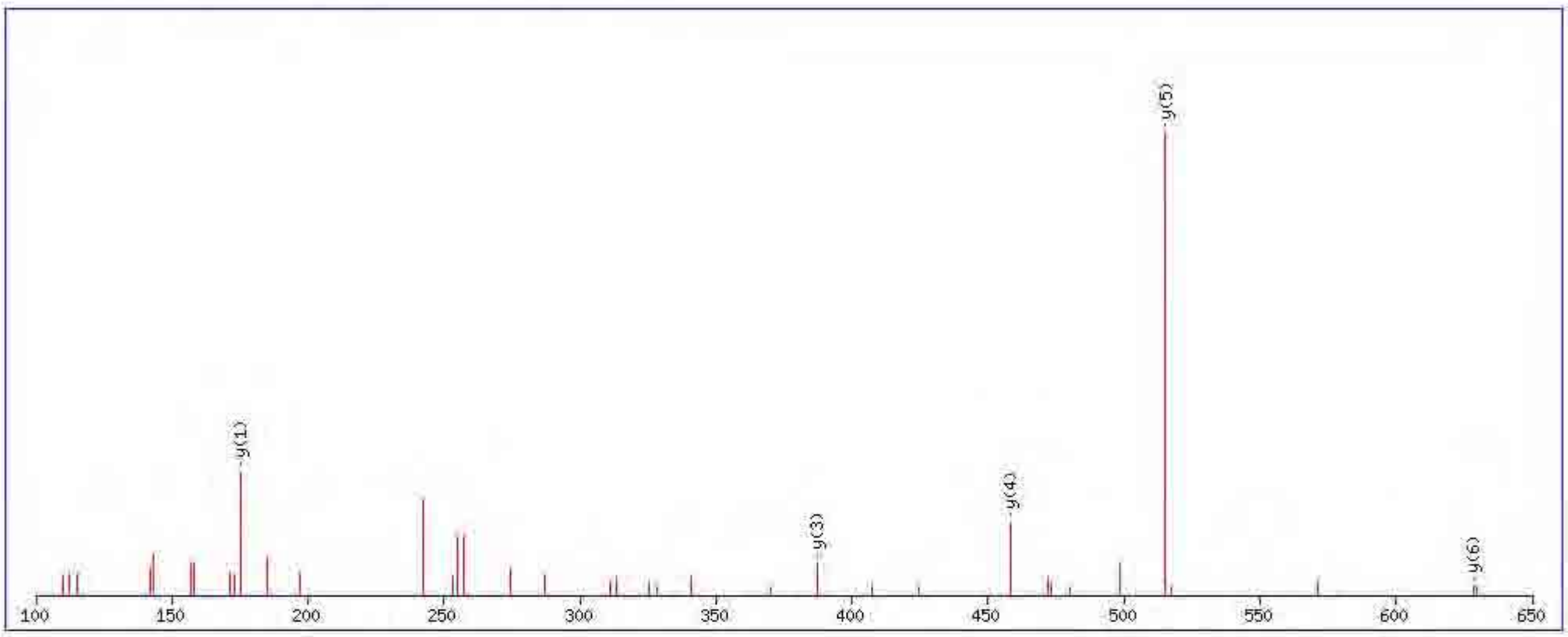
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLGALVR**
Found in **EFTU_HUMAN**, Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2

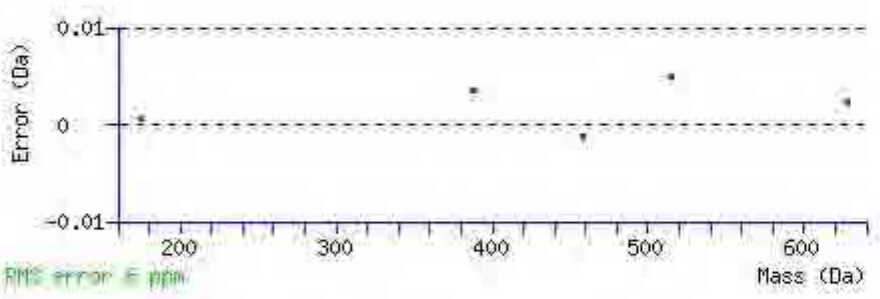
Match to Query 385: 741.449328 from(371.731940,2+) rtinseconds(972) index(4874)
Title: Locus:1.1.1.1314.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

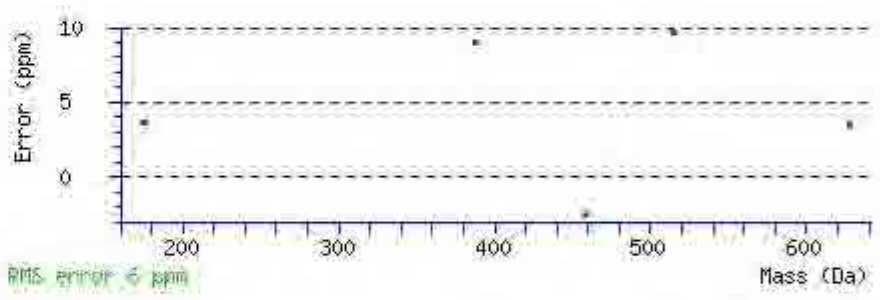
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 741.449707
Ions Score: 50 **Expect:** 0.00087
Matches : 5/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.050203	58.028740	98.023654	49.515465	N					7
2	228.134267	114.570771	211.107718	106.057497	L	*628.414072*	314.710674	611.387523	306.197400	6
3	285.155731	143.081504	268.129182	134.568229	G	*515.330008*	258.168642	498.303459	249.655368	5
4	356.192845	178.600060	339.166296	170.086786	A	*458.308544*	229.657910	441.281995	221.144635	4
5	469.276909	235.142092	452.250360	226.628818	L	*387.271430*	194.139353	370.244881	185.626078	3
6	568.345323	284.676300	551.318774	276.163025	V	274.187366	137.597321	257.160817	129.084046	2
7					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of NLGALVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	741.449707	-0.000379	NLGALVR
47.6	741.449722	-0.000394	GGIGALVR
32.3	741.449722	-0.000394	VQGALVR
32.1	741.449707	-0.000379	NIGGIIR
31.9	741.449722	-0.000394	GGLQVLR
31.9	741.449707	-0.000379	NLQLVR
31.9	741.449707	-0.000379	NLQVIR
31.9	741.449707	-0.000379	NLQVLR
30.8	741.449722	-0.000394	GGIGGILR
27.6	741.449707	-0.000379	NVAAVLR

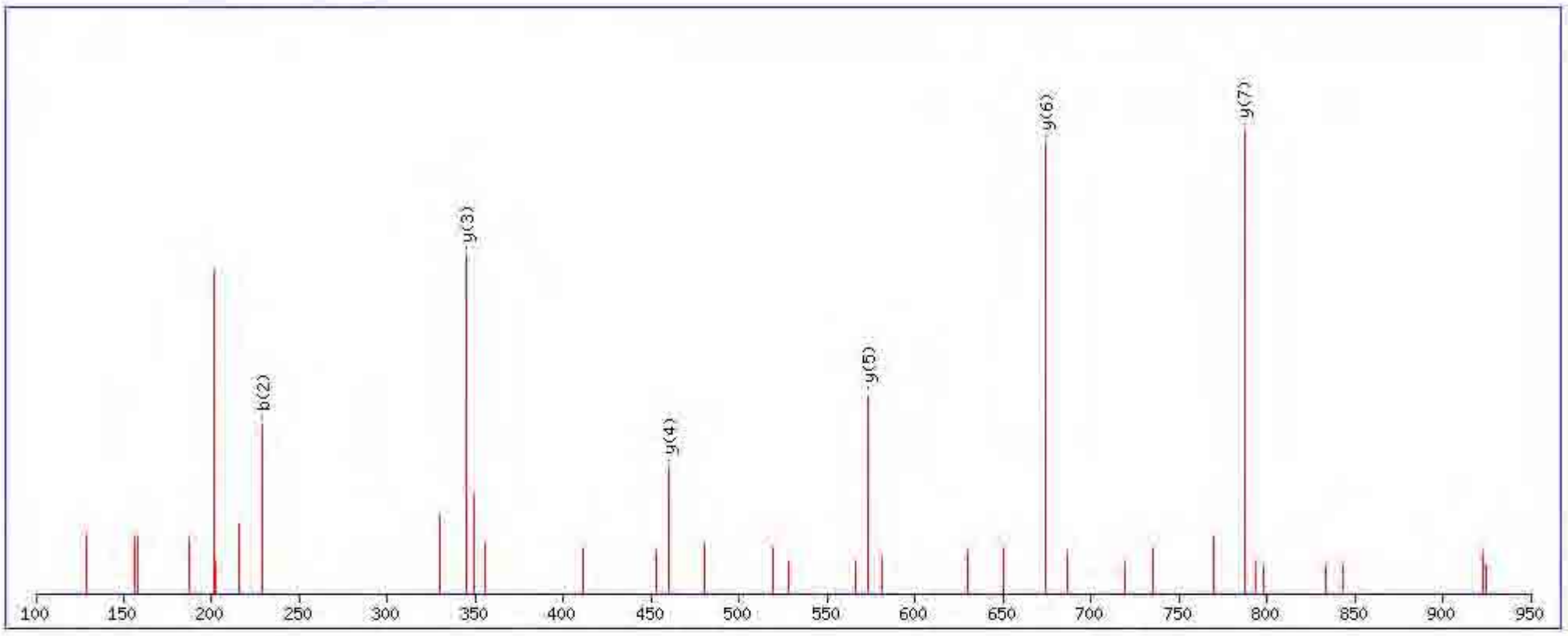
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILTIDIGR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

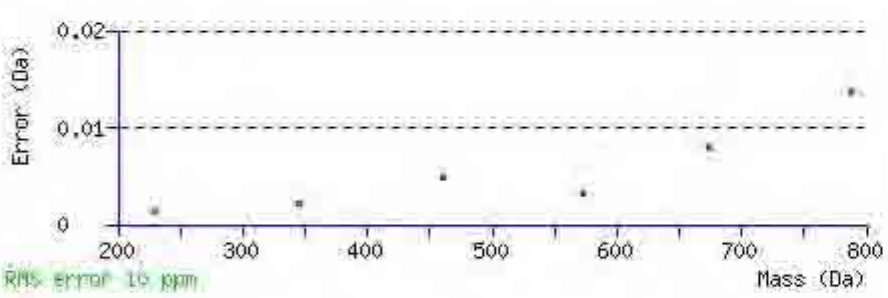
Match to Query 5725: 1014.579388 from(508.296970,2+) rtinseconds(1894) index(15332)
Title: Locus:1.1.1.1827.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

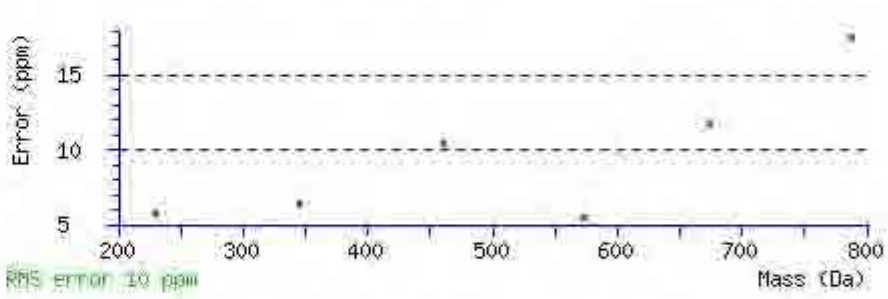
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1014.570953
Ions Score: 37 **Expect:** 0.0059
Matches : 6/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	229.118283	115.062779	211.107718	106.057497	I	900.551294	450.779285	883.524745	442.266011	882.540729	441.774003	8
3	342.202347	171.604811	324.191782	162.599529	L	*787.467230*	394.237253	770.440681	385.723979	769.456665	385.231971	7
4	443.250026	222.128651	425.239461	213.123369	T	*674.383166*	337.695221	657.356617	329.181947	656.372601	328.689939	6
5	556.334090	278.670683	538.323525	269.665401	I	*573.335487*	287.171382	556.308938	278.658107	555.324922	278.166099	5
6	671.361033	336.184155	653.350468	327.178872	D	*460.251423*	230.629350	443.224874	222.116075	442.240858	221.624067	4
7	784.445097	392.726187	766.434532	383.720904	I	*345.224480*	173.115878	328.197931	164.602604			3
8	841.466561	421.236919	823.455996	412.231636	G	232.140416	116.573846	215.113867	108.060572			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DILTIDIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1014.570953	0.008435	DILTIDIGR
12.8	1014.570969	0.008419	DVTTRITLP
11.9	1014.582169	-0.002781	DILTRIER
11.9	1014.570938	0.008450	VELTKLQAN
11.7	1014.570953	0.008435	DILVDGKAGK
11.7	1014.578339	0.001049	DLLLTPKCL
11.6	1014.582169	-0.002781	NNTLLGQKK
11.6	1014.570938	0.008450	NNTPLLSLK
7.6	1014.575012	0.004376	VFVPLPGSTV
5.7	1014.570953	0.008435	EVTPRTALL

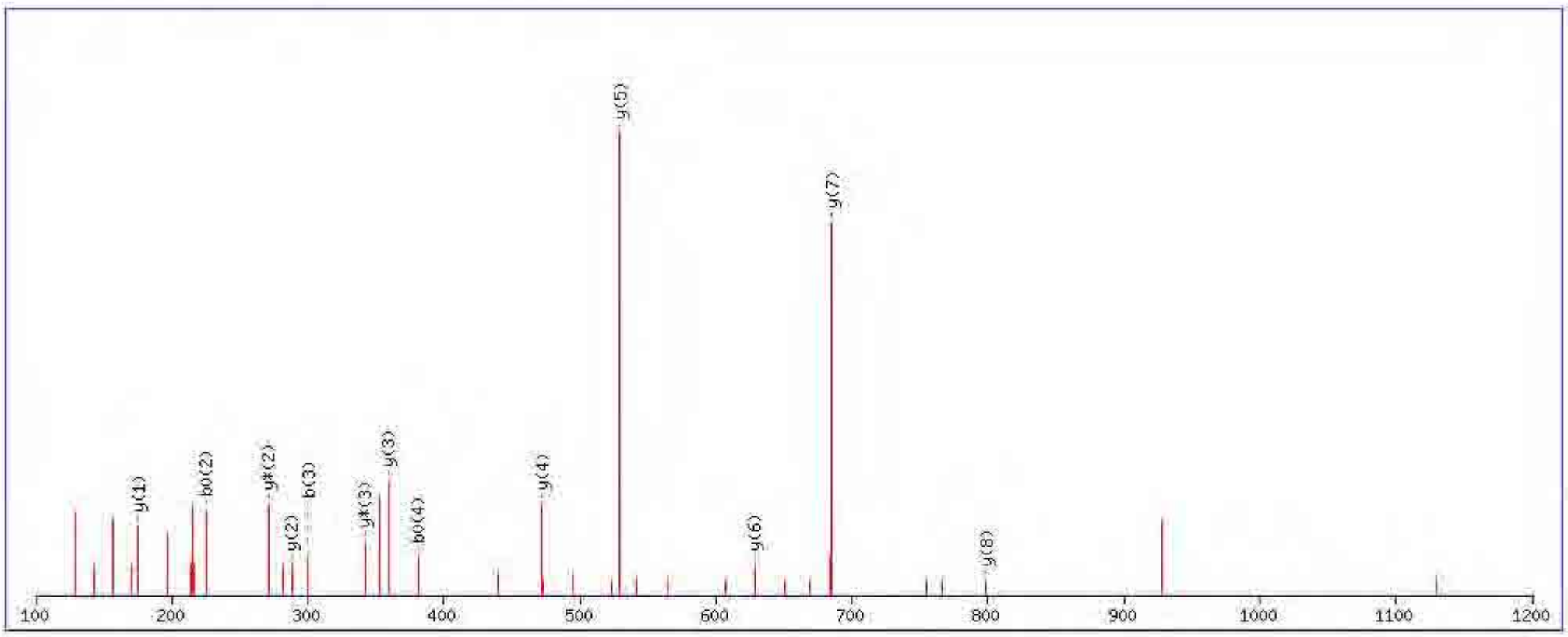
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGVGIALR**
Found in **FABP5_HUMAN**, Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3

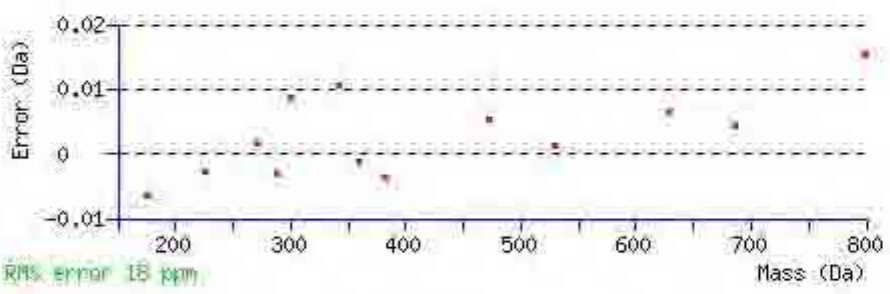
Match to Query 3813: 926.552168 from(464.283360,2+) rtinseconds(1584) index(11481)
Title: Locus:1.1.1.1658.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

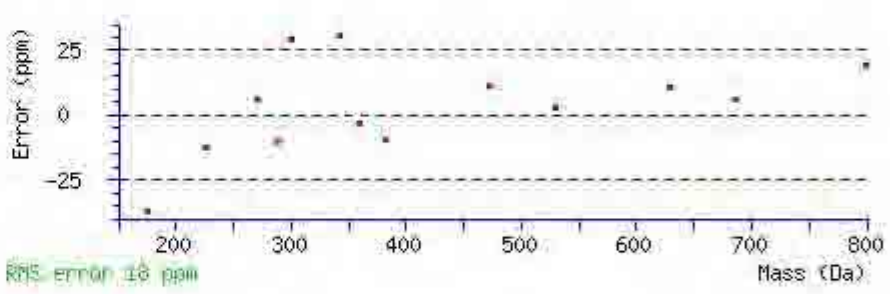
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 926.554901
Ions Score: 48 **Expect:** 0.0017
Matches : 13/64 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					9
2	243.133933	122.070605	225.123368	113.065322	L	*798.519600*	399.763438	781.493051	391.250163	8
3	300.155397	150.581336	282.144832	141.576054	G	*685.435536*	343.221406	668.408987	334.708131	7
4	399.223811	200.115544	381.213246	191.110261	V	*628.414072*	314.710674	611.387523	306.197400	6
5	456.245275	228.626275	438.234710	219.620993	G	*529.345658*	265.176467	512.319109	256.663192	5
6	569.329339	285.168308	551.318774	276.163025	I	*472.324194*	236.665735	455.297645	228.152460	4
7	640.366453	320.686865	622.355888	311.681582	A	*359.240130*	180.123703	342.213581	171.610428	3
8	753.450517	377.228897	735.439952	368.223614	L	*288.203016*	144.605146	271.176467	136.091871	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ELGVGIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	926.554901	-0.002733	ELGVGIALR
26.7	926.554901	-0.002733	ELRGLLQV
12.8	926.554901	-0.002733	LREGPVLK
12.8	926.554901	-0.002733	RLEGILGGL
12.3	926.543686	0.008482	APTIGLAAVV
11.9	926.554901	-0.002733	EGVLGALLR
10.7	926.543671	0.008497	LTGSLPNLL
9.9	926.554901	-0.002733	ELVQAVLR
9.6	926.543671	0.008497	AEVVLGNII
7.2	926.554901	-0.002733	TSLPLGALR

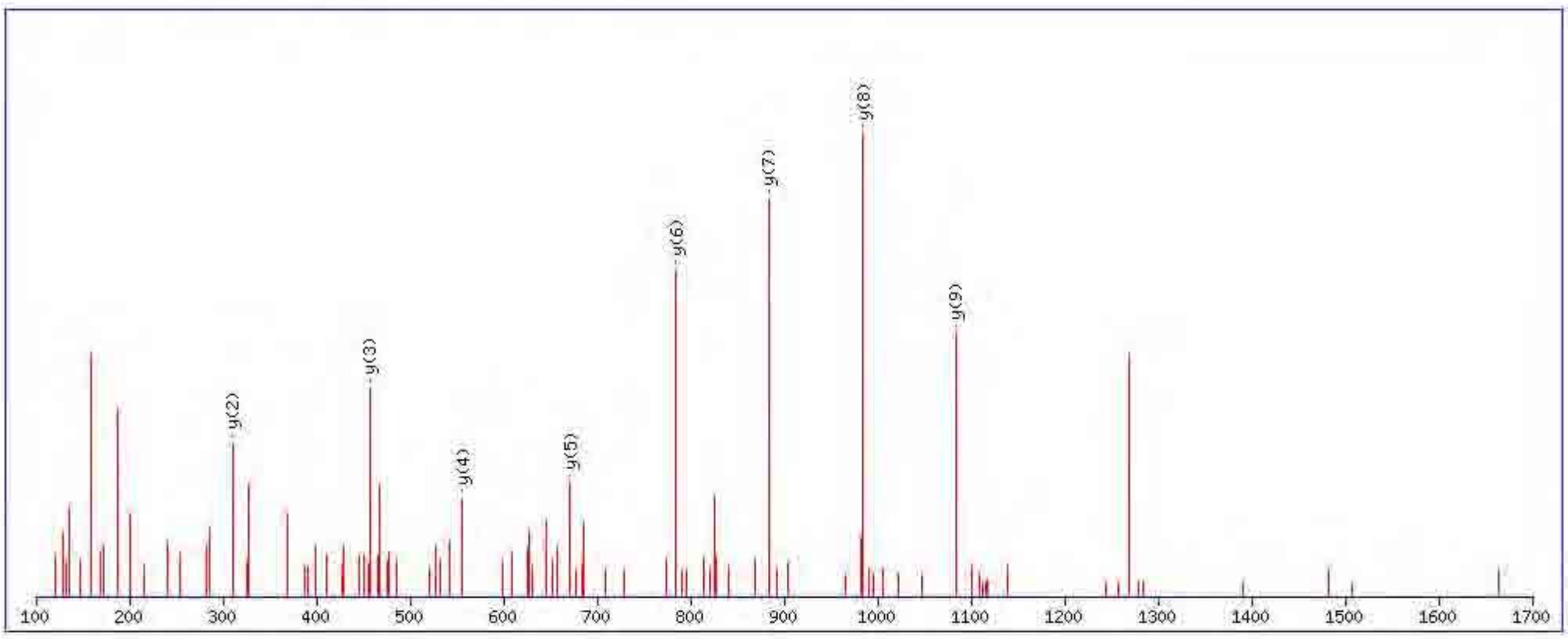
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVVTVIDVFYK**
Found in **FIL A2_HUMAN**, Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1

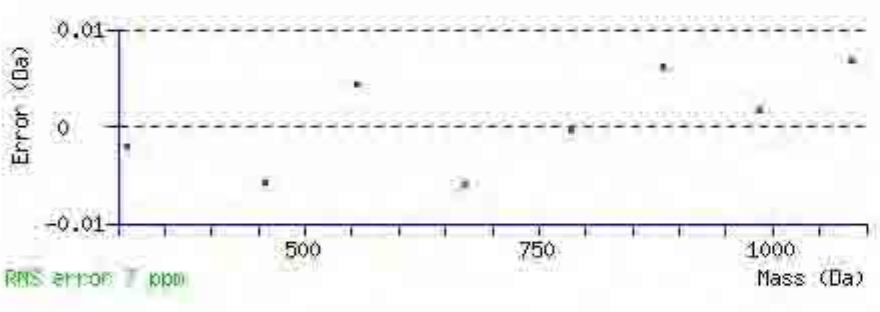
Match to Query 12171: 1268.701968 from(635.358260,2+) rtinseconds(2243) index(19655)
Title: Locus:1.1.1.2018.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

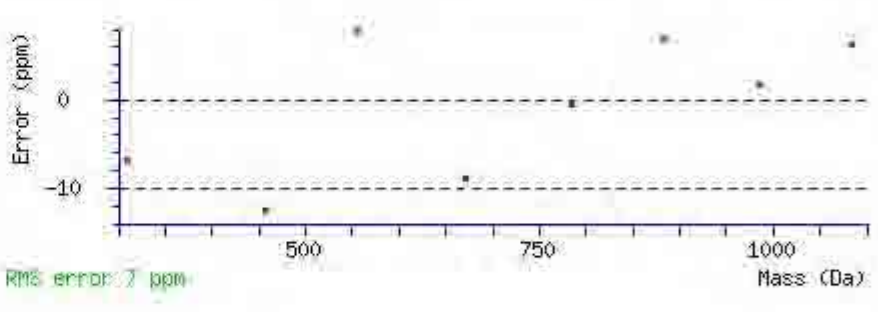
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1268.701660
Ions Score: 67 **Expect:** 1.9e-006
Matches : 8/92 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	187.107718	94.057497	169.097153	85.052214	V	1182.676889	591.842082	1165.650340	583.328808	1164.666324	582.836800	10
3	286.176132	143.591704	268.165567	134.586422	V	*1083.608475*	542.307876	1066.581926	533.794601	1065.597910	533.302593	9
4	387.223811	194.115544	369.213246	185.110261	T	*984.540061*	492.773668	967.513512	484.260394	966.529496	483.768386	8
5	486.292225	243.649751	468.281660	234.644468	V	*883.492382*	442.249829	866.465833	433.736554	865.481817	433.244546	7
6	599.376289	300.191783	581.365724	291.186500	I	*784.423968*	392.715622	767.397419	384.202347	766.413403	383.710339	6
7	714.403232	357.705254	696.392667	348.699972	D	*671.339904*	336.173590	654.313355	327.660315	653.329339	327.168307	5
8	813.471646	407.239461	795.461081	398.234178	V	*556.312961*	278.660119	539.286412	270.146844			4
9	960.540060	480.773668	942.529495	471.768385	F	*457.244547*	229.125911	440.217998	220.612637			3
10	1123.603389	562.305332	1105.592824	553.300050	Y	*310.176133*	155.591704	293.149584	147.078430			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVVTVIDVFYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1268.701660	0.000308	SVVTVIDVFYK
5.3	1268.712875	-0.010907	VSLWPVPVAASK
5.0	1268.708847	-0.006879	LTTAVPSPSKPR
4.7	1268.691086	0.010882	DPGLPKMQVIR
4.5	1268.712845	-0.010877	WVIEAKDLPAK
3.6	1268.708847	-0.006879	VSTAPQQKPIGK
3.4	1268.691071	0.010897	PAMENQVLVIR
0.8	1268.697617	0.004351	TPAKNSVVIPDL
0.6	1268.708862	-0.006894	ESPGVPVAKVVR
0.5	1268.697632	0.004336	VSVEVVTAGGAALP

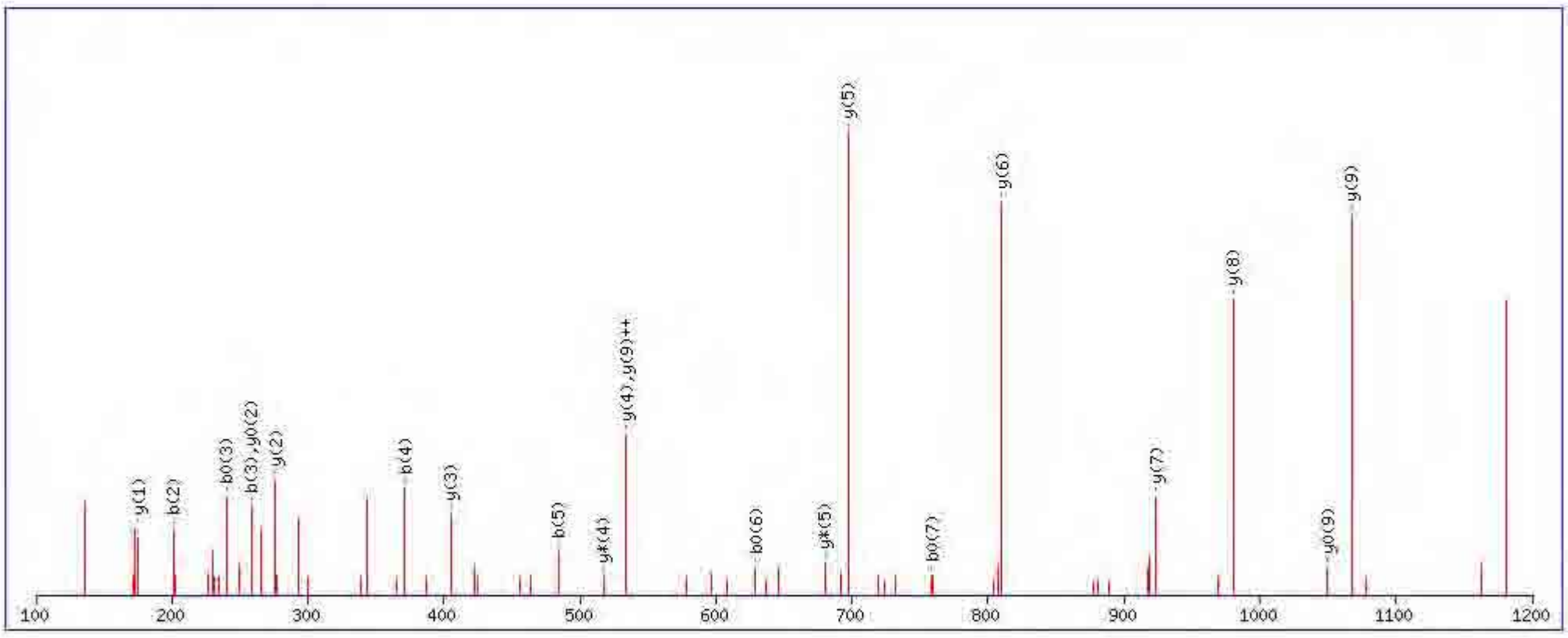
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISGLIYEETR**
Found in **H4_HUMAN**, Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

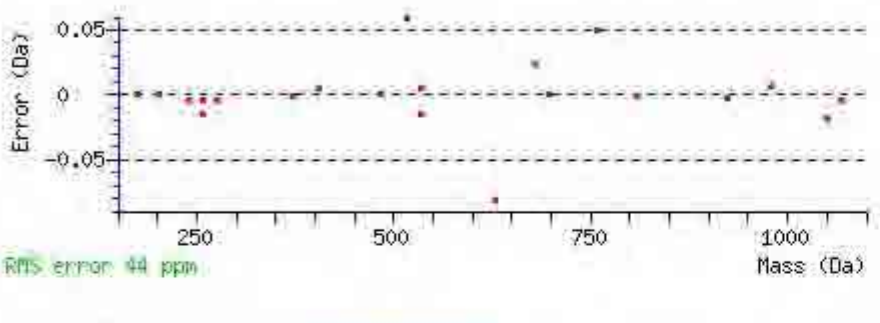
Match to Query 9955: 1179.614688 from(590.814620,2+) rtinseconds(1378) index(8907)
Title: Locus:1.1.1.1545.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

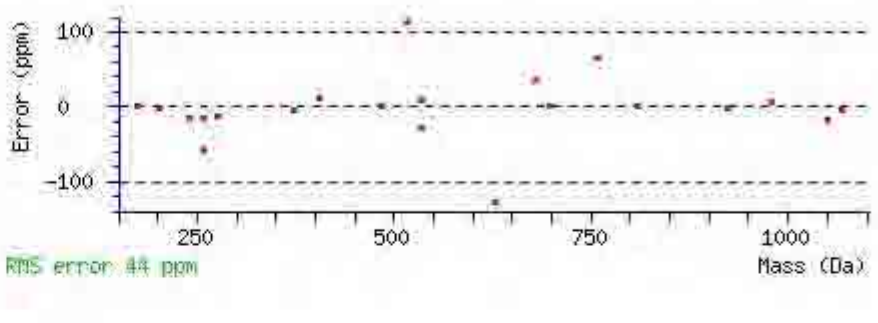
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1179.613525
Ions Score: 63 **Expect:** 8.4e-005
Matches : 21/86 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							10
2	**201.123368**	101.065322	183.112803	92.060039	S	*1067.536766*	534.272021	1050.510217	525.758747	1049.526201	525.266739	9
3	**258.144832**	129.576054	240.134267	120.570771	G	*980.504738*	490.756007	963.478189	482.242733	962.494173	481.750725	8
4	**371.228896**	186.118086	353.218331	177.112803	L	*923.483274*	462.245275	906.456725	453.732001	905.472709	453.239993	7
5	**484.312960**	242.660118	466.302395	233.654835	I	*810.399210*	405.703243	793.372661	397.189969	792.388645	396.697961	6
6	647.376289	324.191783	629.365724	315.186500	Y	*697.315146*	349.161211	680.288597	340.647937	679.304581	340.155929	5
7	776.418882	388.713079	758.408317	379.707797	E	*534.251817*	267.629547	517.225268	259.116272	516.241252	258.624264	4
8	905.461475	453.234376	887.450910	444.229093	E	*405.209224*	203.108250	388.182675	194.594975	387.198659	194.102967	3
9	1006.509154	503.758215	988.498589	494.752933	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
10					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ISGLIYEETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	1179.613525	0.001163	ISGLIYEETR
19.1	1179.610855	0.003833	PSGLHNQQKR
18.3	1179.613586	0.001102	SPGPPPPVGVKT
15.6	1179.624771	-0.010083	GAELPTHPSKK
14.4	1179.613525	0.001163	LKAEPAAPPAAP
14.2	1179.613556	0.001132	GSLPITNSFTK
12.2	1179.613525	0.001163	LQEIQTAYSK
11.5	1179.613556	0.001132	VTAVLKSQGYD
11.0	1179.624786	-0.010098	SVAPLPPQRSP
10.8	1179.620956	-0.006268	LSVPATFMLVS

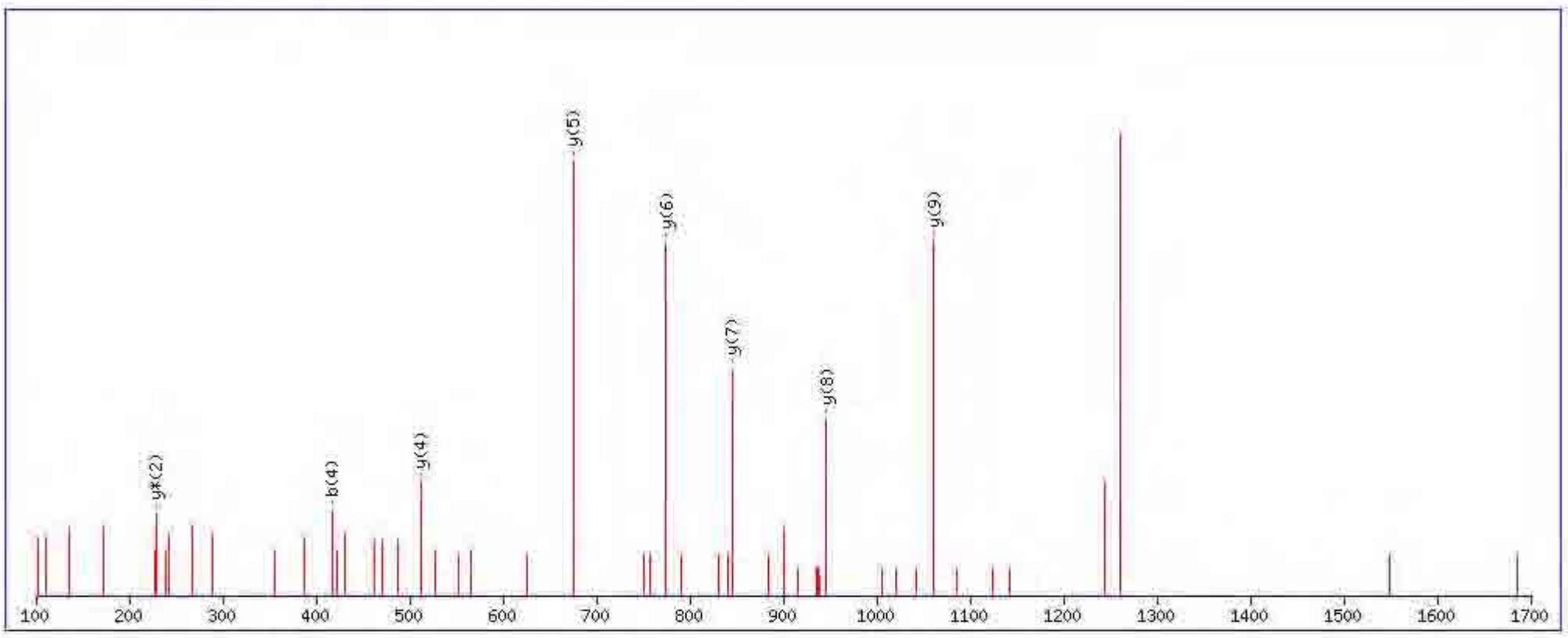
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEDTAVYYCAR**
Found in **HV302_HUMAN**, Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1

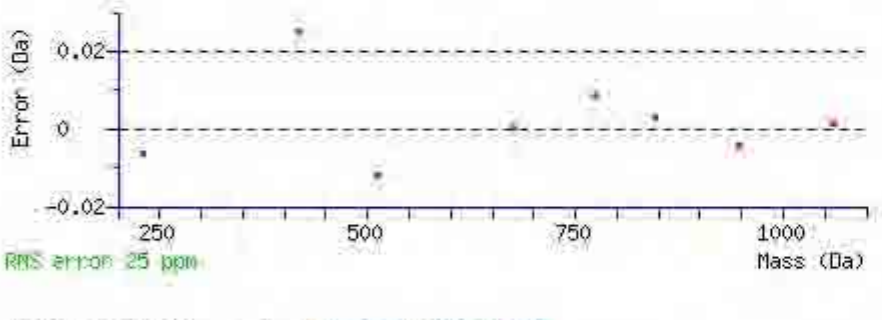
Match to Query 11967: 1260.550408 from(631.282480,2+) rtinseconds(1136) index(6151)
Title: Locus:1.1.1.1410.24
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

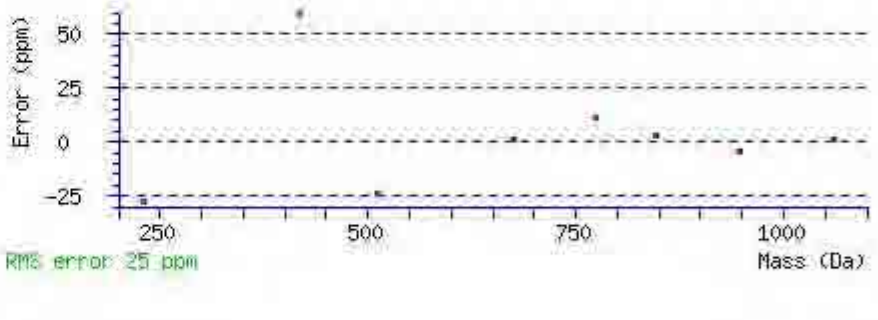
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1260.544464
Ions Score: 45 **Expect:** 0.00037
Matches : 8/84 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	201.086983	101.047130	183.076418	92.041847	E	1190.514652	595.760964	1173.488103	587.247690	1172.504087	586.755682	10
3	316.113926	158.560601	298.103361	149.555319	D	*1061.472059*	531.239668	1044.445510	522.726393	1043.461494	522.234385	9
4	417.161605	209.084441	399.151040	200.079158	T	*946.445116*	473.726196	929.418567	465.212922	928.434551	464.720914	8
5	488.198719	244.602998	470.188154	235.597715	A	*845.397437*	423.202357	828.370888	414.689082			7
6	587.267133	294.137205	569.256568	285.131922	V	*774.360323*	387.683800	757.333774	379.170525			6
7	750.330462	375.668869	732.319897	366.663587	Y	*675.291909*	338.149593	658.265360	329.636318			5
8	913.393791	457.200534	895.383226	448.195251	Y	*512.228580*	256.617928	495.202031	248.104654			4
9	1016.402976	508.705126	998.392411	499.699844	C	349.165251	175.086264	332.138702	166.572989			3
10	1087.440090	544.223683	1069.429525	535.218401	A	246.156066	123.581671	229.129517	115.068397			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AEDTAVYYCAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	1260.544464	0.005944	AEDTAVYYCAR
44.8	1260.544464	0.005944	AEBTAVYYCAR
44.8	1260.544464	0.005944	AZBTAVYYCAR
7.8	1260.547852	0.002556	CPSEAGAMTQPAV
7.2	1260.544495	0.005913	CPDFVEGPEPR
7.2	1260.562241	-0.011833	SLDLDDWPRE
5.9	1260.544510	0.005898	SPSTHTMAPWV
5.4	1260.547012	0.003396	AETLPGSGDSGPGT
2.4	1260.540466	0.009942	EACPPNLTGDGR
1.4	1260.544510	0.005898	VTGCPPFDEHK

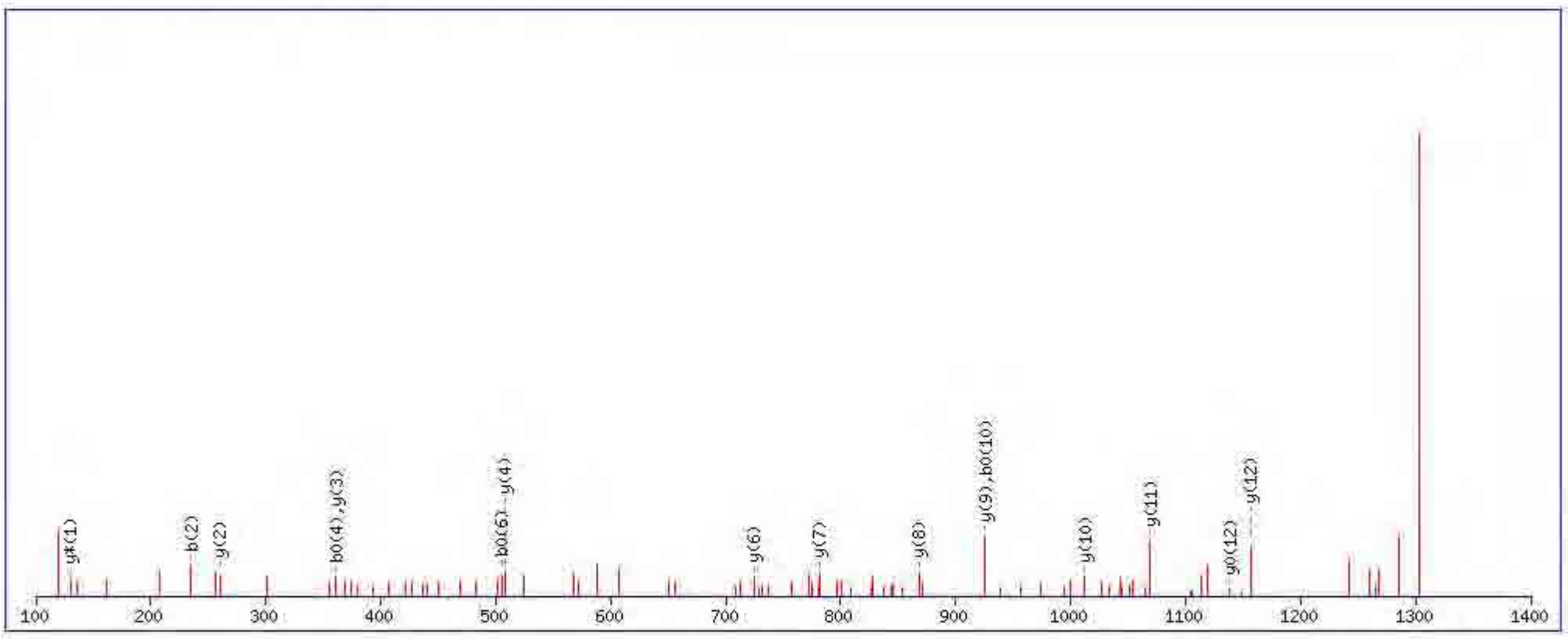
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSGSGTDFTLK**
Found in **KV201_HUMAN**, Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1

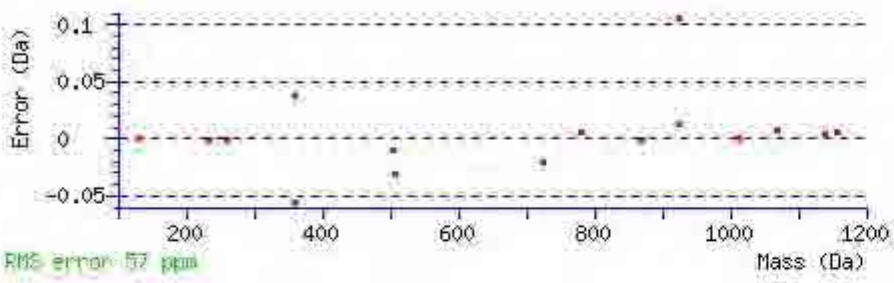
Match to Query 12981: 1302.600488 from(652.307520,2+) rtinseconds(1325) index(8200)
Title: Locus:1.1.1.1516.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

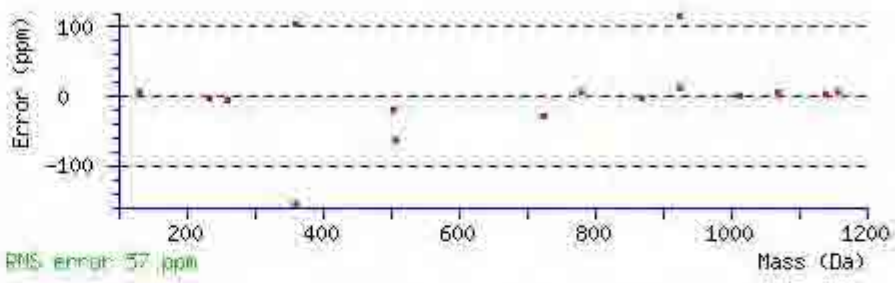
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1302.609222
Ions Score: 54 Expect: 4.6e-005
Matches : 16/114 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	235.107718	118.057497	217.097153	109.052214	S	*1156.548059*	578.777667	1139.521510	570.264393	1138.537494	569.772385	12
3	292.129182	146.568229	274.118617	137.562946	G	*1069.516031*	535.261653	1052.489482	526.748379	1051.505466	526.256371	11
4	379.161210	190.084243	361.150645	181.078960	S	*1012.494567*	506.750921	995.468018	498.237647	994.484002	497.745639	10
5	436.182674	218.594975	418.172109	209.589692	G	*925.462539*	463.234907	908.435990	454.721633	907.451974	454.229625	9
6	523.214702	262.110989	505.204137	253.105707	S	*868.441075*	434.724176	851.414526	426.210901	850.430510	425.718893	8
7	580.236166	290.621721	562.225601	281.616439	G	*781.409047*	391.208161	764.382498	382.694887	763.398482	382.202879	7
8	681.283845	341.145561	663.273280	332.140278	T	*724.387583*	362.697429	707.361034	354.184155	706.377018	353.692147	6
9	796.310788	398.659032	778.300223	389.653750	D	623.339904	312.173590	606.313355	303.660315	605.329339	303.168307	5
10	943.379202	472.193239	925.368637	463.187956	F	*508.312961*	254.660118	491.286412	246.146844	490.302396	245.654836	4
11	1044.426881	522.717078	1026.416316	513.711796	T	*361.244547*	181.125911	344.217998	172.612637	343.233982	172.120629	3
12	1157.510945	579.259110	1139.500380	570.253828	L	*260.196868*	130.602072	243.170319	122.088797			2
13					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSGSGSGTDFTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	1302.609222	-0.008734	FSGSGSGTDFTLK
53.9	1302.609222	-0.008734	FSGSGSGTBFTLK
7.3	1302.591431	0.009057	FSAKMPNASFST
7.2	1302.593933	0.006555	EQAPDISPKSDT
6.8	1302.606689	-0.006201	FSLGYMPYPGR
6.4	1302.609192	-0.008704	SFSGFSISQSKE
6.3	1302.591446	0.009042	FLVPDHVNMSE
6.2	1302.613419	-0.012931	MVMYLNMLRT
6.0	1302.591431	0.009057	FSAKMPNASFST
5.6	1302.597977	0.002511	FTAESYTVLGDT

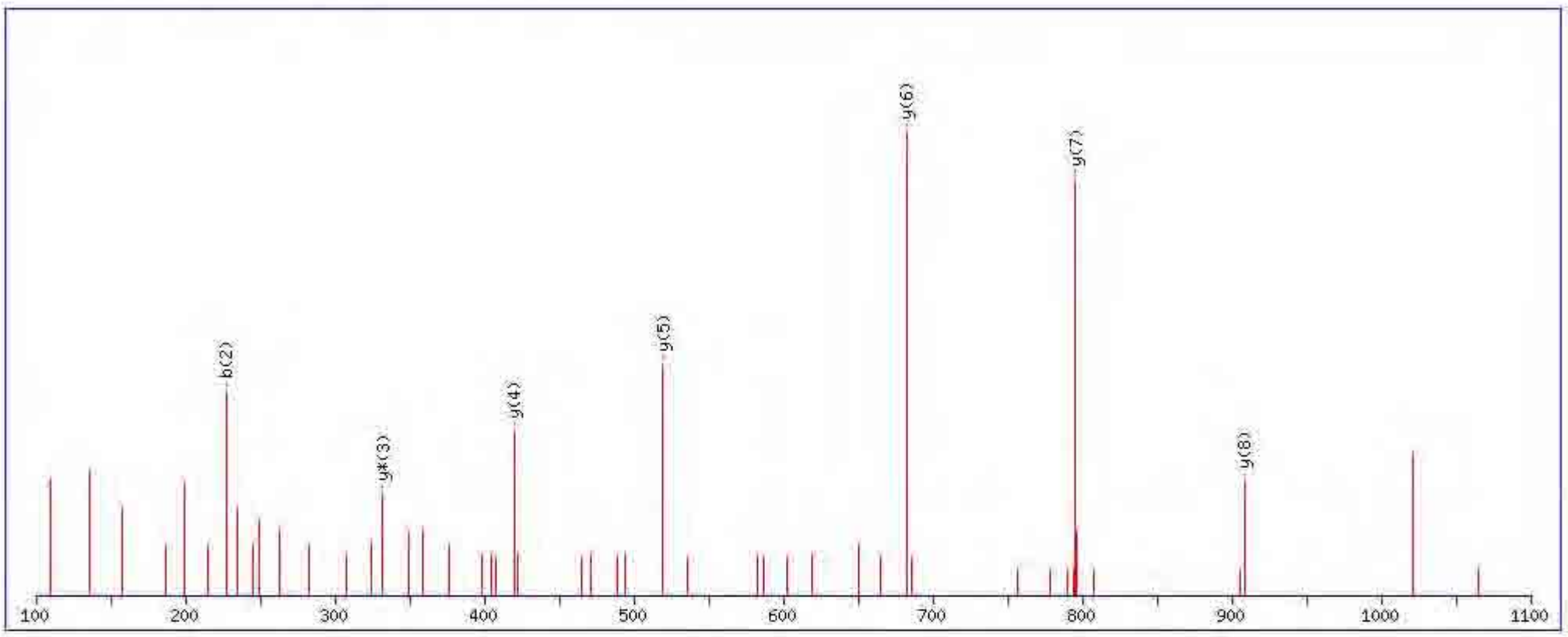
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYVASSR**
Found in **KV304_HUMAN**, Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1

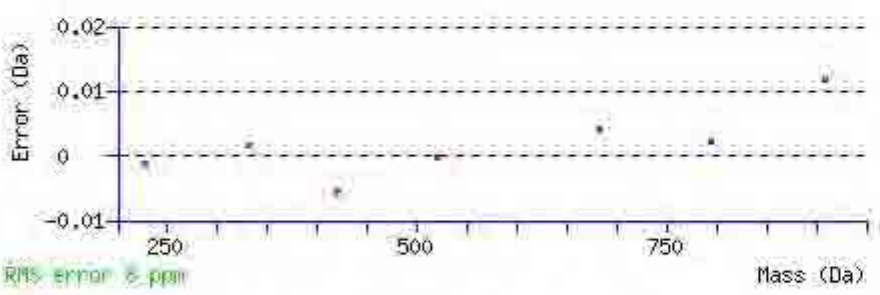
Match to Query 5824: 1020.600388 from(511.307470,2+) rtinseconds(1478) index(10227)
Title: Locus:1.1.1.1600.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

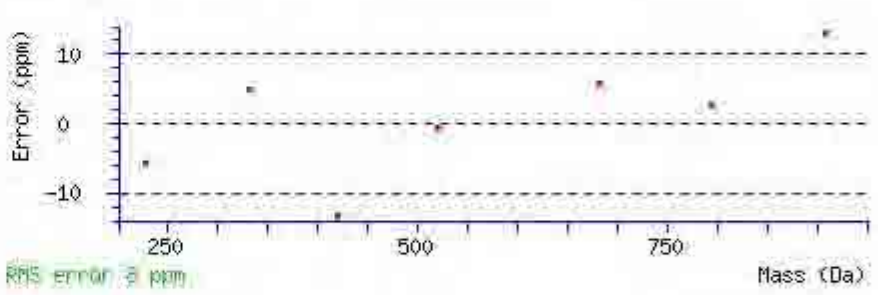
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1020.596756
Ions Score: 41 **Expect:** 0.004
Matches : 7/66 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*908.519993*	454.763635	891.493444	446.250360	890.509428	445.758352	8
3	340.259468	170.633372			I	*795.435929*	398.221603	778.409380	389.708328	777.425364	389.216320	7
4	503.322797	252.165036			Y	*682.351865*	341.679571	665.325316	333.166296	664.341300	332.674288	6
5	602.391211	301.699244			V	*519.288536*	260.147906	502.261987	251.634632	501.277971	251.142624	5
6	673.428325	337.217801			A	*420.220122*	210.613699	403.193573	202.100424	402.209557	201.608416	4
7	760.460353	380.733814	742.449788	371.728532	S	349.183008	175.095142	332.156459	166.581867	331.172443	166.089859	3
8	847.492381	424.249828	829.481816	415.244546	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIYVASSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1020.596756	0.003632	LLIYVASSR
17.4	1020.596771	0.003617	PLIPPISPR
13.9	1020.607986	-0.007598	ILLQEHIR
13.9	1020.607986	-0.007598	LLPHKELR
13.9	1020.596771	0.003617	PLIPPISPR
13.9	1020.596786	0.003602	PLPVPPTLR
12.5	1020.600784	-0.000396	LLYIFKQP
11.9	1020.596771	0.003617	PLIPPISPR
11.2	1020.596756	0.003632	IILAILDHN
11.2	1020.596771	0.003617	IILHGAELVG

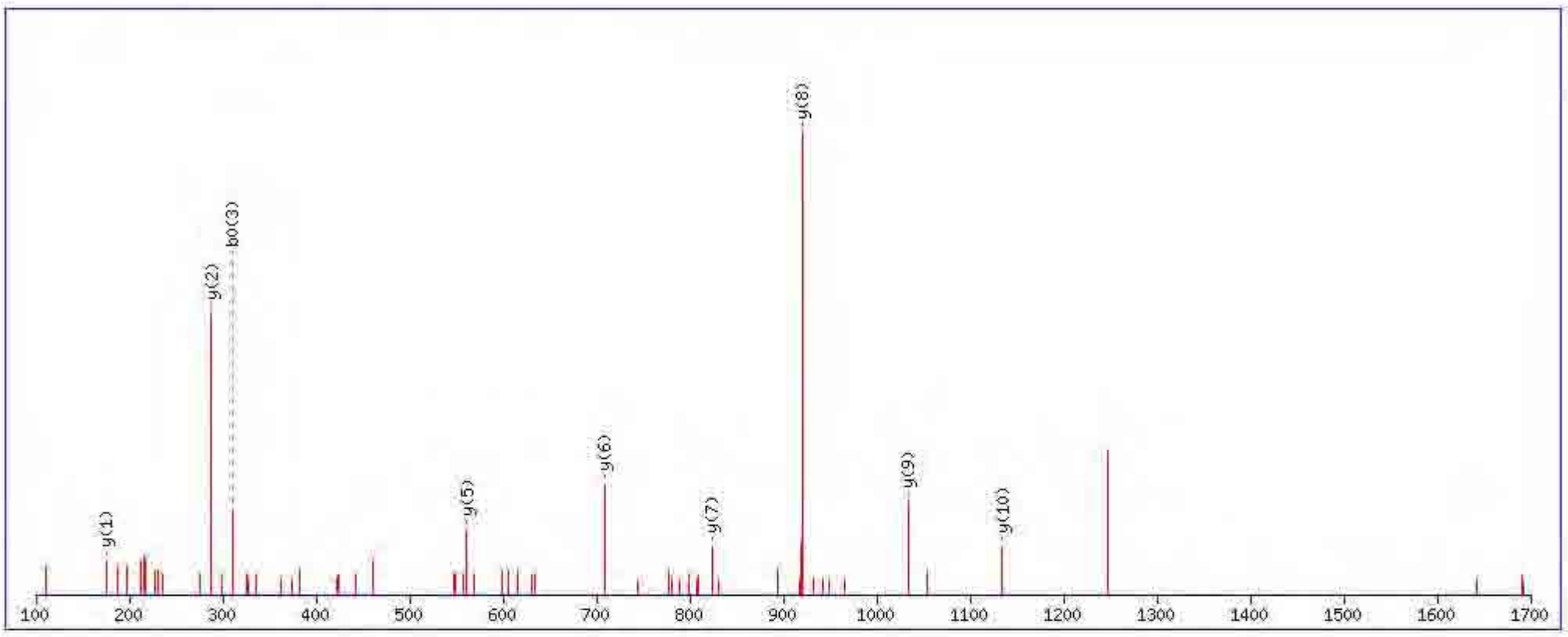
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLPDFTGDLR**
Found in **LBP_HUMAN**, Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3

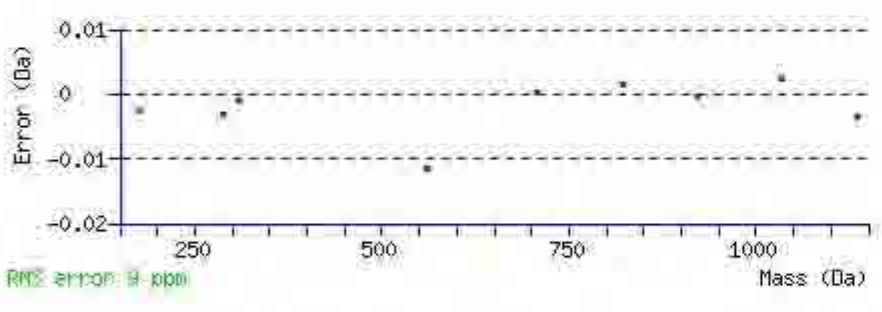
Match to Query 11694: 1246.660388 from(624.337470,2+) rtinseconds(2085) index(17694)
Title: Locus:1.1.1.1932.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

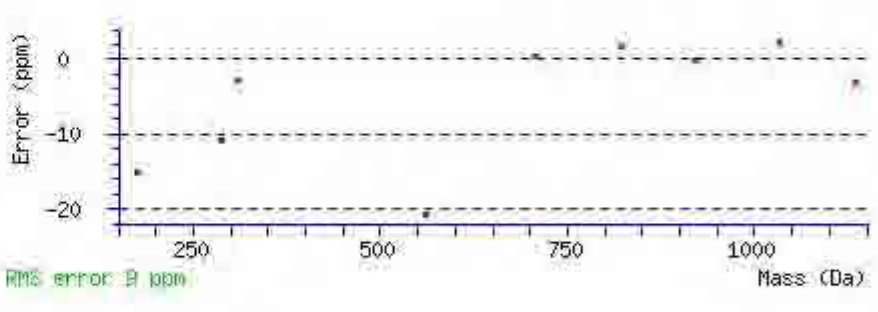
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1246.655762
Ions Score: 72 **Expect:** 7.1e-006
Matches : 9/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	*1134.578966*	567.793121	1117.552417	559.279847	1116.568401	558.787839	10
3	328.223083	164.615179	310.212518	155.609897	L	*1033.531287*	517.269282	1016.504738	508.756007	1015.520722	508.263999	9
4	425.275847	213.141561	407.265282	204.136279	P	*920.447223*	460.727249	903.420674	452.213975	902.436658	451.721967	8
5	540.302790	270.655033	522.292225	261.649750	D	*823.394459*	412.200868	806.367910	403.687593	805.383894	403.195585	7
6	687.371204	344.189240	669.360639	335.183957	F	*708.367516*	354.687396	691.340967	346.174122	690.356951	345.682114	6
7	788.418883	394.713079	770.408318	385.707797	T	*561.299102*	281.153189	544.272553	272.639915	543.288537	272.147907	5
8	845.440347	423.223812	827.429782	414.218529	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	960.467290	480.737283	942.456725	471.732000	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1073.551354	537.279315	1055.540789	528.274032	L	*288.203016*	144.605146	271.176467	136.091871			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLPDFTGDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	1246.655762	0.004626	ITLPDFTGDLR
16.1	1246.655731	0.004657	PLPLSYEQIR
15.6	1246.655762	0.004626	PTPPGQPPISPK
15.5	1246.655731	0.004657	LTIIQDPEYR
15.5	1246.656616	0.003772	LTLFMAVPPCR
15.5	1246.653076	0.007312	PTPGQRLHPGR
15.1	1246.655746	0.004642	LDVLVNNAYAGV
14.9	1246.659103	0.001285	LTPEIMKEVR
14.2	1246.659119	0.001269	PTDTAMLTLLR
13.6	1246.655746	0.004642	PPESPPLLPPR

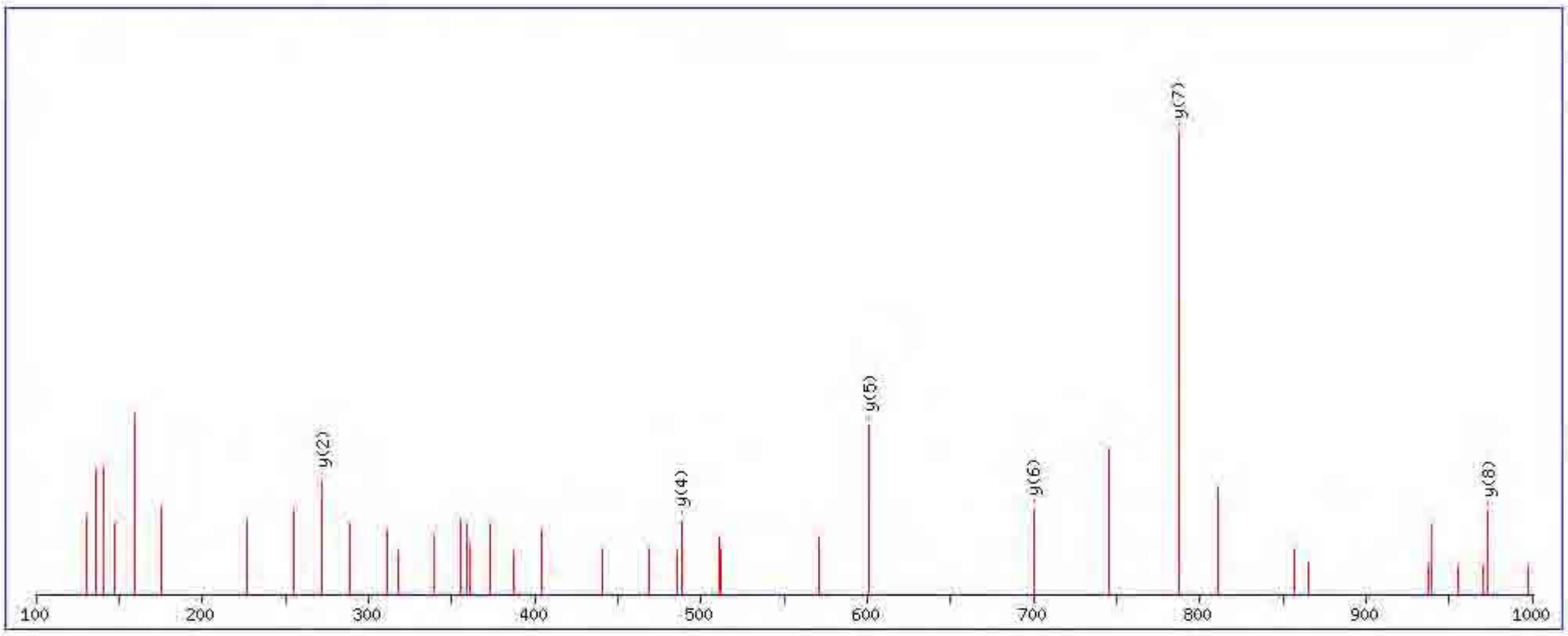
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IWSVLESPR**
Found in **MAMC2_HUMAN**, MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3

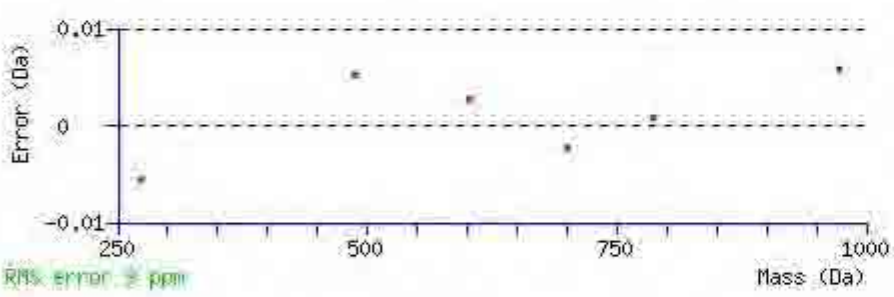
Match to Query 7371: 1085.588308 from(543.801430,2+) rtinseconds(1688) index(12810)
Title: Locus:1.1.1.1715.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

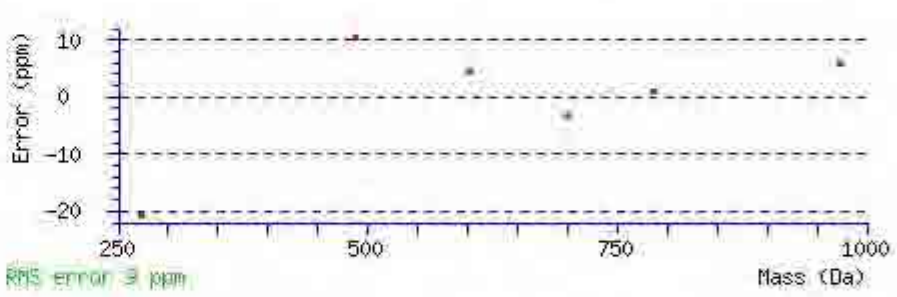
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1085.586929
Ions Score: 47 **Expect:** 0.0027
Matches : 6/72 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	300.170653	150.588965			W	*973.510156*	487.258716	956.483607	478.745442	955.499591	478.253434	8
3	387.202681	194.104979	369.192116	185.099696	S	*787.430843*	394.219060	770.404294	385.705785	769.420278	385.213777	7
4	486.271095	243.639186	468.260530	234.633903	V	*700.398815*	350.703046	683.372266	342.189771	682.388250	341.697763	6
5	599.355159	300.181218	581.344594	291.175935	L	*601.330401*	301.168839	584.303852	292.655564	583.319836	292.163556	5
6	728.397752	364.702514	710.387187	355.697232	E	*488.246337*	244.626807	471.219788	236.113532	470.235772	235.621524	4
7	815.429780	408.218528	797.419215	399.213246	S	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
8	912.482544	456.744910	894.471979	447.739628	P	*272.171716*	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IWSVLESPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	1085.586929	0.001379	IWSVLESPR
18.7	1085.596817	-0.008509	IDADAIVEKI
18.7	1085.590958	-0.002650	LWWLPVEK
15.9	1085.596832	-0.008524	LGSEVLEQVL
10.2	1085.590302	-0.001994	VLSGLECIPR
9.7	1085.586929	0.001379	PAFGPLEALR
9.7	1085.582916	0.005392	PTSTVKNSPR
9.7	1085.596848	-0.008540	SSVLTLIPQP
9.6	1085.582916	0.005392	IVSPDAGGAKR
8.3	1085.586945	0.001363	WISVSPLPR

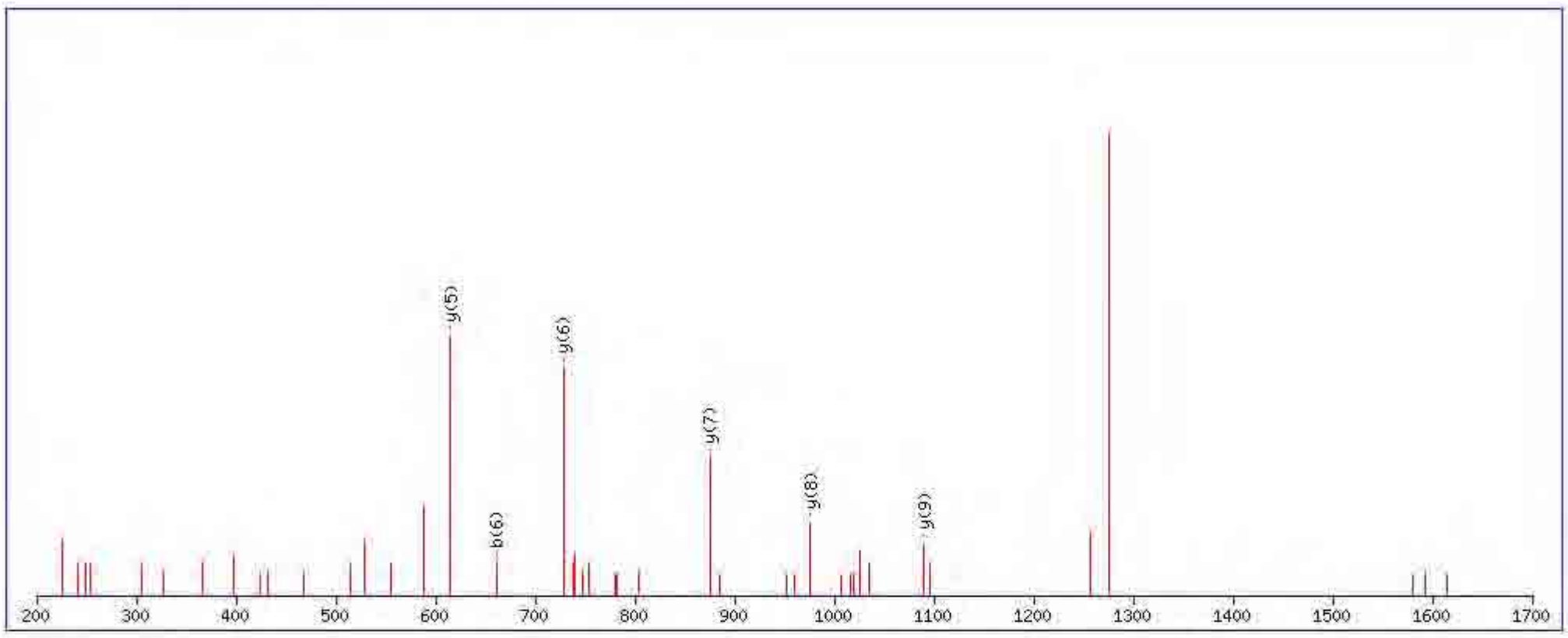
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NANTFISPQQR**
Found in **MGP_HUMAN**, Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2

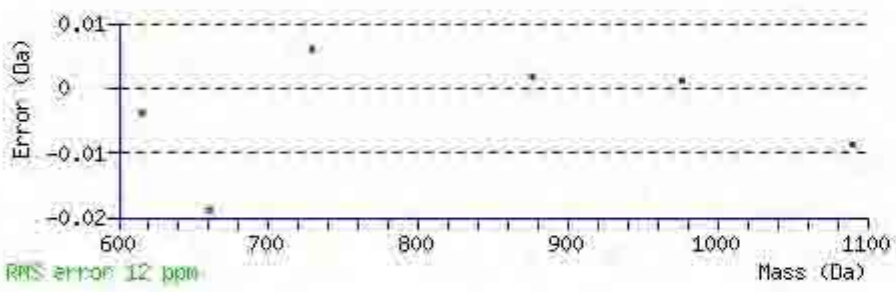
Match to Query 12275: 1274.648208 from(638.331380,2+) rtinseconds(937) index(4534)
Title: Locus:1.1.1.1294.21
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

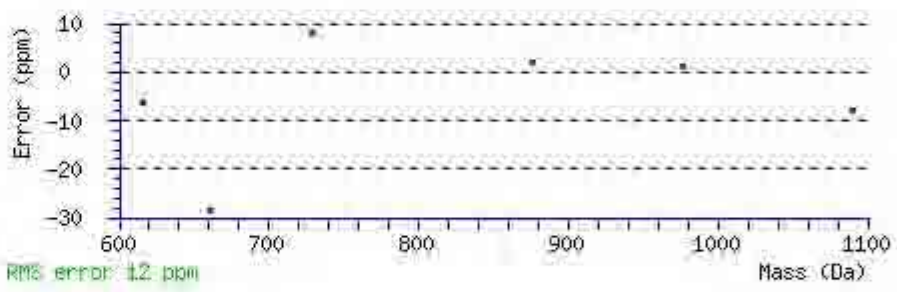
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1274.636734
Ions Score: 32 **Expect:** 0.01
Matches : 6/106 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	186.087317	93.547296	169.060768	85.034022			A	1161.601098	581.304187	1144.574549	572.790913	1143.590533	572.298905	10
3	300.130244	150.568760	283.103695	142.055486			N	*1090.563984*	545.785630	1073.537435	537.272356	1072.553419	536.780348	9
4	401.177923	201.092600	384.151374	192.579325	383.167358	192.087317	T	*976.521057*	488.764167	959.494508	480.250892	958.510492	479.758884	8
5	548.246337	274.626807	531.219788	266.113532	530.235772	265.621524	F	*875.473378*	438.240327	858.446829	429.727053	857.462813	429.235045	7
6	661.330401	331.168839	644.303852	322.655564	643.319836	322.163556	I	*728.404964*	364.706120	711.378415	356.192846	710.394399	355.700838	6
7	748.362429	374.684853	731.335880	366.171578	730.351864	365.679570	S	*615.320900*	308.164088	598.294351	299.650814	597.310335	299.158806	5
8	845.415193	423.211235	828.388644	414.697960	827.404628	414.205952	P	528.288872	264.648074	511.262323	256.134800			4
9	973.473771	487.240524	956.447222	478.727249	955.463206	478.235241	Q	431.236108	216.121692	414.209559	207.608417			3
10	1101.532349	551.269813	1084.505800	542.756538	1083.521784	542.264530	Q	303.177530	152.092403	286.150981	143.579128			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NANTFISPQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1274.636734	0.011474	NANTFISPQQR
10.6	1274.650665	-0.002457	EGTLFPERTLP
10.6	1274.642792	0.005416	TPSDMPLLELK
9.1	1274.639465	0.008743	SVPTFTVIPEGP
9.1	1274.639465	0.008743	SVPTFTVIPEGP
8.1	1274.657852	-0.009644	GNRSLSLTENGK
7.1	1274.650650	-0.002442	DLEGEAFLPLR
7.1	1274.636261	0.011947	ITGEIMHALKM
6.8	1274.650620	-0.002412	LAAAANEAYTAPL
6.5	1274.636749	0.011459	WLVDTQDSRR

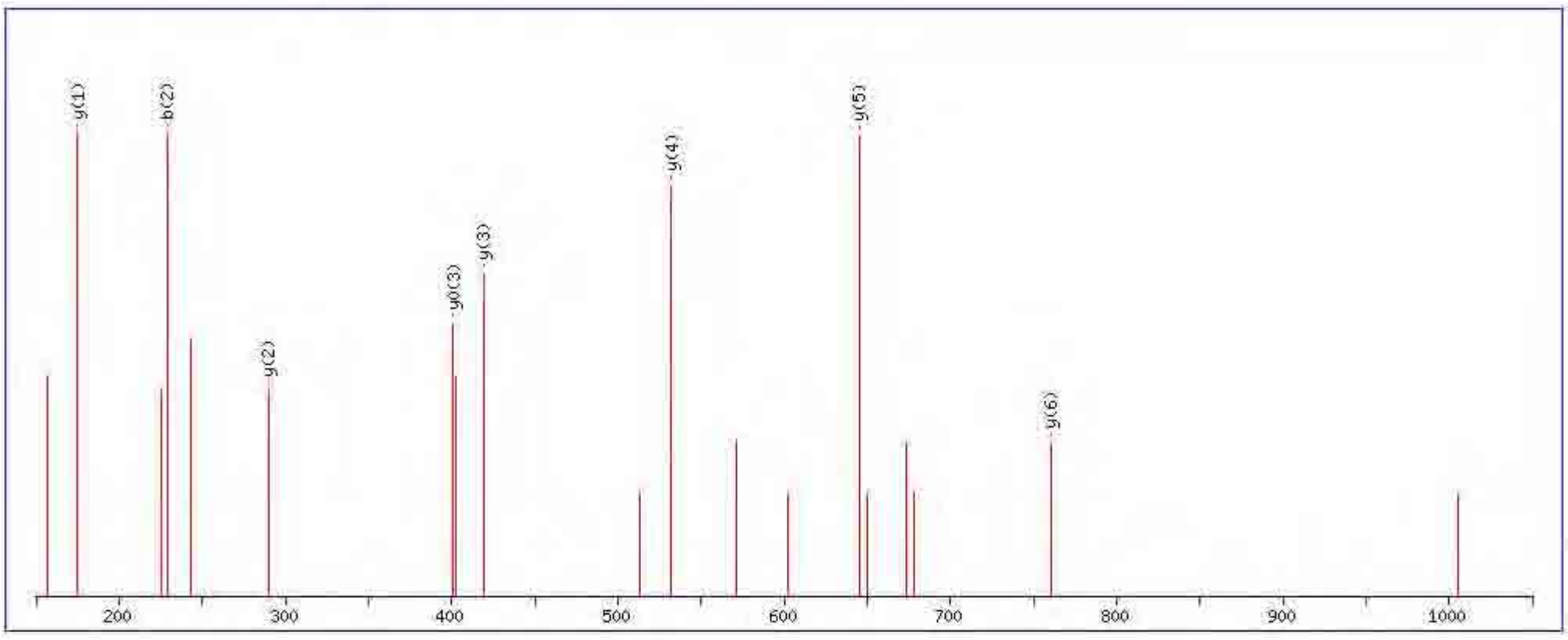
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDLLEDR**
Found in **GANAB_HUMAN**, Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3

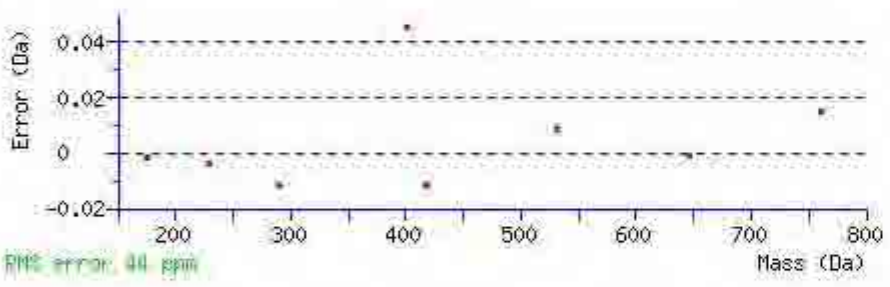
Match to Query 2569: 872.456428 from(437.235490,2+) rtinseconds(1364) index(8718)
Title: Locus:1.1.1.1538.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

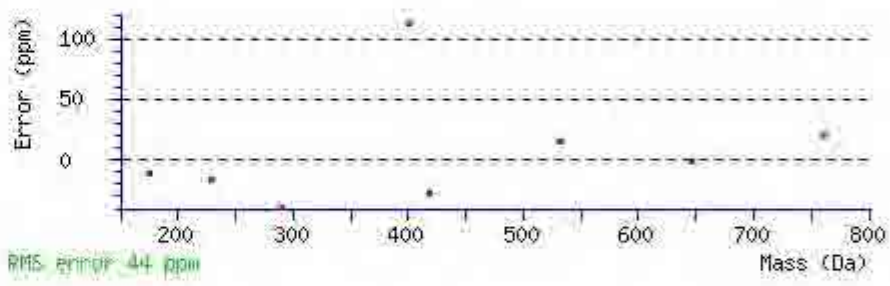
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 872.460327
Ions Score: 49 **Expect:** 0.0071
Matches : 8/56 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	229.118283	115.062779	211.107718	106.057497	D	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
3	342.202347	171.604811	324.191782	162.599529	L	*645.356616*	323.181946	628.330067	314.668672	627.346051	314.176664	5
4	455.286411	228.146843	437.275846	219.141561	L	*532.272552*	266.639914	515.246003	258.126640	514.261987	257.634632	4
5	584.329004	292.668140	566.318439	283.662858	E	*419.188488*	210.097882	402.161939	201.584607	401.177923	201.092599	3
6	699.355947	350.181612	681.345382	341.176329	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LDLLEDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	872.460327	-0.003899	LDLLEDR
32.8	872.460327	-0.003899	LLDIEDR
32.8	872.460327	-0.003899	LVELEDR
30.9	872.460342	-0.003914	LDPPGKSK
30.9	872.460342	-0.003914	LDPPGSKK
25.2	872.460327	-0.003899	LEVIERD
25.2	872.460327	-0.003899	LIDIERD
21.7	872.460327	-0.003899	DLLLDER
20.3	872.460327	-0.003899	DLLEIDR
20.2	872.460342	-0.003914	IDPKTGNI

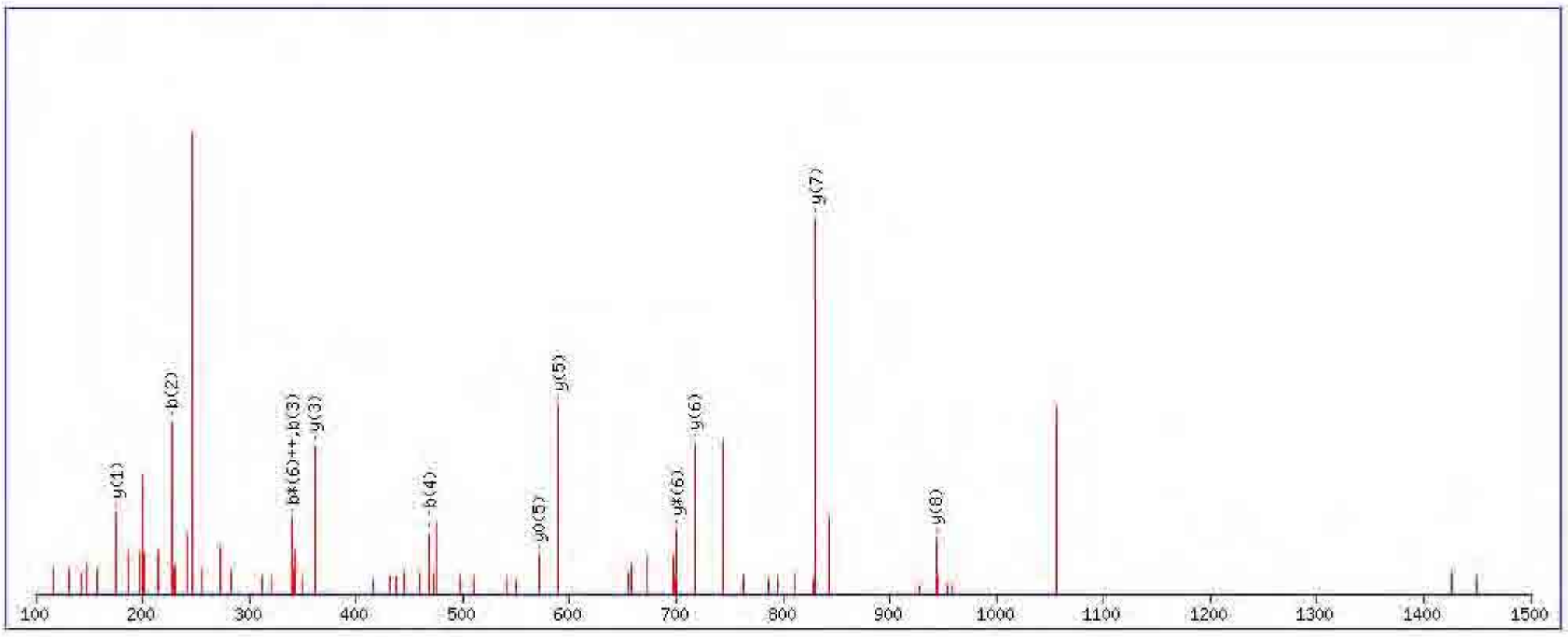
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLIKVEEGR**
Found in **NR4A3_HUMAN**, Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=2 SV=3

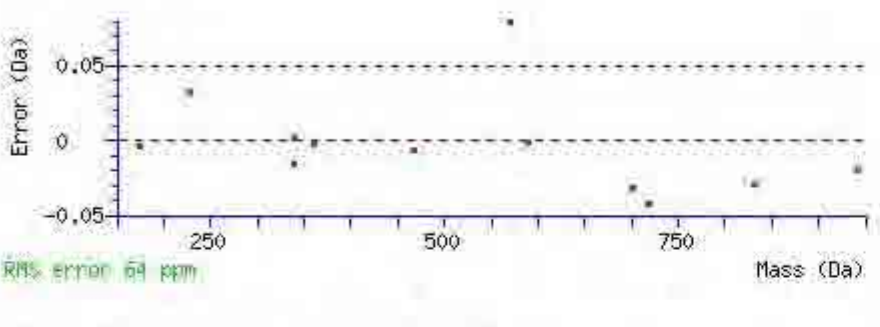
Match to Query 6637: 1055.600468 from(528.807510,2+) rtinseconds(1543) index(10950)
Title: Locus:1.1.1.1636.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

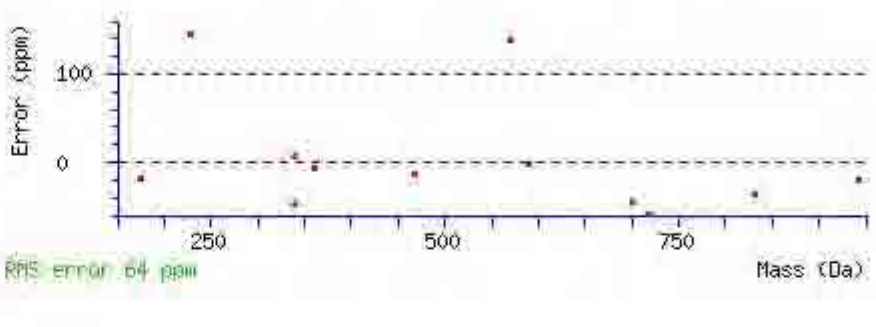
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597488
Variable modifications:
P1 : Oxidation (P)
Ions Score: 41 **Expect:** 0.0088
Matches : 12/76 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116					P							9
2	227.139019	114.073147					L	*943.557107*	472.282192	926.530558	463.768917	925.546542	463.276909	8
3	340.223083	170.615179					I	*830.473043*	415.740160	813.446494	407.226885	812.462478	406.734877	7
4	468.318046	234.662661	451.291497	226.149386			K	*717.388979*	359.198128	700.362430	350.684853	699.378414	350.192845	6
5	567.386460	284.196868	550.359911	275.683594			V	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	E	490.225602	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	825.471646	413.239461	808.445097	404.726187	807.461081	404.234179	E	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	882.493110	441.750193	865.466561	433.236919	864.482545	432.744911	G	232.140416	116.573846	215.113867	108.060571			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PLIKVEEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1055.597488	0.002980	PLIKVEEGR
41.1	1055.597504	0.002964	LLPQLTSPR
26.5	1055.597488	0.002980	LLKLDPADR
24.3	1055.608704	-0.008236	ILLREAEGR
24.3	1055.608704	-0.008236	LLLRAEGER
20.1	1055.597488	0.002980	LGPLALETAR
19.8	1055.597488	0.002980	ILSLPEGTAR
18.4	1055.597488	0.002980	LPASLSLPAR
17.9	1055.597504	0.002964	LSIPGPLTSR
16.8	1055.608734	-0.008266	ITVLRDPAR

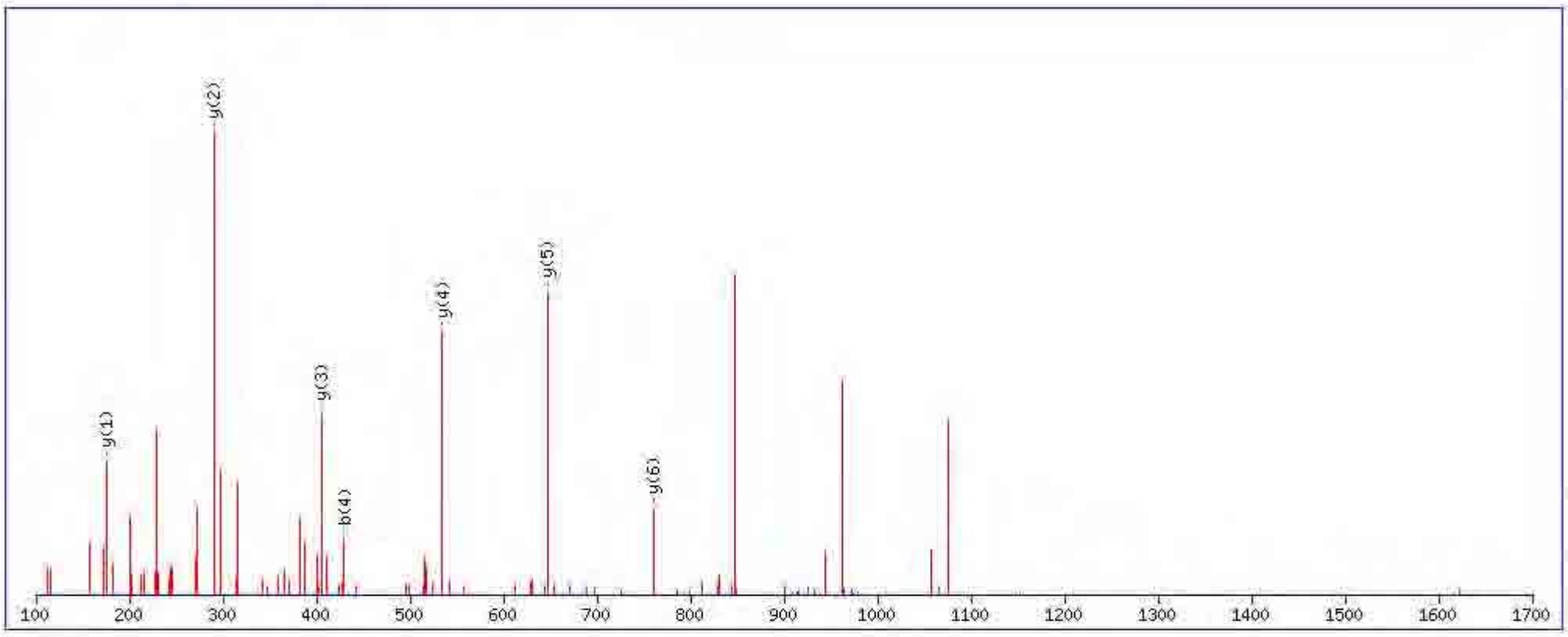
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTVIIEDDR**
Found in **PARD3_HUMAN**, Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2

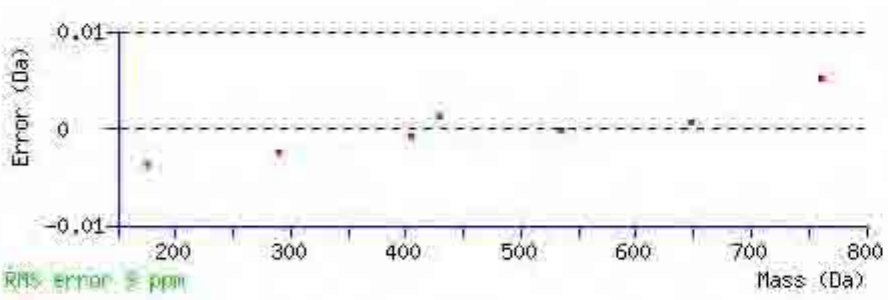
Match to Query 7105: 1074.519568 from(538.267060,2+) rtinseconds(1225) index(7154)
Title: Locus:1.1.1.1460.13
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

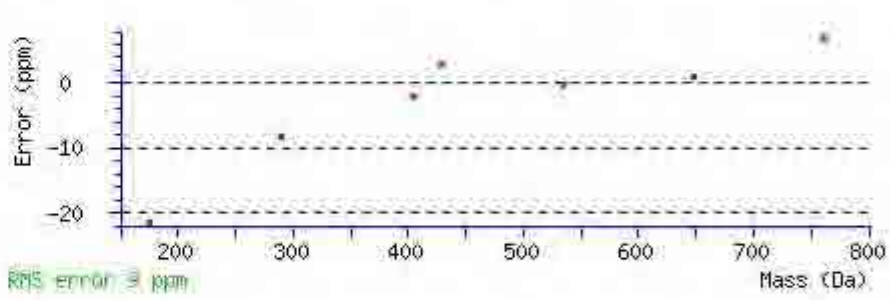
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.519318
Ions Score: 49 **Expect:** 0.0026
Matches : 7/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	217.081898	109.044587	199.071333	100.039304	T	960.499652	480.753464	943.473103	472.240190	942.489087	471.748182	8
3	316.150312	158.578794	298.139747	149.573512	V	859.451973	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	429.234376	215.120826	411.223811	206.115544	I	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
5	542.318440	271.662858	524.307875	262.657576	I	*647.299495*	324.153386	630.272946	315.640111	629.288930	315.148103	5
6	671.361033	336.184155	653.350468	327.178872	E	*534.215431*	267.611354	517.188882	259.098079	516.204866	258.606071	4
7	786.387976	393.697626	768.377411	384.692343	D	*405.172838*	203.090057	388.146289	194.576782	387.162273	194.084774	3
8	901.414919	451.211097	883.404354	442.205815	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DTVIIEDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.0	1074.519318	0.000250	DTVIIEDDR
33.2	1074.519287	0.000281	LEEGLEETR
32.6	1074.526688	-0.007120	LDSMAIEALP
29.5	1074.523331	-0.003763	EKLYPPSPP
24.3	1074.526703	-0.007135	GSPMEISLPI
22.4	1074.512772	0.006796	NSLNPEVMR
20.5	1074.524017	-0.004449	MGGSPRALDR
20.5	1074.526688	-0.007120	LDSMAIEALP
20.3	1074.523331	-0.003763	EKLYPPSPP
20.1	1074.520645	-0.001077	LWTRNDDR

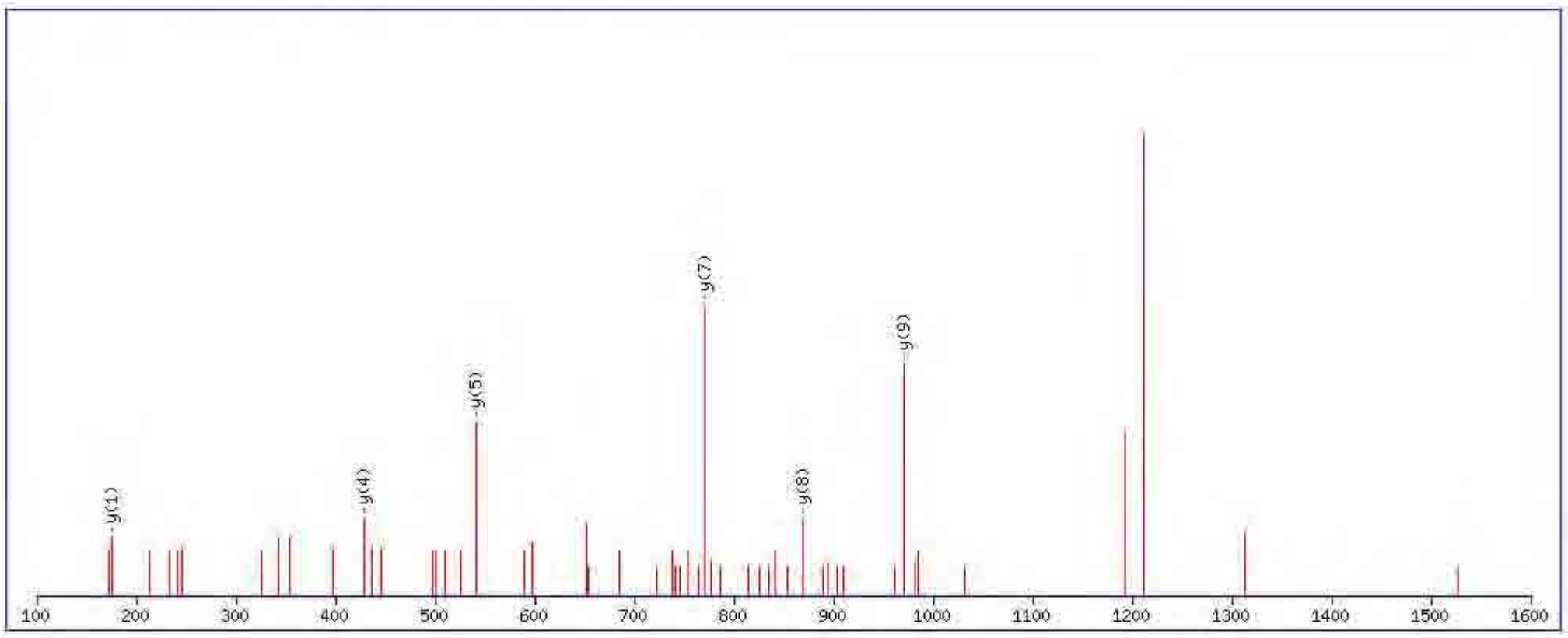
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QITVNDLPVGR**
Found in **PRDX1_HUMAN**, Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

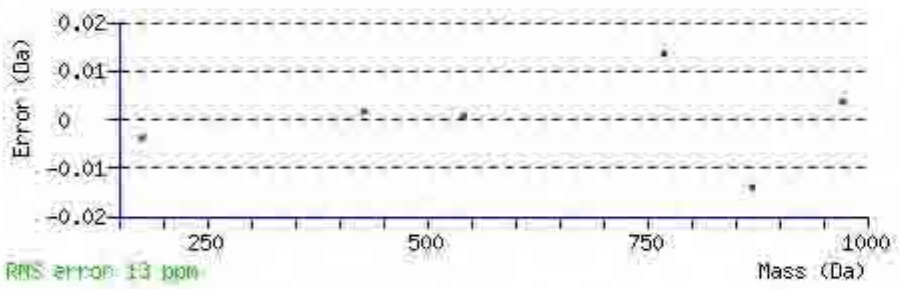
Match to Query 10837: 1210.670568 from(606.342560,2+) rtinseconds(1498) index(10460)
Title: Locus:1.1.1.1611.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

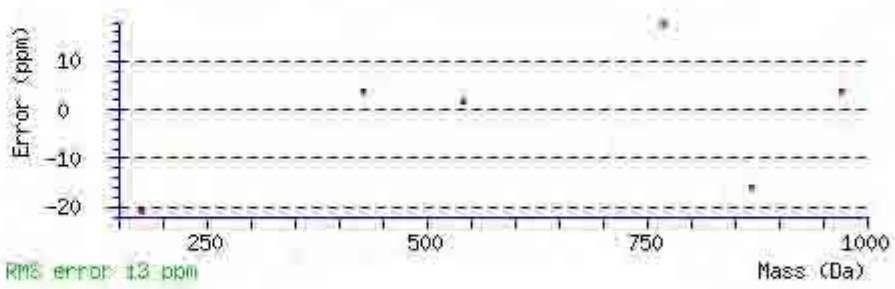
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1210.666992
Ions Score: 47 **Expect:** 0.0021
Matches : 6/106 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	242.149918	121.578597	225.123369	113.065323			I	1083.615685	542.311481	1066.589136	533.798206	1065.605120	533.306198	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	*970.531621*	485.769449	953.505072	477.256174	952.521056	476.764166	9
4	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	V	*869.483942*	435.245609	852.457393	426.732335	851.473377	426.240327	8
5	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	N	*770.415528*	385.711402	753.388979	377.198128	752.404963	376.706120	7
6	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	D	656.372601	328.689939	639.346052	320.176664	638.362036	319.684656	6
7	784.419945	392.713611	767.393396	384.200336	766.409380	383.708328	L	*541.345658*	271.176467	524.319109	262.663193			5
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	P	*428.261594*	214.634435	411.235045	206.121160			4
9	980.541123	490.774200	963.514574	482.260925	962.530558	481.768917	V	331.208830	166.108053	314.182281	157.594778			3
10	1037.562587	519.284932	1020.536038	510.771657	1019.552022	510.279649	G	232.140416	116.573846	215.113867	108.060571			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QITVNDLPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.3	1210.666992	0.003576	QITVNDLPVGR
22.2	1210.678192	-0.007624	RGEVVEAKPAR
21.7	1210.666962	0.003606	LQPTSAAPISAR
21.4	1210.666992	0.003576	PIQSTAGAVPVR
19.1	1210.678207	-0.007639	PKPKTSPRPR
12.3	1210.666977	0.003591	PKISPQKPPR
12.3	1210.682236	-0.011668	PKSLPTHLFR
11.6	1210.666977	0.003591	LGKELQTGTHK
11.5	1210.678223	-0.007655	TVIQTAGRPPR
11.5	1210.678223	-0.007655	TVIQTAGRPPR

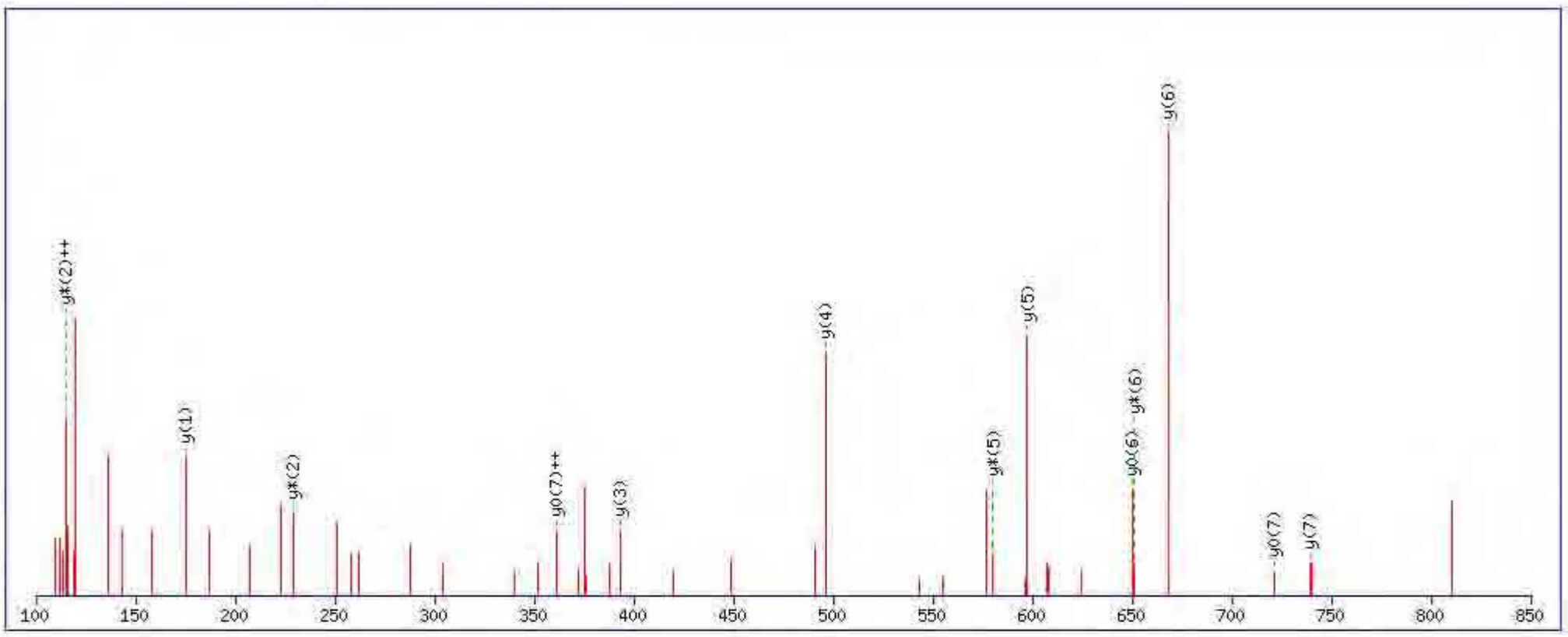
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAATCFAR**
Found in **PA2GA_HUMAN**, Phospholipase A2, membrane associated OS=Homo sapiens GN=PLA2G2A PE=1 SV=2

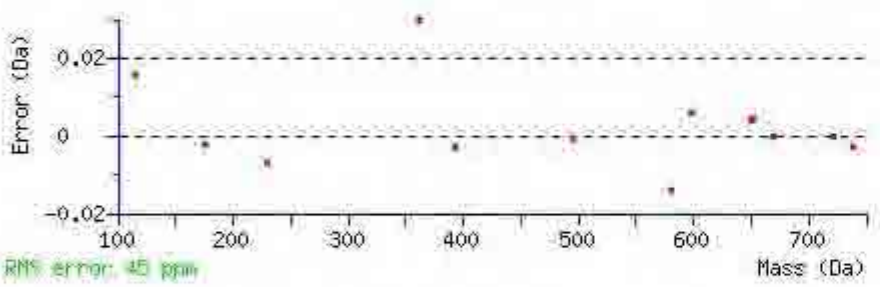
Match to Query 1203: 809.386468 from(405.700510,2+) rtinseconds(695) index(2288)
Title: Locus:1.1.1.1158.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

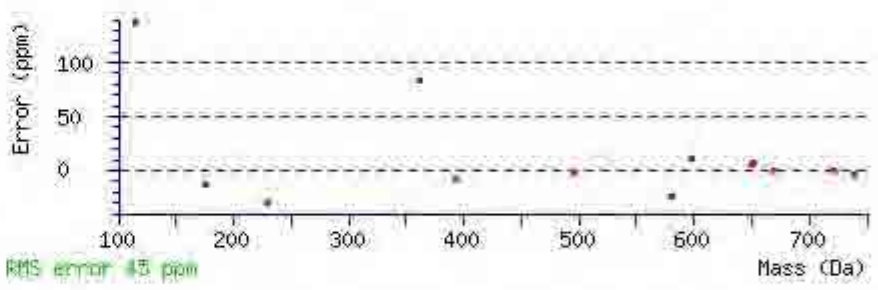
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 809.385391
Ions Score: 37 **Expect:** 0.0052
Matches : 13/56 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							8
2	143.081504	72.044390			A	*739.355572*	370.181424	722.329023	361.668150	721.345007	361.176142	7
3	214.118618	107.562947			A	*668.318458*	334.662867	651.291909	326.149593	650.307893	325.657585	6
4	315.166297	158.086786	297.155732	149.081504	T	*597.281344*	299.144310	580.254795	290.631036	579.270779	290.139028	5
5	418.175482	209.591379	400.164917	200.586097	C	*496.233665*	248.620471	479.207116	240.107196			4
6	565.243896	283.125586	547.233331	274.120304	F	*393.224480*	197.115878	376.197931	188.602604			3
7	636.281010	318.644143	618.270445	309.638861	A	246.156066	123.581671	229.129517	115.068397			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AAATCFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	809.385391	0.001077	AAATCFAR
7.7	809.391937	-0.005469	AAPPPPTQ
7.4	809.391922	-0.005454	DPPGEKPA
6.2	809.391937	-0.005469	AAPPPPTQ
5.8	809.391937	-0.005469	AAPPPPTQ
5.2	809.388779	-0.002311	GRTCMVK
4.8	809.391937	-0.005469	DLPGPQAP
4.8	809.391937	-0.005469	DLPGPQAP
3.9	809.391922	-0.005454	AAPAAPPPA
3.9	809.393265	-0.006797	AWGHPSR

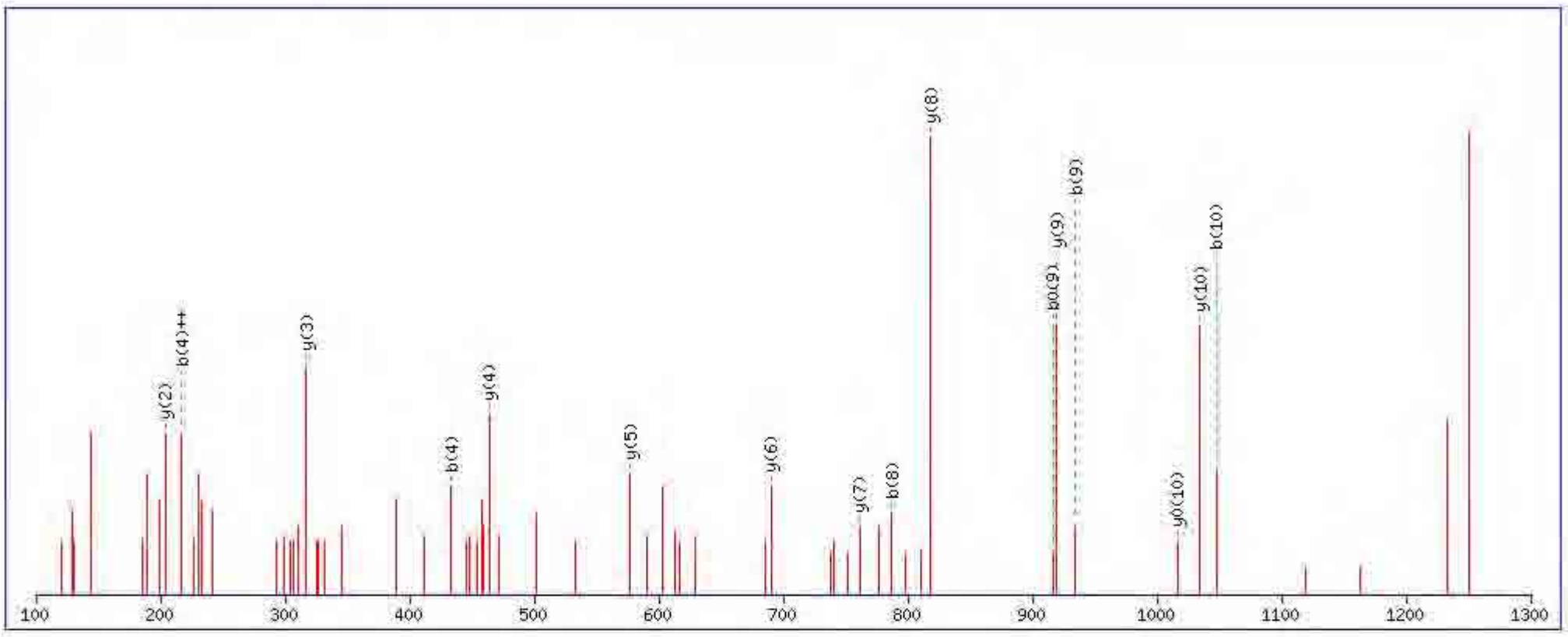
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTDTGALLFIGK**
Found in **PEDF_HUMAN**, Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4

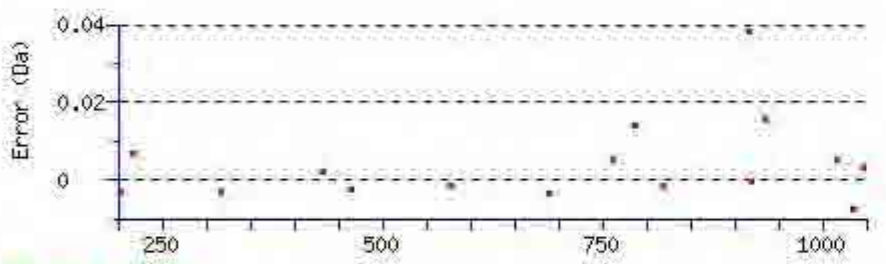
Match to Query 11764: 1249.656368 from(625.835460,2+) rtinseconds(2006) index(16618)
Title: Locus:1.1.1.1889.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

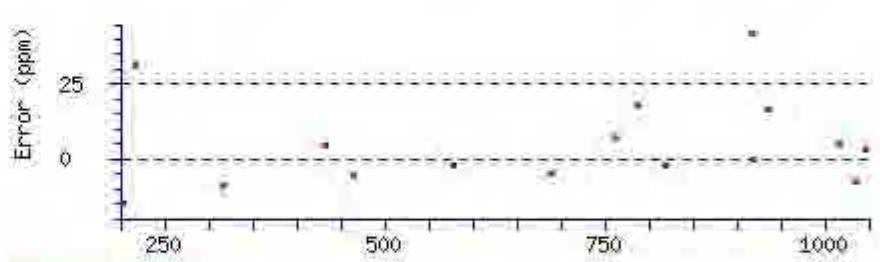
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1249.655426
Ions Score: 64 Expect: 2.5e-005
Matches : 17/94 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							12
2	217.081898	109.044587	199.071333	100.039304	T	1135.635753	568.321514	1118.609204	559.808240	1117.625188	559.316232	11
3	332.108841	166.558058	314.098276	157.552776	D	1034.588074	517.797675	1017.561525	509.284401	1016.577509	508.792393	10
4	433.156520	217.081898	415.145955	208.076616	T	919.561131	460.284203	902.534582	451.770929	901.550566	451.278921	9
5	490.177984	245.592630	472.167419	236.587347	G	818.513452	409.760364	801.486903	401.247089			8
6	561.215098	281.111187	543.204533	272.105905	A	761.491988	381.249632	744.465439	372.736357			7
7	674.299162	337.653219	656.288597	328.647937	L	690.454874	345.731075	673.428325	337.217800			6
8	787.383226	394.195251	769.372661	385.189969	L	577.370810	289.189043	560.344261	280.675768			5
9	934.451640	467.729458	916.441075	458.724176	F	464.286746	232.647011	447.260197	224.133736			4
10	1047.535704	524.271490	1029.525139	515.266207	I	317.218332	159.112804	300.191783	150.599529			3
11	1104.557168	552.782222	1086.546603	543.776939	G	204.134268	102.570772	187.107719	94.057497			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DTDTGALLFIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.3	1249.655426	0.000942	DTDTGALLFIGK
14.2	1249.666656	-0.010288	ATFLQISTVDR
10.4	1249.658798	-0.002430	SGGMIVITSILGS
9.7	1249.656281	0.000087	LCCIFLLQQIG
8.4	1249.666611	-0.010243	SFAASLRELEK
7.3	1249.655426	0.000942	KGLSDFLGVISD
7.0	1249.648895	0.007473	MALTQGPLTFR
7.0	1249.656281	0.000087	KLNCFPVLMGI
5.7	1249.666626	-0.010258	RYLQLTQSEL
5.7	1249.655411	0.000957	VKGYLLPDDSK

Mascot: http://www.matrixscience.com

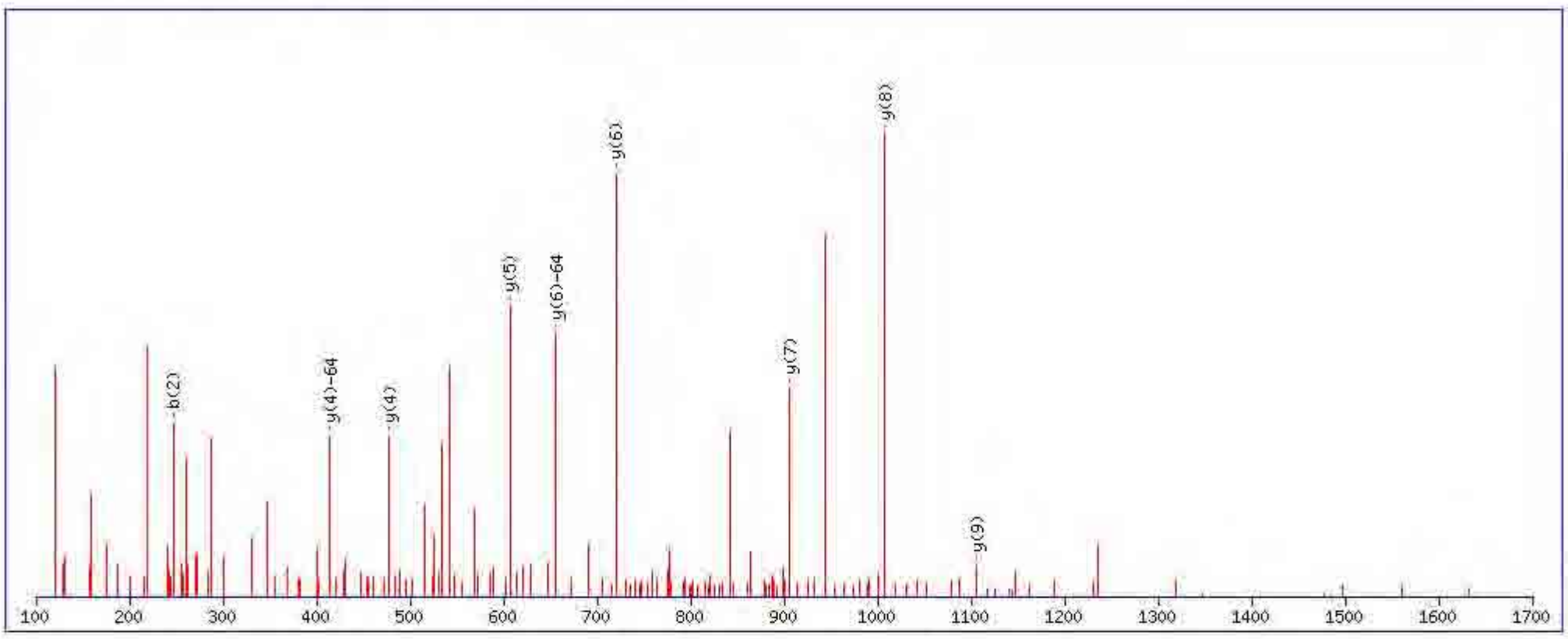
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVTWIEGVMR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

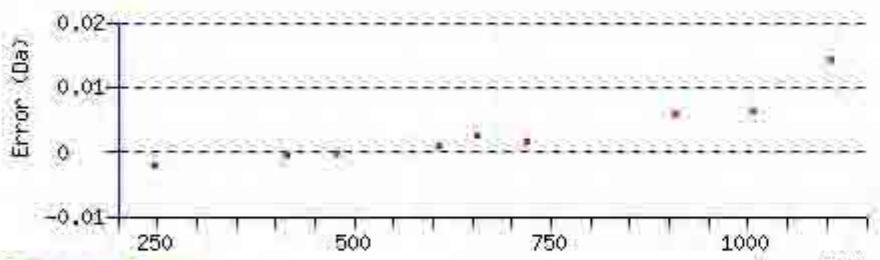
Match to Query 11824: 1252.628148 from(627.321350,2+) rtinseconds(1815) index(14279)
Title: Locus:1.1.1.1783.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

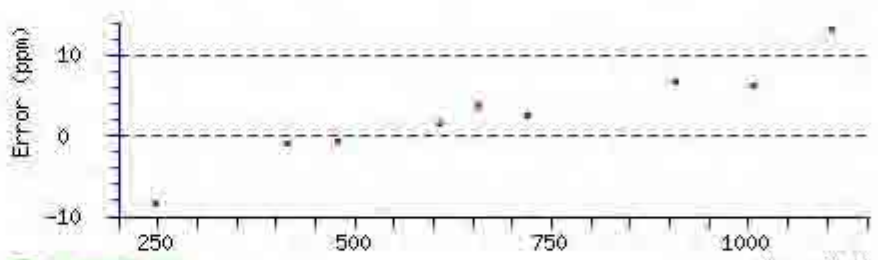
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1252.627441
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 46 **Expect:** 0.0012
Matches : 9/124 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							10
2	247.144104	124.075690			V	*1106.566293*	553.786785	1089.539744	545.273510	1088.555728	544.781502	9
3	348.191783	174.599529	330.181218	165.594247	T	*1007.497879*	504.252578	990.471330	495.739303	989.487314	495.247295	8
4	534.271096	267.639186	516.260531	258.633904	W	*906.450200*	453.728738	889.423651	445.215464	888.439635	444.723456	7
5	647.355160	324.181218	629.344595	315.175936	I	*720.370887*	360.689082	703.344338	352.175807	702.360322	351.683799	6
6	776.397753	388.702515	758.387188	379.697232	E	*607.286823*	304.147050	590.260274	295.633775	589.276258	295.141767	5
7	833.419217	417.213247	815.408652	408.207964	G	*478.244230*	239.625753	461.217681	231.112479			4
8	932.487631	466.747454	914.477066	457.742171	V	421.222766	211.115021	404.196217	202.601746			3
9	1079.523031	540.265154	1061.512466	531.259871	M	322.154352	161.580814	305.127803	153.067540			2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FVTWIEGVMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1252.627441	0.000707	FVTWIEGVMR
14.2	1252.616180	0.011968	MAAFPLEPKFA
12.3	1252.616211	0.011937	FQALFPMGPLT
7.9	1252.637344	-0.009196	MVTSSFPISVAV
6.6	1252.616028	0.012120	RTPGDAPGTPPR
6.1	1252.616028	0.012120	RTPGDAPGTPPR
5.3	1252.616211	0.011937	FQALFPMGPLT
5.2	1252.620026	0.008122	FSPYREGPIR
4.9	1252.616180	0.011968	MAAFPLEPKFA
4.4	1252.623383	0.004765	MEAFGNAKTLR

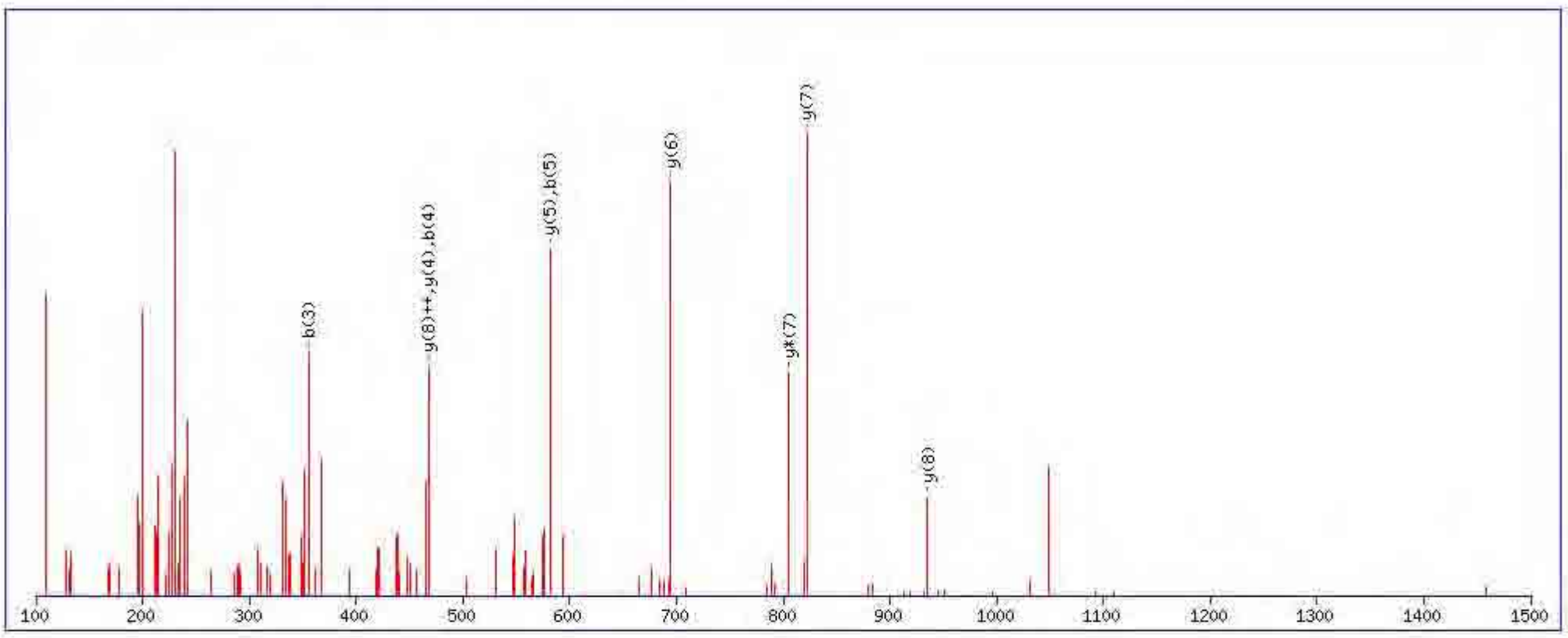
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPQLPPRVP**
Found in **F205A_HUMAN**, Protein FAM205A OS=Homo sapiens GN=FAM205A PE=2 SV=4

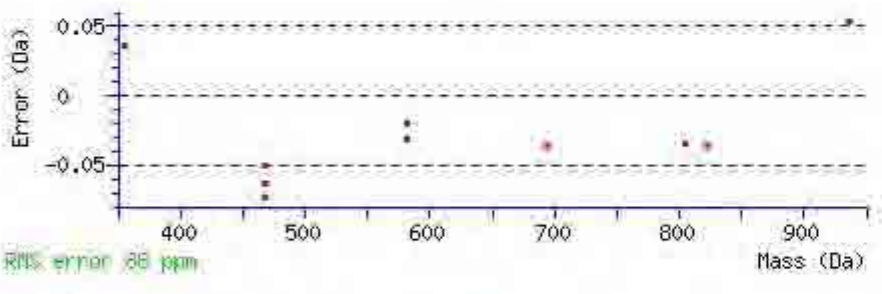
Match to Query 6477: 1047.605268 from(524.809910,2+) rtinseconds(1449) index(9825)
Title: Locus:1.1.1.1584.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

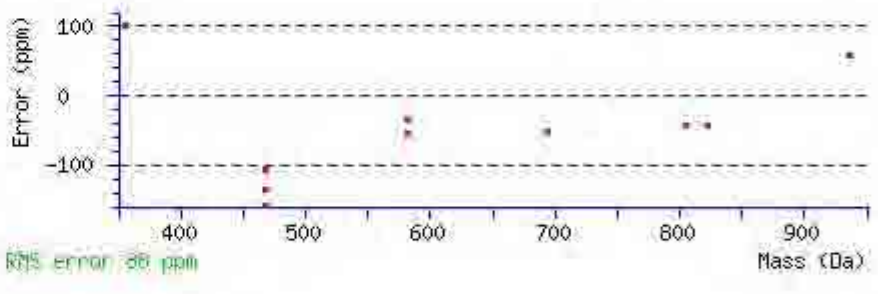
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1047.607681
Variable modifications:
P2 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 40 **Expect:** 0.0078
Matches : 10/56 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308			L					9
2	227.139019	114.073147			P	*935.530894*	468.269085	918.504345	459.755810	8
3	**355.197597**	178.102436	338.171048	169.589162	Q	*822.483215*	411.745246	805.456666	403.231971	7
4	**468.281661**	234.644468	451.255112	226.131194	L	*694.424637*	347.715956	677.398088	339.202682	6
5	**581.329340**	291.168308	564.302791	282.655034	P	*581.340573*	291.173925	564.314024	282.660650	5
6	678.382104	339.694690	661.355555	331.181416	P	*468.292894*	234.650085	451.266345	226.136810	4
7	834.483215	417.745246	817.456666	409.231971	R	371.240130	186.123703	354.213581	177.610428	3
8	933.551629	467.279452	916.525080	458.766178	V	215.139019	108.073147			2
9					P	116.070605	58.538940			1





NCBI **BLAST** search of LPQLPPRVP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.8	1047.607681	-0.002413	LPQLPPRVP
28.6	1047.607666	-0.002398	LLQIAGISPH
28.6	1047.607666	-0.002398	LLQLNHPTL
28.6	1047.607681	-0.002413	LPQLPPRVP
28.6	1047.607681	-0.002413	LPQLPPRVP
16.9	1047.596420	0.008848	PPLYSALKK
16.6	1047.596436	0.008832	LILQEGTFK
16.6	1047.596436	0.008832	PLPKAYTVK
14.7	1047.607666	-0.002398	PPQPPKKPK
14.5	1047.599792	0.005476	IIKEGMLTK

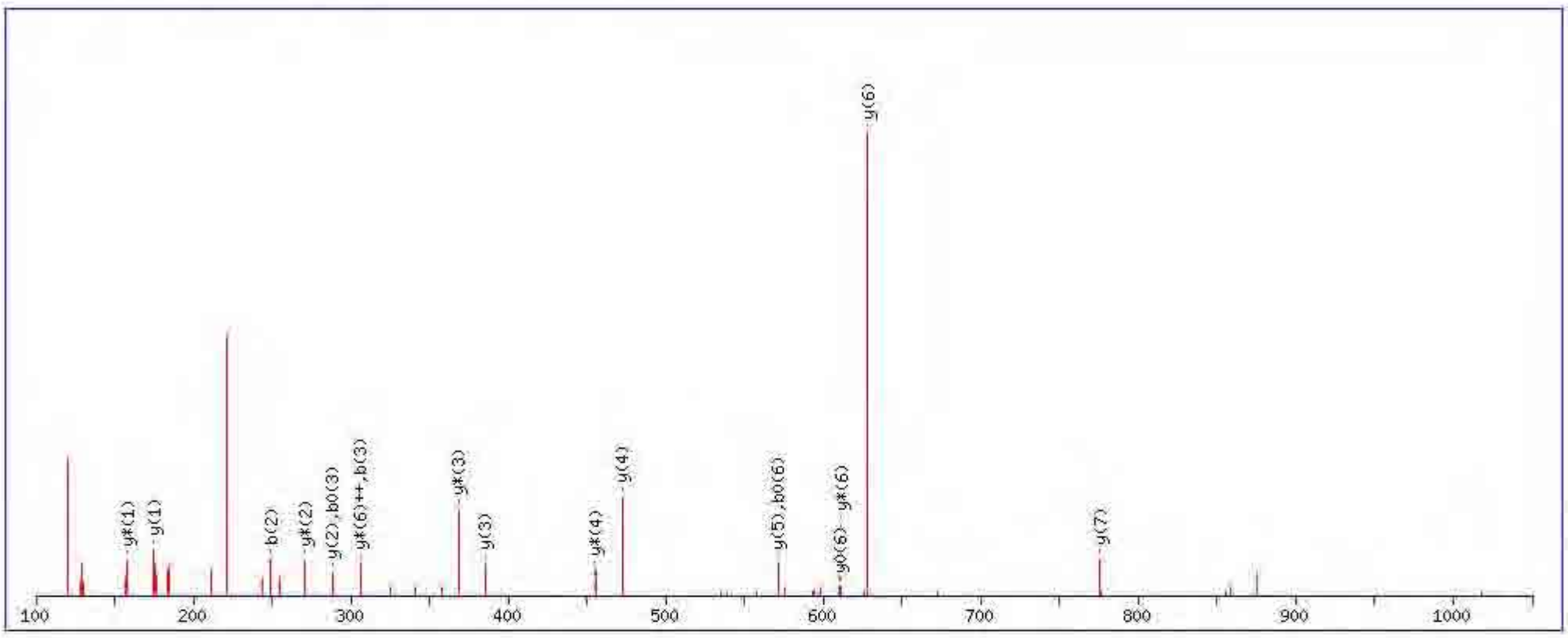
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFGVSPLR**
Found in **XP32_HUMAN**, Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1

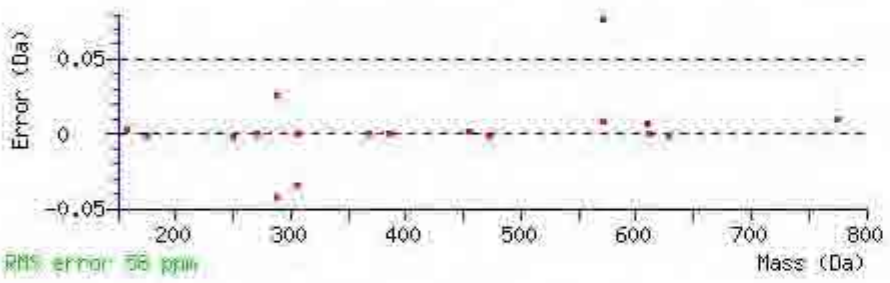
Match to Query 2644: 875.482268 from(438.748410,2+) rtinseconds(1291) index(7883)
Title: Locus:1.1.1.1497.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

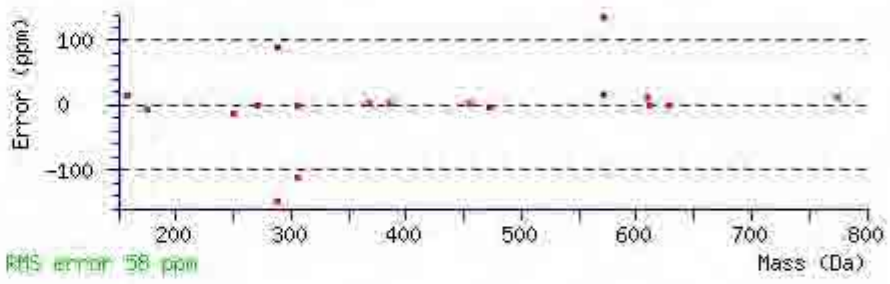
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 875.486511
Ions Score: 51 **Expect:** 0.00018
Matches : 18/64 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	249.123369	125.065322	231.112804	116.060040	F	775.446100	388.226688	758.419551	379.713414	757.435535	379.221406	7
3	306.144833	153.576054	288.134268	144.570772	G	628.377686	314.692481	611.351137	306.179207	610.367121	305.687199	6
4	405.213247	203.110261	387.202682	194.104979	V	571.356222	286.181749	554.329673	277.668475	553.345657	277.176467	5
5	492.245275	246.626275	474.234710	237.620993	S	472.287808	236.647542	455.261259	228.134268	454.277243	227.642260	4
6	589.298039	295.152658	571.287474	286.147375	P	385.255780	193.131528	368.229231	184.618254			3
7	702.382103	351.694690	684.371538	342.689407	L	288.203016	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TFGVSPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	875.486511	-0.004243	TFGVSPLR
10.3	875.486496	-0.004228	SGLFSPIR
10.2	875.486496	-0.004228	FTAPTAIR
9.5	875.486511	-0.004243	FGTVPISR
9.2	875.486481	-0.004213	FEKSPLR
9.2	875.486496	-0.004228	PPPLSPPR
9.1	875.478653	0.003615	KPVMVIGT
8.3	875.486496	-0.004228	TFIPDKR
7.0	875.475281	0.006987	TGFVDIPK
7.0	875.486511	-0.004243	TPPPVPPR

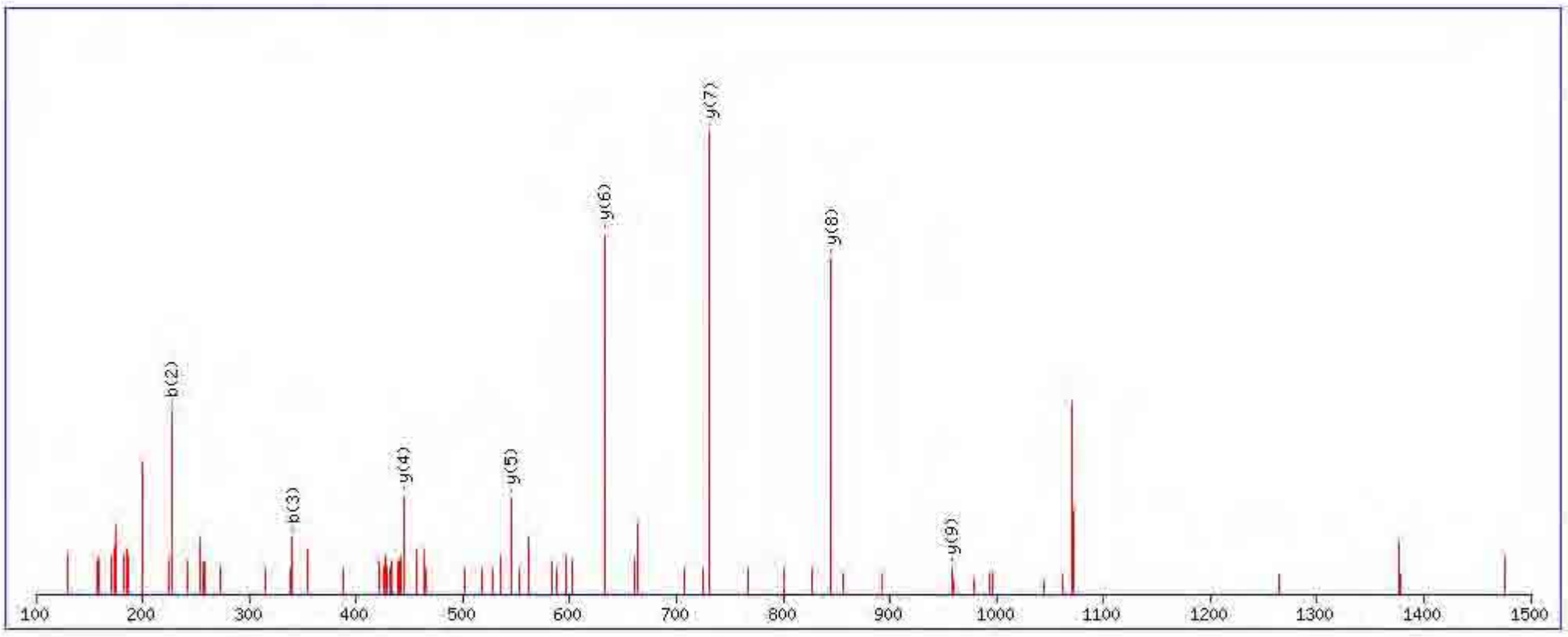
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

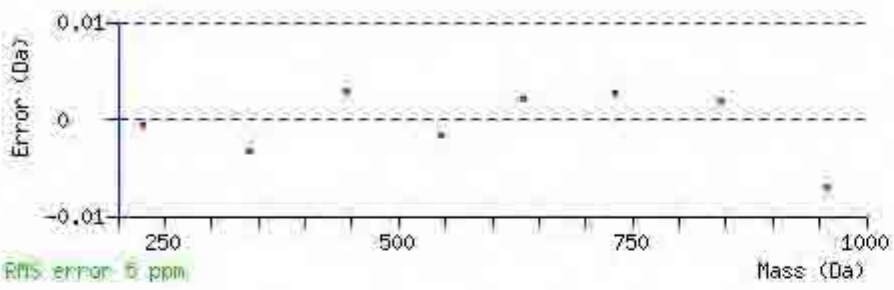
Match to Query 6980: 1069.645968 from(535.830260,2+) rtinseconds(1377) index(8898)
Title: Locus:1.1.1.1545.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_1.mgf

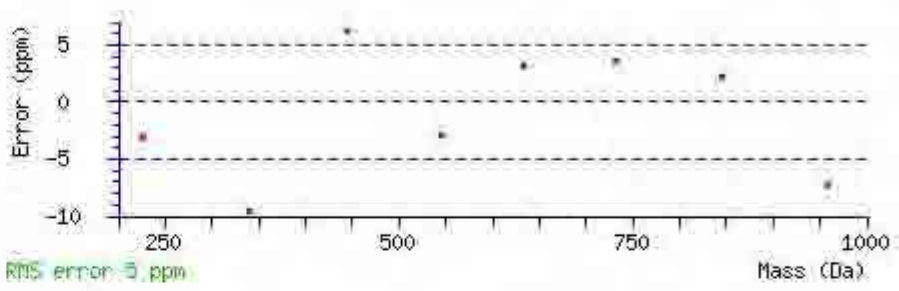
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 53 **Expect:** 0.00025
Matches : 8/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	844.488694	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	731.404630	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	632.336216	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	444.256509	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	1069.649536	-0.003568	LLIVSTPTAR
24.3	1069.638321	0.007647	IPLVPSKVSV
24.3	1069.638306	0.007662	LLPVLLSTAQ
23.4	1069.649506	-0.003538	LLLDALREK
23.4	1069.653564	-0.007596	LLLWVSVVAA
23.4	1069.649521	-0.003553	PLLSVKELR
16.3	1069.639633	0.006335	LLWPTRLR
14.4	1069.649521	-0.003553	LLIIRSAPAT
12.5	1069.638290	0.007678	LLLLLQDKD
12.5	1069.649521	-0.003553	LLPLLRSDK

Sibling 1 – technical replicate # 2

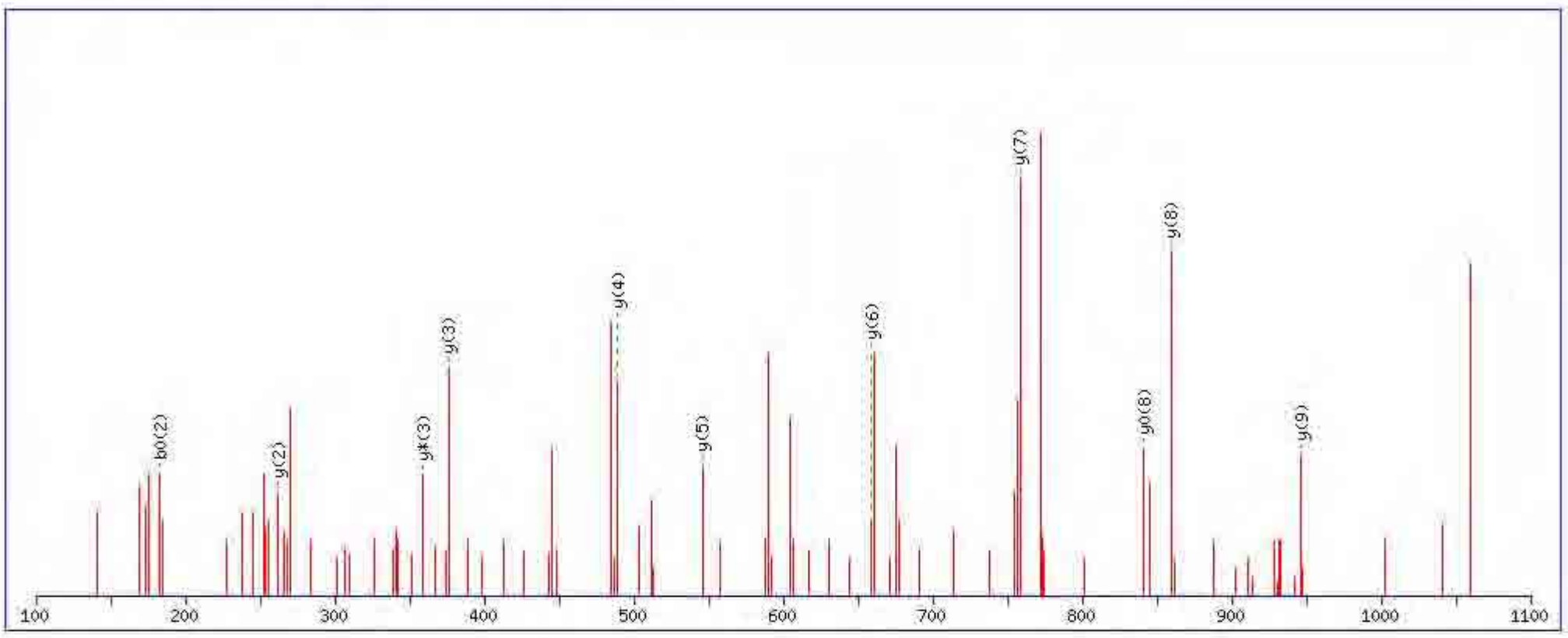
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISTVIGPNDQ**
Found in **ALMS1_HUMAN**, Alstrom syndrome protein 1 OS=Homo sapiens GN=ALMS1 PE=1 SV=3

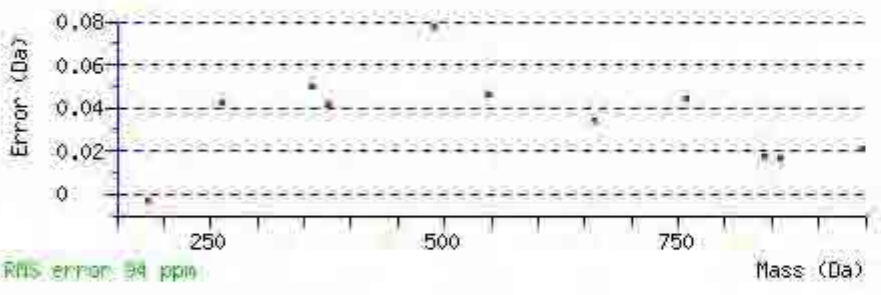
Match to Query 6518: 1058.527768 from(530.271160,2+) rtinseconds(858) index(3363)
Title: Locus:1.1.1.1295.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

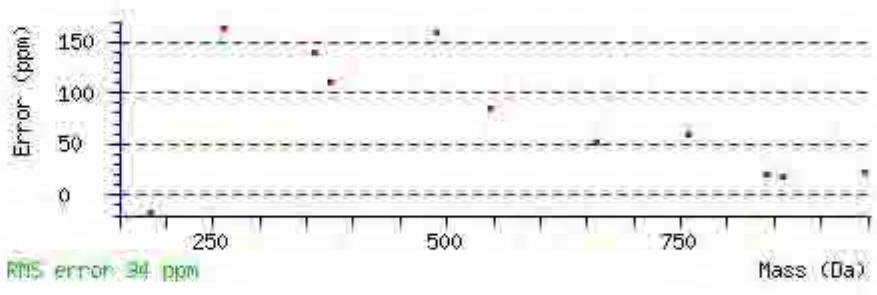
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1058.524414
Variable modifications:
P7 : Oxidation (P)
Ions Score: 46 **Expect:** 0.0031
Matches : 11/90 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							10
2	201.123368	101.065322			183.112803	92.060039	S	*946.447617*	473.727447	929.421068	465.214172	928.437052	464.722164	9
3	302.171047	151.589161			284.160482	142.583879	T	*859.415589*	430.211433	842.389040	421.698158	841.405024	421.206150	8
4	401.239461	201.123369			383.228896	192.118086	V	*758.367910*	379.687593	741.341361	371.174319	740.357345	370.682311	7
5	514.323525	257.665401			496.312960	248.660118	I	*659.299496*	330.153386	642.272947	321.640112	641.288931	321.148104	6
6	571.344989	286.176133			553.334424	277.170850	G	*546.215432*	273.611354	529.188883	265.098080	528.204867	264.606072	5
7	684.392668	342.699972			666.382103	333.694690	P	*489.193968*	245.100622	472.167419	236.587348	471.183403	236.095340	4
8	798.435595	399.721436	781.409046	391.208161	780.425030	390.716153	N	*376.146289*	188.576783	359.119740	180.063508	358.135724	179.571500	3
9	913.462538	457.234907	896.435989	448.721633	895.451973	448.229625	D	*262.103362*	131.555319	245.076813	123.042045	244.092797	122.550037	2
10							Q	147.076419	74.041848	130.049870	65.528573			1





NCBI **BLAST** search of ISTVIGPNDQ
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	1058.524414	0.003354	ISTVIGPNDQ
18.2	1058.517883	0.009885	PSPTGGLMQR
18.0	1058.535645	-0.007877	PSSGLLSPGGR
17.2	1058.535629	-0.007861	PTSAPPSKSR
17.1	1058.535629	-0.007861	PTAVNLADSR
12.3	1058.525742	0.002026	PSAFHKGGSR
11.7	1058.535614	-0.007846	LSSLNPQER
11.4	1058.535629	-0.007861	LTTPPSSNSR
11.1	1058.517868	0.009900	PSSLSIHMR
11.0	1058.535629	-0.007861	LSTQPAPASR

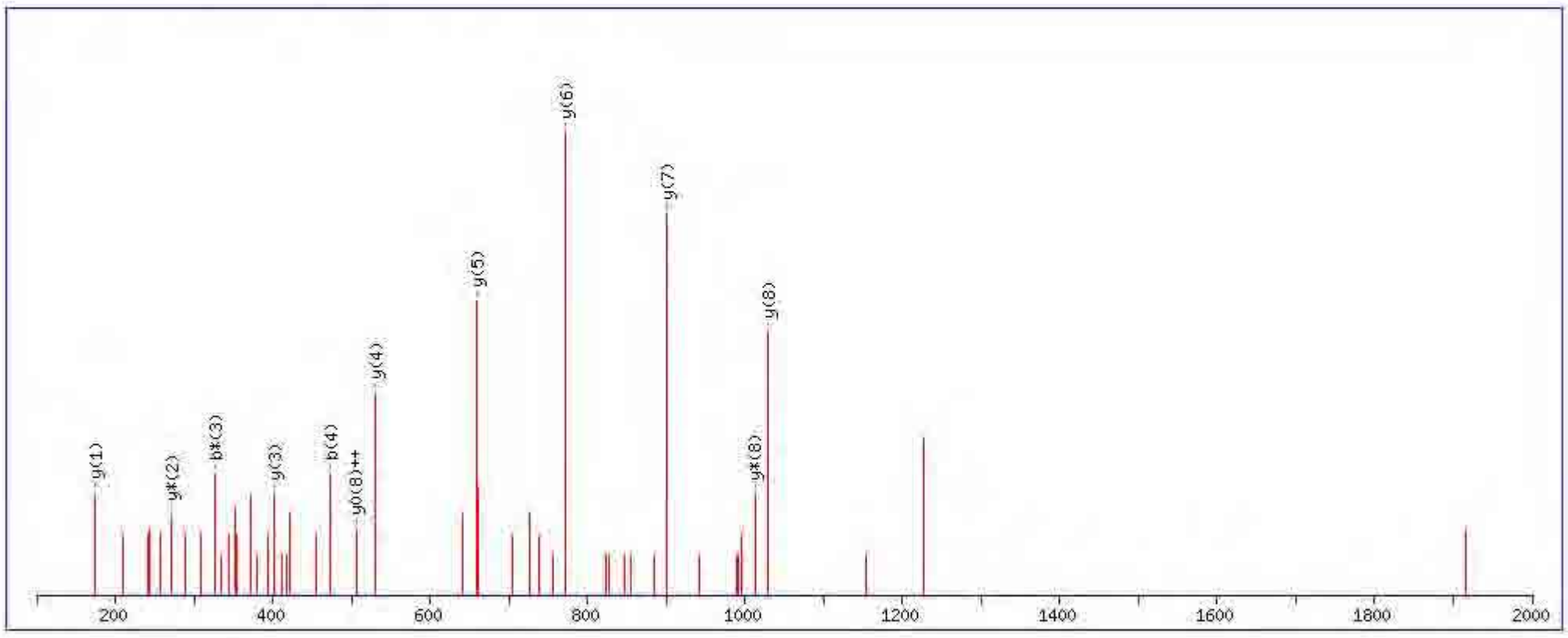
Mascot Search Results

Peptide View

MS/MS Fragmentation of TNQELQEINR
Found in ANXA2_HUMAN, Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

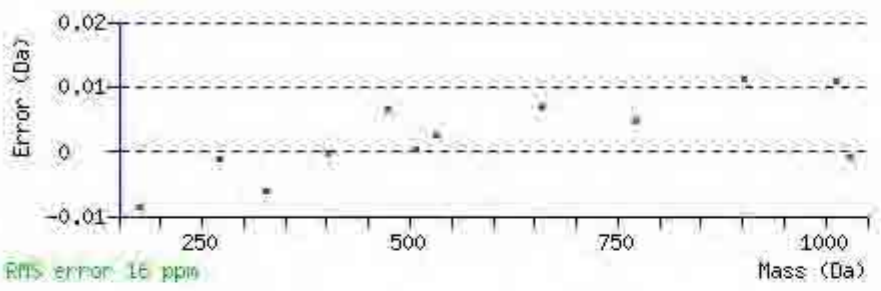
Match to Query 11352: 1243.620748 from(622.817650,2+) rtinseconds(897) index(3701)
Title: Locus:1.1.1.1317.26
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

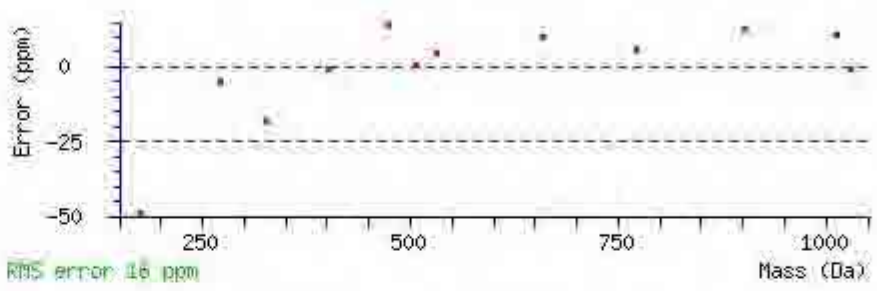
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1243.615646
Ions Score: 46 **Expect:** 0.0016
Matches : 12/100 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	N	1143.575276	572.291276	1126.548727	563.778002	1125.564711	563.285994	9
3	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	*1029.532349*	515.269813	1012.505800	506.756538	1011.521784	506.264530	8
4	473.199053	237.103164	456.172504	228.589890	455.188488	228.097882	E	*901.473771*	451.240524	884.447222	442.727249	883.463206	442.235241	7
5	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	L	*772.431178*	386.719227	755.404629	378.205953	754.420613	377.713945	6
6	714.341695	357.674486	697.315146	349.161211	696.331130	348.669203	Q	*659.347114*	330.177195	642.320565	321.663921	641.336549	321.171913	5
7	843.384288	422.195782	826.357739	413.682508	825.373723	413.190500	E	*531.288536*	266.147906	514.261987	257.634632	513.277971	257.142624	4
8	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	I	*402.245943*	201.626609	385.219394	193.113335			3
9	1070.511279	535.759278	1053.484730	527.246003	1052.500714	526.753995	N	289.161879	145.084577	272.135330	136.571303			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNQELQEINR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1243.615646	0.005102	TNQELQEINR
15.6	1243.615662	0.005086	AKGSEGEQGPLR
11.2	1243.615662	0.005086	SQQLQEKQQQ
10.0	1243.630920	-0.010172	YYTGTQSRIR
9.3	1243.615677	0.005071	ASGTTQQADIPR
9.0	1243.608459	0.012289	DLDELIVQHY
8.9	1243.615662	0.005086	SETSPVPEARR
8.7	1243.629608	-0.008860	TNASVPSIPLDV
8.6	1243.630905	-0.010157	HYSPTKELNR
8.5	1243.630905	-0.010157	KESQPAIWNR

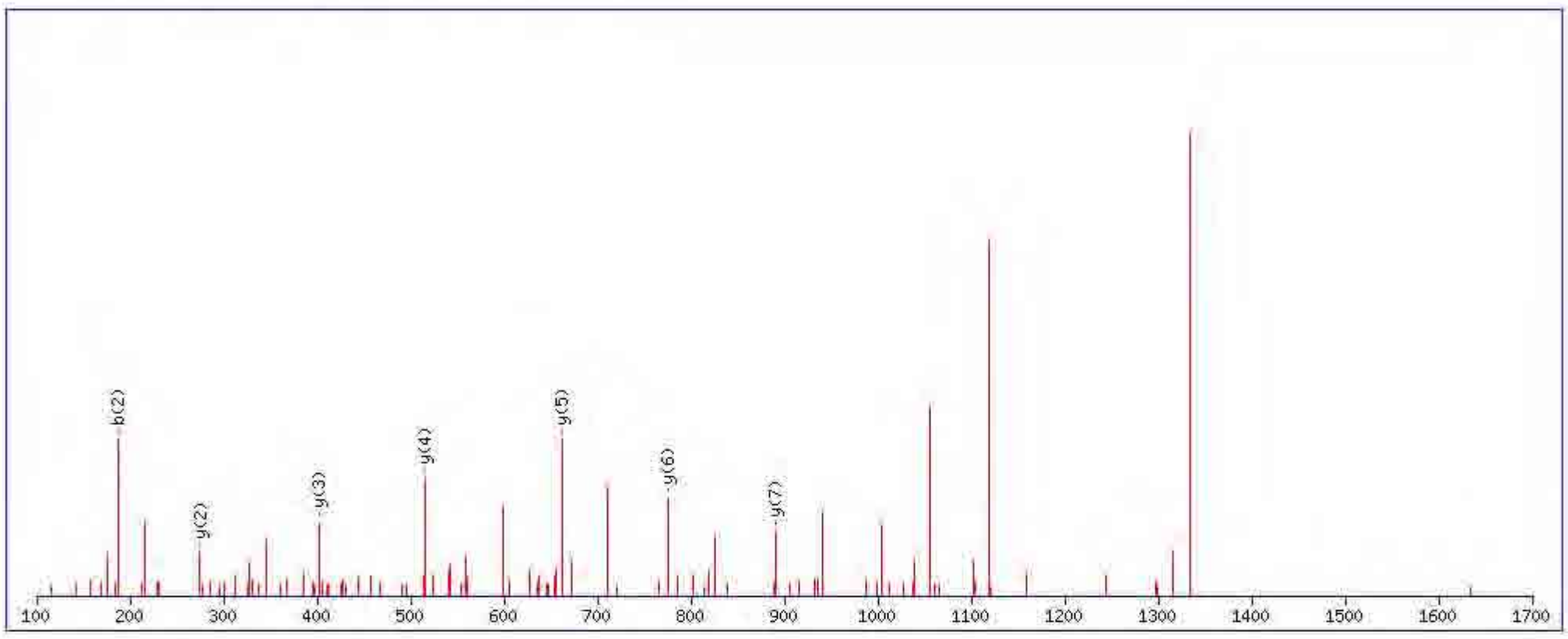
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSGISDPFLQVR**
Found in **AP1G1_HUMAN**, AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5

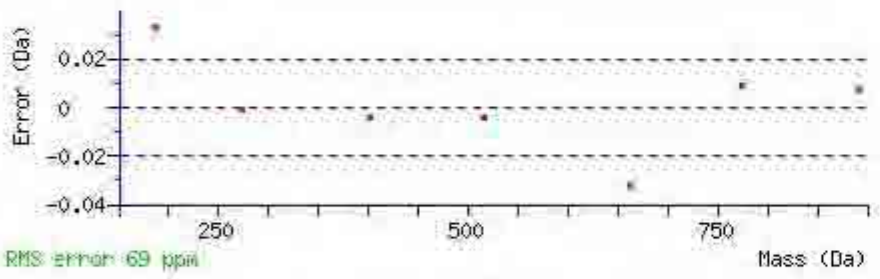
Match to Query 13329: 1332.691128 from(667.352840,2+) rtinseconds(1493) index(10024)
Title: Locus:1.1.1.1651.24
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

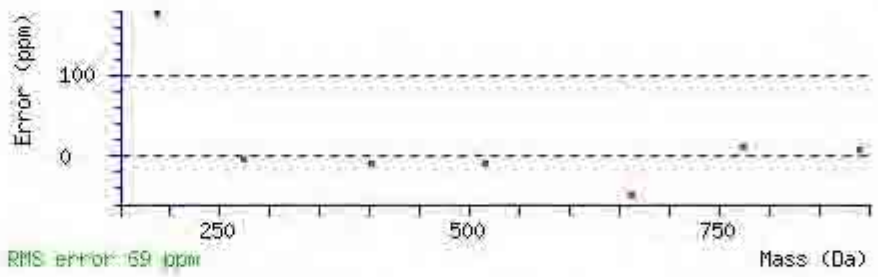
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1332.703781
Variable modifications:
P7 : Oxidation (P)
Ions Score: 37 **Expect:** 0.011
Matches : 7/100 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							12
2	187.107718	94.057497			169.097153	85.052214	S	1234.642628	617.824952	1217.616079	609.311677	1216.632063	608.819669	11
3	244.129182	122.568229			226.118617	113.562946	G	1147.610600	574.308938	1130.584051	565.795664	1129.600035	565.303655	10
4	357.213246	179.110261			339.202681	170.104978	I	1090.589136	545.798206	1073.562587	537.284931	1072.578571	536.792923	9
5	444.245274	222.626275			426.234709	213.620992	S	977.505072	489.256174	960.478523	480.742899	959.494507	480.250891	8
6	559.272217	280.139747			541.261652	271.134464	D	*890.473044*	445.740160	873.446495	437.226885	872.462479	436.734877	7
7	672.319896	336.663586			654.309331	327.658303	P	*775.446101*	388.226689	758.419552	379.713414			6
8	819.388310	410.197793			801.377745	401.192510	F	*662.398422*	331.702849	645.371873	323.189574			5
9	932.472374	466.739825			914.461809	457.734542	L	*515.330008*	258.168642	498.303459	249.655368			4
10	1060.530952	530.769114	1043.504403	522.255839	1042.520387	521.763831	Q	*402.245944*	201.626610	385.219395	193.113335			3
11	1159.599366	580.303321	1142.572817	571.790047	1141.588801	571.298038	V	*274.187366*	137.597321	257.160817	129.084047			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VSGISDPFLQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1332.703781	-0.012653	VSGISDPFLQVR
15.2	1332.686035	0.005093	VPDGMVGFIIGRG
13.8	1332.686005	0.005123	WVEVASMKVPR
12.7	1332.700577	-0.009449	ACNIMLLGAQRK
11.3	1332.686035	0.005093	VPDGMVGFIIGRG
11.1	1332.689346	0.001782	EGLQLMNLMLR
10.6	1332.688492	0.002636	TLDKEGLSESVR
9.6	1332.686020	0.005108	WLVTCATEVGVR
9.1	1332.689346	0.001782	EGLQLMNLMLR
8.4	1332.678635	0.012493	FTLTAQNGVGPGR

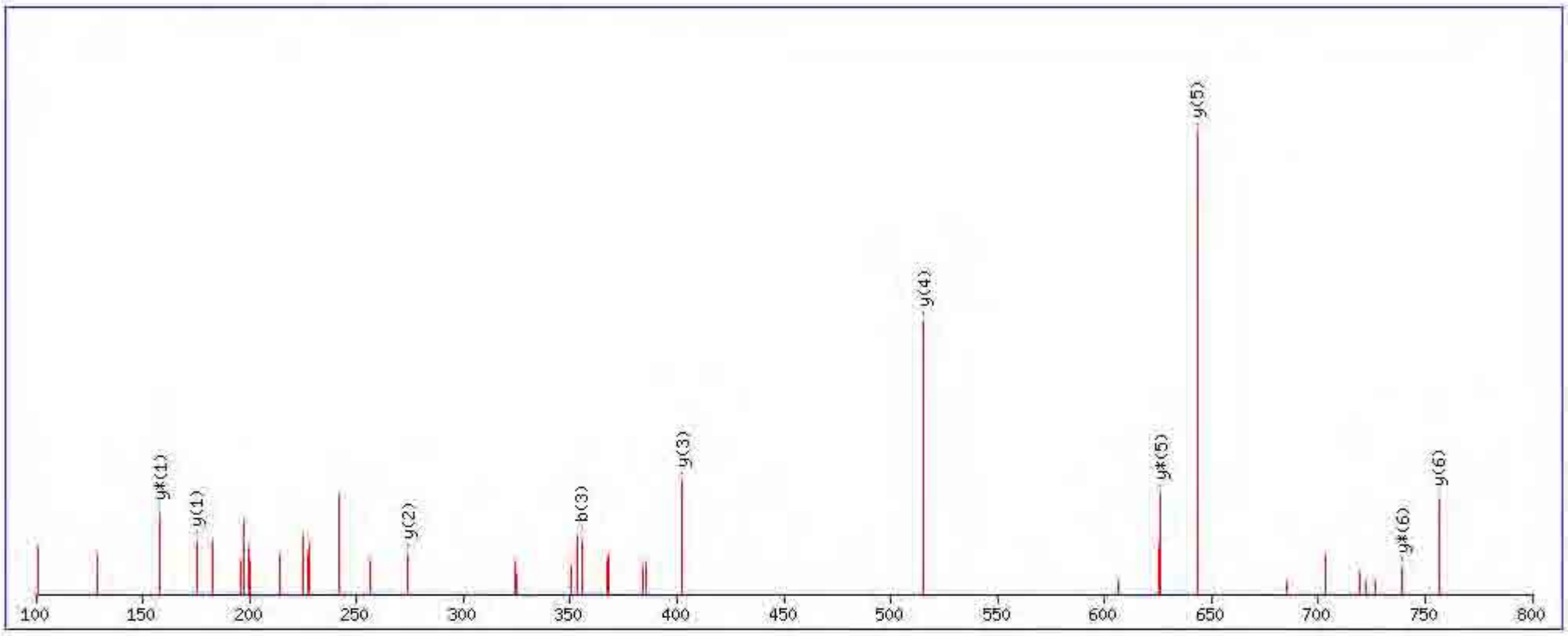
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLKPQVR**
Found in **L2GL2_HUMAN**, Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=1 SV=2

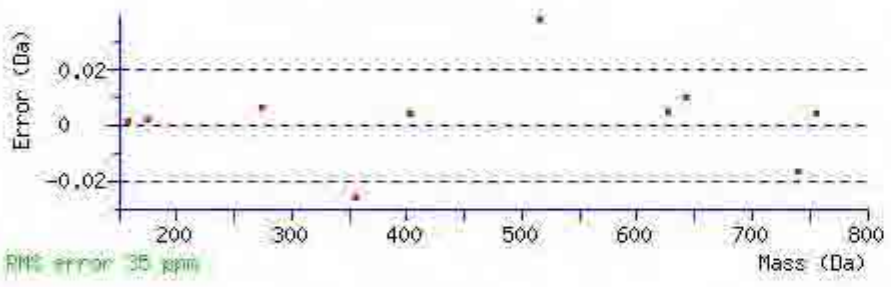
Match to Query 2428: 868.549968 from(435.282260,2+) rtinseconds(1336) index(7957)
Title: Locus:1.1.1.1566.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

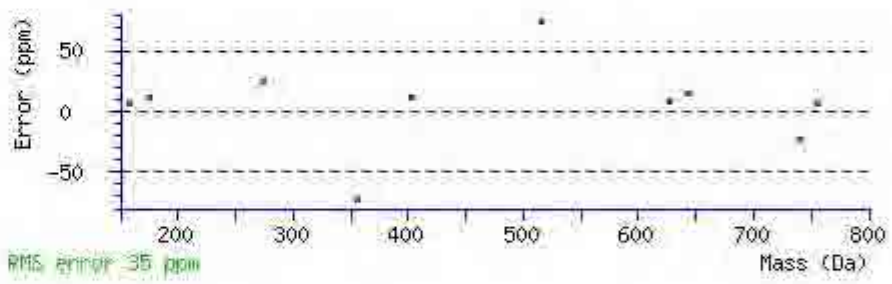
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 868.549423
Variable modifications:
P4 : Oxidation (P)
Ions Score: 36 **Expect:** 0.0072
Matches : 10/44 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			L					7
2	227.175404	114.091340			L	*756.472650*	378.739963	739.446101	370.226689	6
3	355.270367	178.138822	338.243818	169.625547	K	*643.388586*	322.197931	626.362037	313.684657	5
4	468.318046	234.662661	451.291497	226.149387	P	*515.293623*	258.150450	498.267074	249.637175	4
5	596.376624	298.691950	579.350075	290.178676	Q	*402.245944*	201.626610	385.219395	193.113335	3
6	695.445038	348.226157	678.418489	339.712883	V	*274.187366*	137.597321	257.160817	129.084046	2
7					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of LLKPQVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	868.549423	0.000545	LLKPQVR
36.1	868.549423	0.000545	LLQLAGVR
36.1	868.549423	0.000545	PLQLKVR
31.0	868.549408	0.000560	ILQLNLR
31.0	868.549423	0.000545	IPKLVQR
31.0	868.549423	0.000545	LIKPVQR
31.0	868.549423	0.000545	LLKPVQR
31.0	868.549408	0.000560	PLKLINR
26.4	868.549423	0.000545	LKIPQVR
24.6	868.549423	0.000545	LLKQPVR

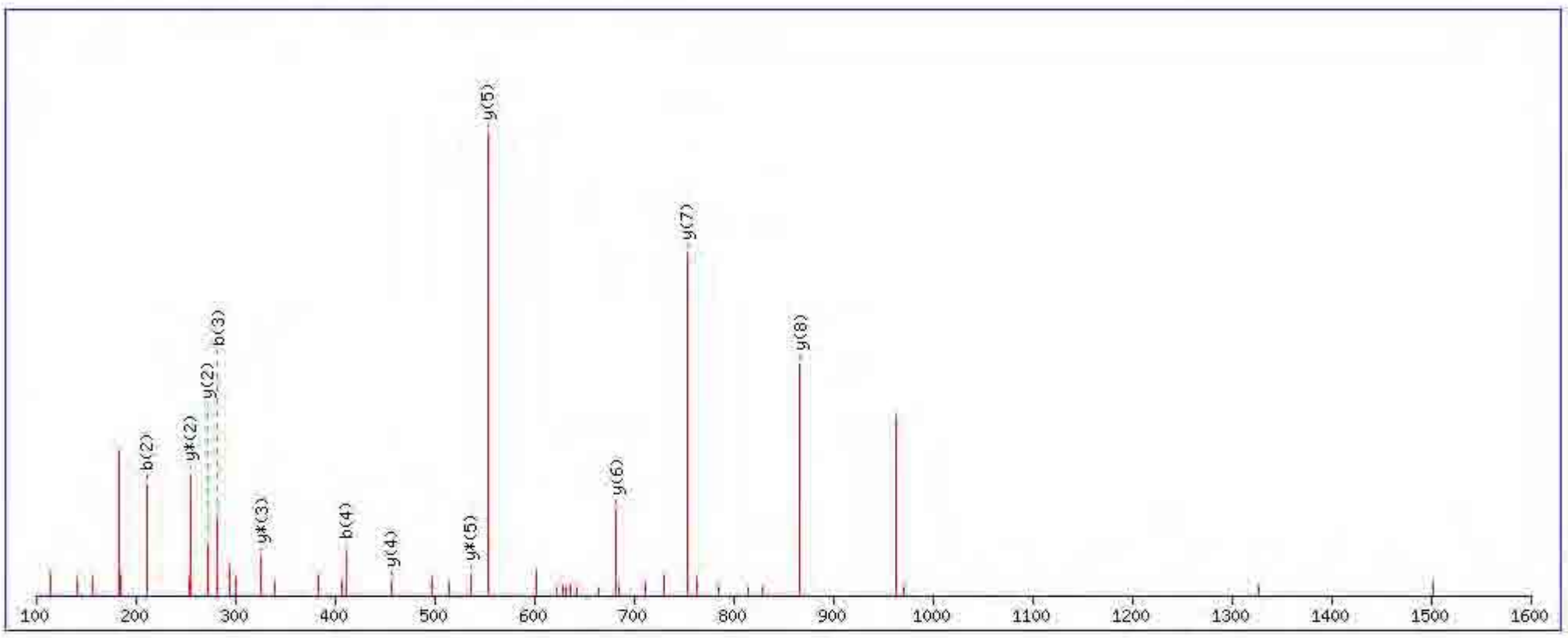
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLAEPLAPR**
Found in **LFNG_HUMAN**, Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2

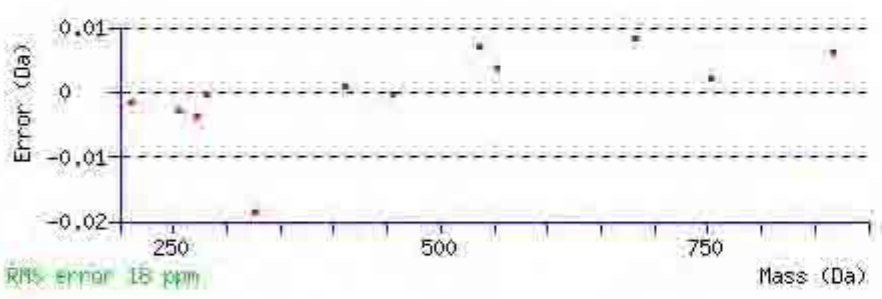
Match to Query 4449: 962.552288 from(482.283420,2+) rtinseconds(1150) index(5936)
Title: Locus:1.1.1.1461.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

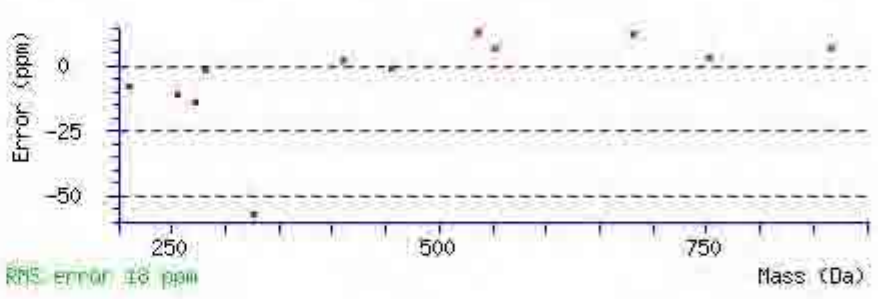
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 962.554886
Ions Score: 40 **Expect:** 0.01
Matches : 12/64 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	98.060040	49.533658			P							9
2	211.144104	106.075690			L	866.509429	433.758353	849.482880	425.245078	848.498864	424.753070	8
3	282.181218	141.594247			A	753.425365	377.216321	736.398816	368.703046	735.414800	368.211038	7
4	411.223811	206.115544	393.213246	197.110261	E	682.388251	341.697764	665.361702	333.184489	664.377686	332.692481	6
5	508.276575	254.641926	490.266010	245.636643	P	553.345658	277.176467	536.319109	268.663193			5
6	621.360639	311.183958	603.350074	302.178675	L	456.292894	228.650085	439.266345	220.136811			4
7	692.397753	346.702515	674.387188	337.697232	A	343.208830	172.108053	326.182281	163.594779			3
8	789.450517	395.228897	771.439952	386.223614	P	272.171716	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PLAEPLAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.8	962.554886	-0.002598	PLAEPLAPR
21.7	962.554901	-0.002613	PLALPSPPR
14.4	962.554901	-0.002613	PLALPSPPR
14.4	962.554916	-0.002628	PPALTPVPR
13.5	962.554901	-0.002613	PPLSLPPAR
12.9	962.547028	0.005260	VMKELSLK
11.4	962.554901	-0.002613	PLALPSPPR
11.4	962.543671	0.008617	PPAPIPDLK
11.4	962.543671	0.008617	PPAVPEIPK
7.5	962.543671	0.008617	APIEVQPLP

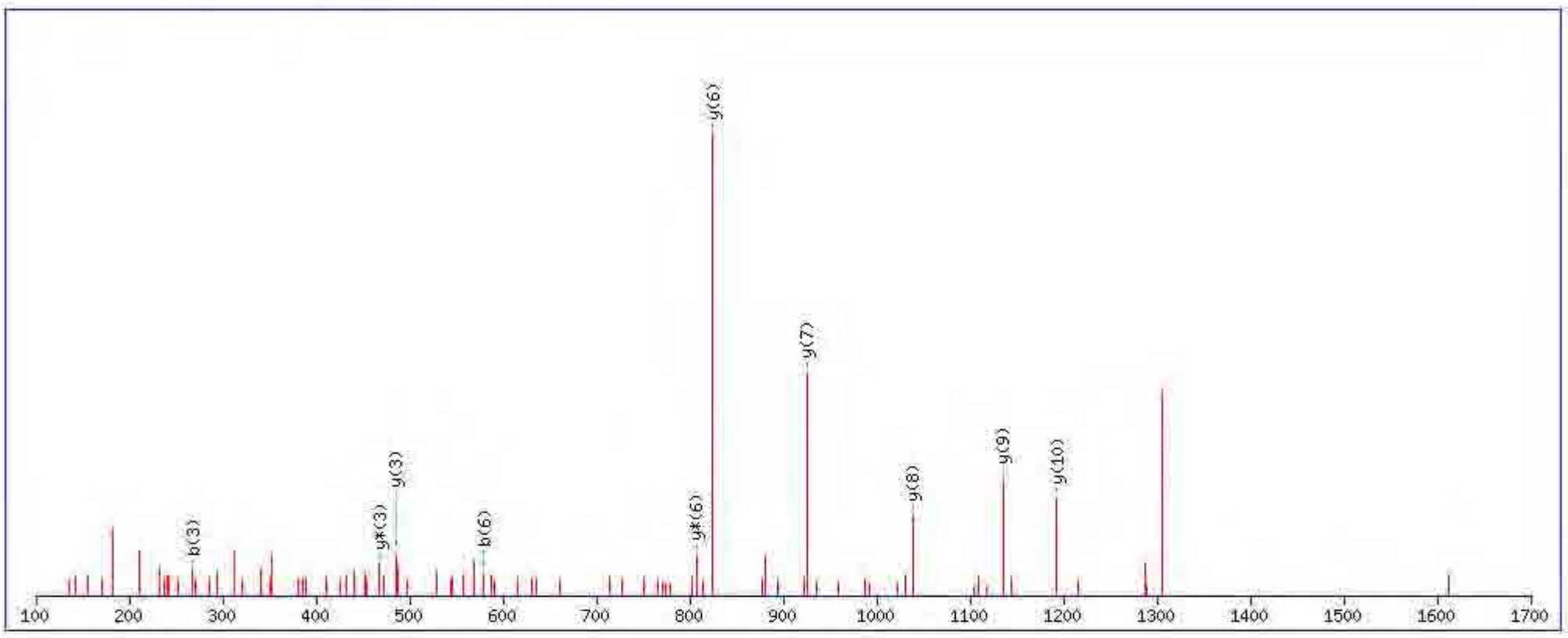
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPITPLEFYR**
Found in **BLMH_HUMAN**, Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1

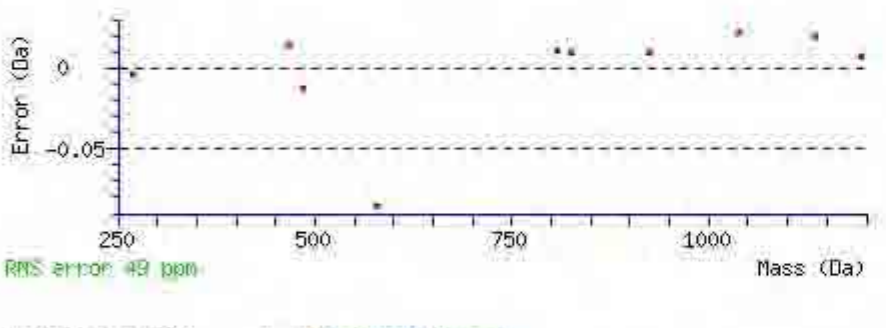
Match to Query 12746: 1304.719688 from(653.367120,2+) rtinseconds(2095) index(17487)
Title: Locus:1.1.1.1982.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

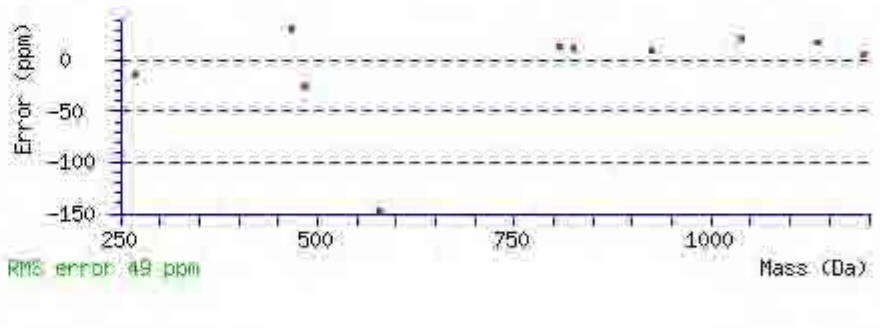
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1304.712860
Ions Score: 32 **Expect:** 0.011
Matches : 10/86 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	*1192.636087*	596.821682	1175.609538	588.308407	1174.625522	587.816399	10
3	**268.165568**	134.586422			P	*1135.614623*	568.310949	1118.588074	559.797675	1117.604058	559.305667	9
4	381.249632	191.128454			I	*1038.561859*	519.784568	1021.535310	511.271293	1020.551294	510.779285	8
5	482.297311	241.652293	464.286746	232.647011	T	*925.477795*	463.242536	908.451246	454.729261	907.467230	454.237253	7
6	**579.350075**	290.178676	561.339510	281.173393	P	*824.430116*	412.718696	807.403567	404.205422	806.419551	403.713414	6
7	692.434139	346.720708	674.423574	337.715425	L	727.377352	364.192314	710.350803	355.679039	709.366787	355.187031	5
8	821.476732	411.242004	803.466167	402.236722	E	614.293288	307.650282	597.266739	299.137007	596.282723	298.644999	4
9	968.545146	484.776211	950.534581	475.770929	F	*485.250695*	243.128985	468.224146	234.615711			3
10	1131.608475	566.307876	1113.597910	557.302593	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGPITPLEFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1304.712860	0.006828	IGPITPLEFYR
10.6	1304.720078	-0.000390	LGPVESLQGHLR
7.5	1304.720062	-0.000374	LSLPAPEPPGRR
7.2	1304.708847	0.010841	IGLPGHQEVEVK
7.0	1304.720062	-0.000374	LSLPAPEPPGRR
5.3	1304.708847	0.010841	LGGSAIPLPPSHK
4.7	1304.731308	-0.011620	GLSPGALLPRHR
1.4	1304.731323	-0.011635	PLVIRGHTPSGR
0.4	1304.712189	0.007499	VLAKNNALTMSK
0.3	1304.708832	0.010856	NASPVQVKTAYK

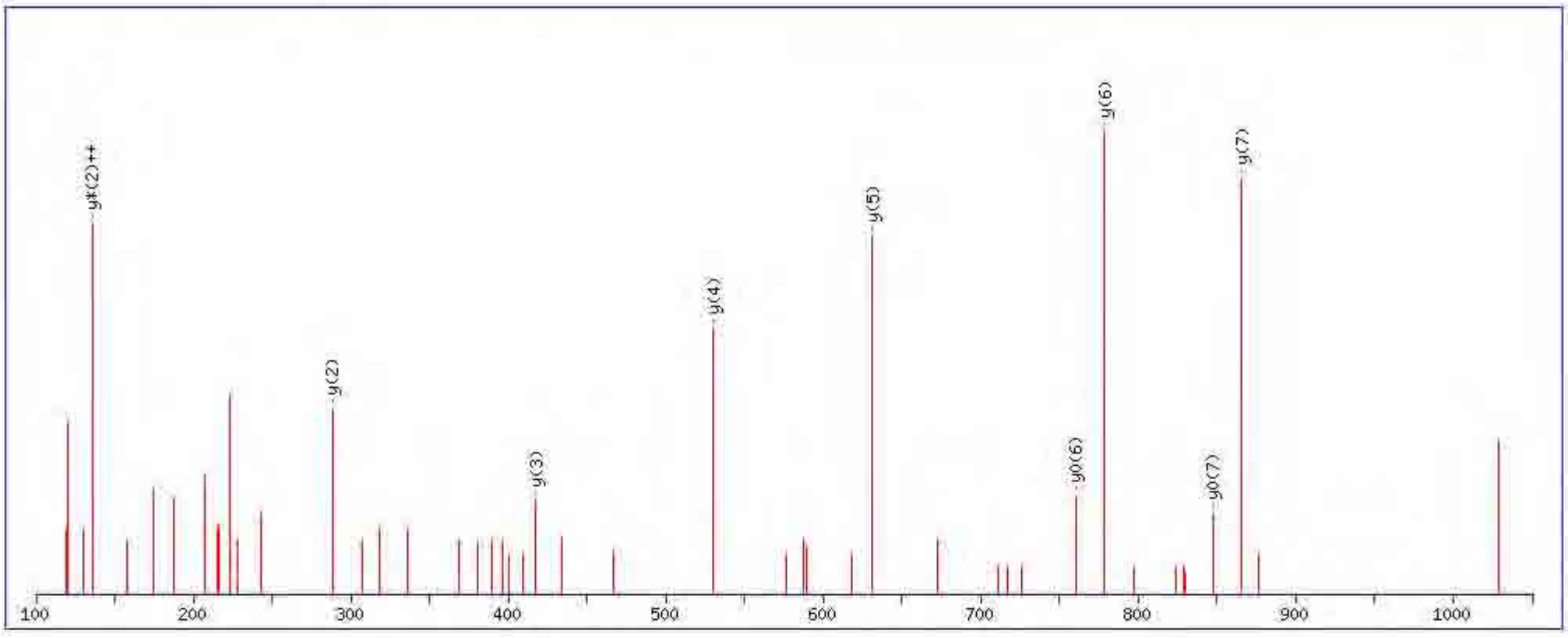
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFTIELR**
Found in **CBPB2_HUMAN**, Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

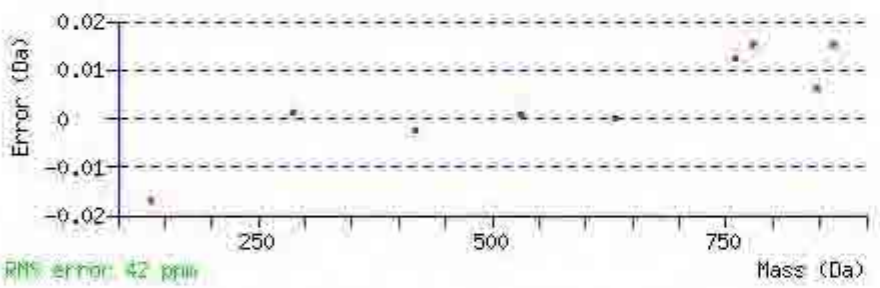
Match to Query 5813: 1027.529248 from(514.771900,2+) rtinseconds(1829) index(14074)
Title: Locus:1.1.1.1836.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

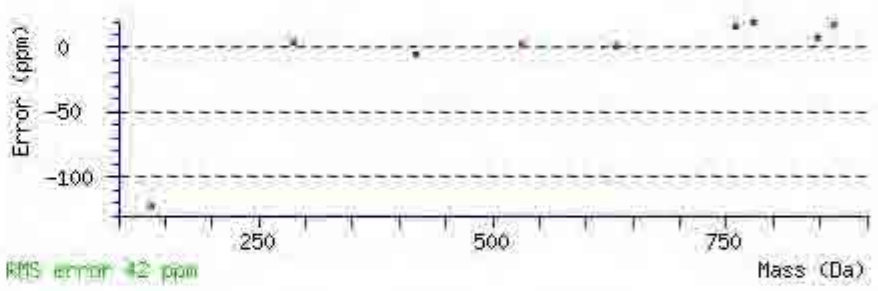
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1027.533829
Ions Score: 41 **Expect:** 0.0082
Matches : 9/64 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							8
2	251.102633	126.054954	233.092068	117.049672	S	*865.477794*	433.242535	848.451245	424.729261	847.467229	424.237253	7
3	398.171047	199.589161	380.160482	190.583879	F	*778.445766*	389.726521	761.419217	381.213247	760.435201	380.721239	6
4	499.218726	250.113001	481.208161	241.107719	T	*631.377352*	316.192314	614.350803	307.679040	613.366787	307.187032	5
5	612.302790	306.655033	594.292225	297.649751	I	*530.329673*	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	741.345383	371.176330	723.334818	362.171047	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
7	854.429447	427.718362	836.418882	418.713079	L	*288.203016*	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YSFTIELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	1027.533829	-0.004581	YSFTIELR
12.5	1027.529800	-0.000552	DNAPTIEIR
7.2	1027.529800	-0.000552	AEAGGLPELR
6.6	1027.537888	-0.008640	LFVGLGFPY
6.4	1027.522614	0.006634	YSVAEVFIT
6.3	1027.531143	-0.001895	LHSHHELR
6.3	1027.529800	-0.000552	AQLGEPELR
6.0	1027.529816	-0.000568	EAAAVPTTPR
6.0	1027.523300	0.005948	CPRVPATPR
3.9	1027.529831	-0.000583	GGVIPATEPR

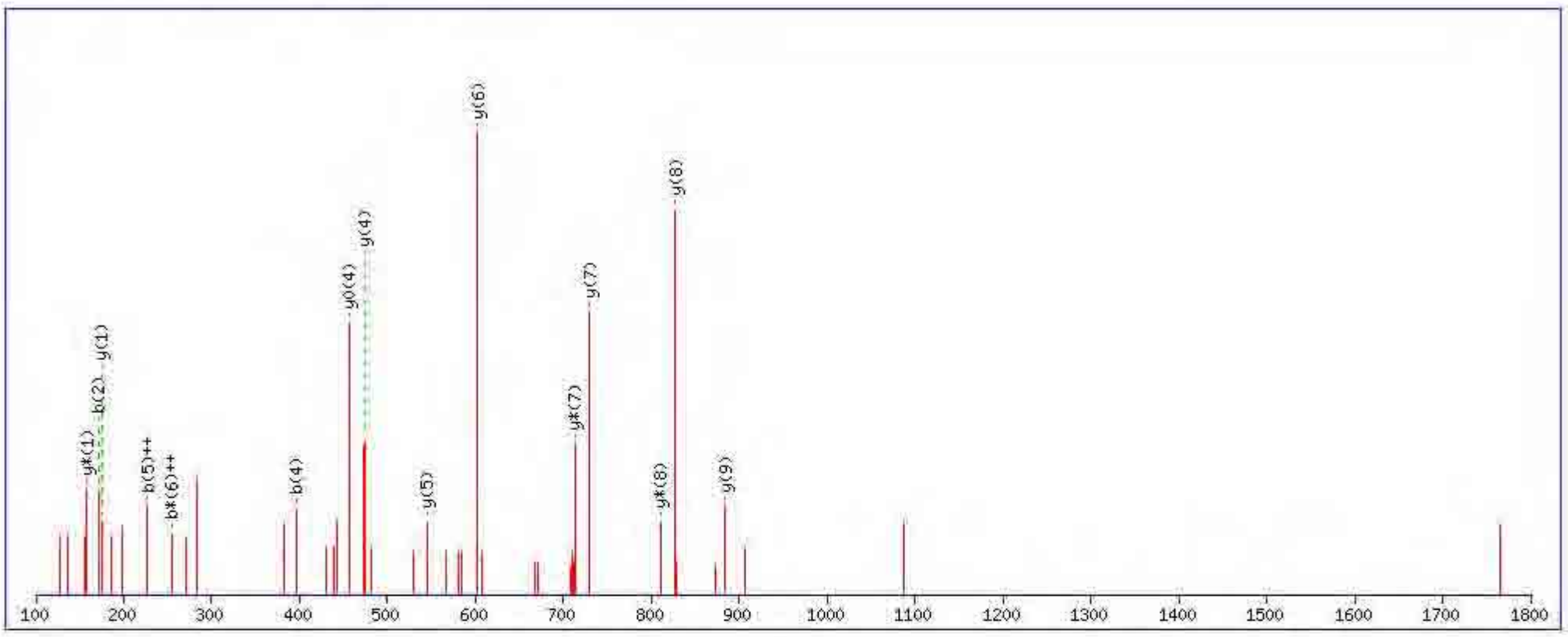
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPKGAPGER**
Found in **CO9A3_HUMAN**, Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2

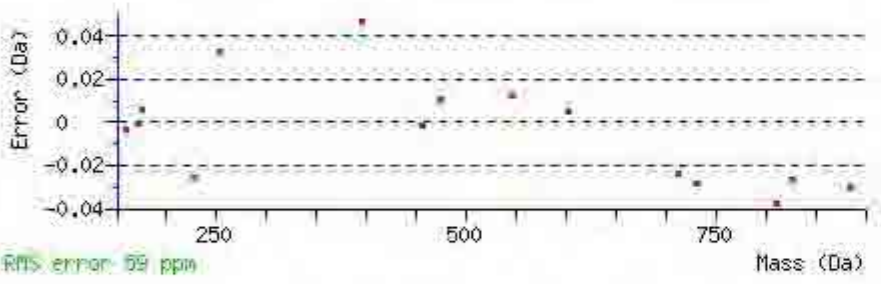
Match to Query 5172: 996.495488 from(499.255020,2+) rtinseconds(552) index(1036)
Title: Locus:1.1.1.1125.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

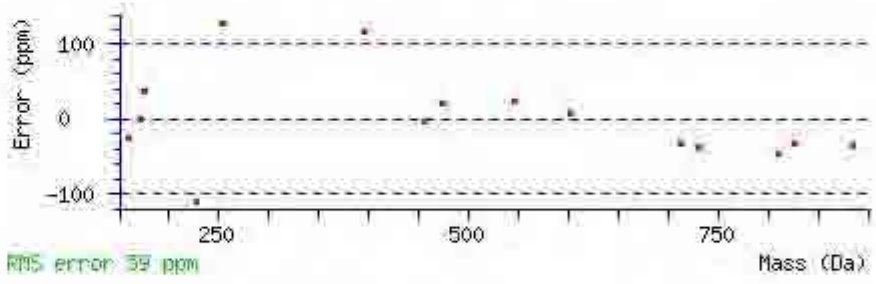
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 996.498856
Variable modifications:
P1 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 44 Expect: 0.0068
Matches : 15/84 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.054955	57.531116					P							10
2	171.076419	86.041847					G	*884.458457*	442.732867	867.431908	434.219592	866.447892	433.727584	9
3	268.129183	134.568229					P	*827.436993*	414.222135	810.410444	405.708860	809.426428	405.216852	8
4	396.224146	198.615711	379.197597	190.102436			K	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	7
5	453.245610	227.126443	436.219061	218.613168			G	*602.289266*	301.648271	585.262717	293.134997	584.278701	292.642989	6
6	524.282724	262.645000	507.256175	254.131726			A	*545.267802*	273.137539	528.241253	264.624265	527.257237	264.132257	5
7	637.330403	319.168840	620.303854	310.655565			P	*474.230688*	237.618982	457.204139	229.105708	456.220123	228.613700	4
8	694.351867	347.679572	677.325318	339.166297			G	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
9	823.394460	412.200868	806.367911	403.687594	805.383895	403.195586	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PGPKGAPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.3	996.498856	-0.003368	PGPKGAPGER
27.9	996.498856	-0.003368	PGPQAGAGAGAK
24.3	996.487625	0.007863	PGPKGDPGEK
20.6	996.498856	-0.003368	PGPAGPKGER
20.6	996.498856	-0.003368	PGPAGPRGEK
18.7	996.498871	-0.003383	LGPPQGGSPR
18.3	996.498871	-0.003383	PGQPGLPGSR
17.8	996.487625	0.007863	IGPEVPDDR
17.2	996.498871	-0.003383	PGPSGPPGKR
17.1	996.498856	-0.003368	PGPKGAPGER

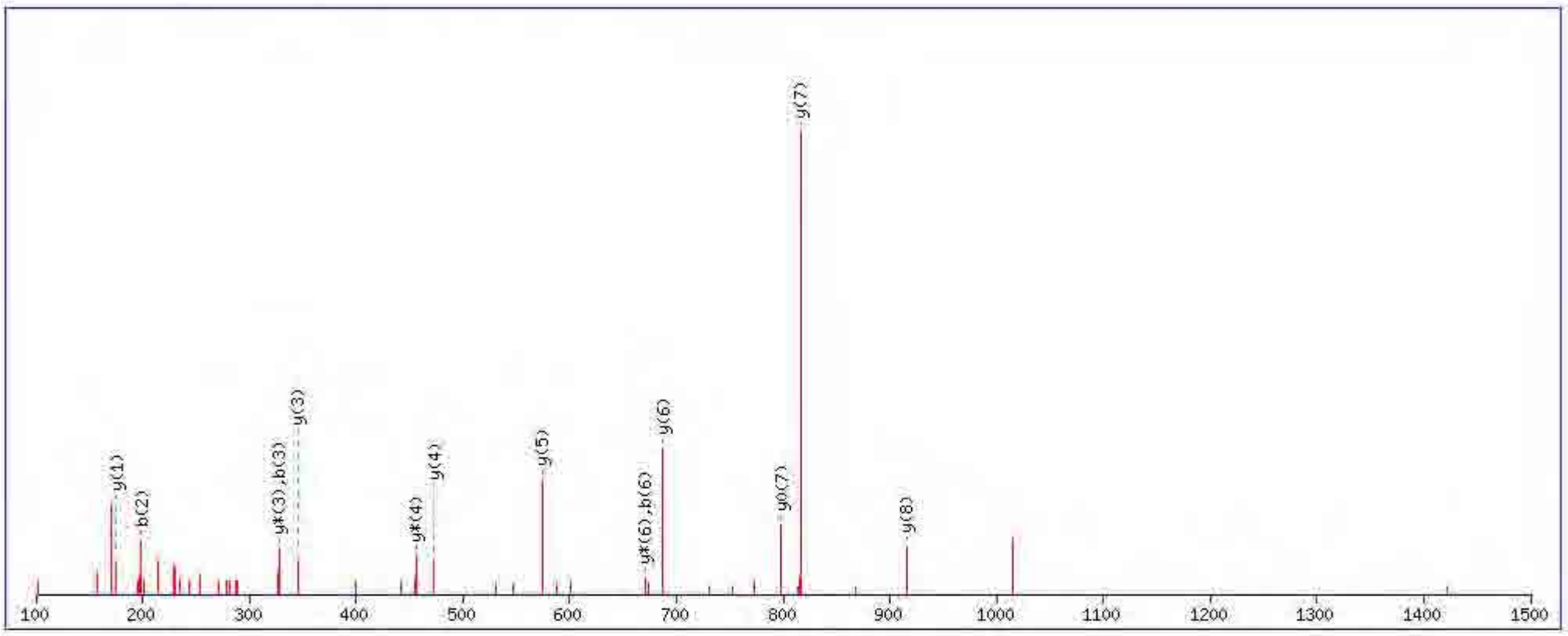
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVELTQGLR**
Found in **CLC11_HUMAN**, C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1

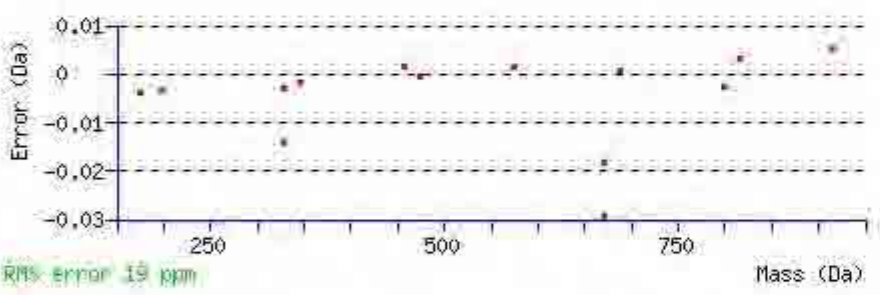
Match to Query 5543: 1013.587748 from(507.801150,2+) rtinseconds(1271) index(7297)
Title: Locus:1.1.1.1529.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

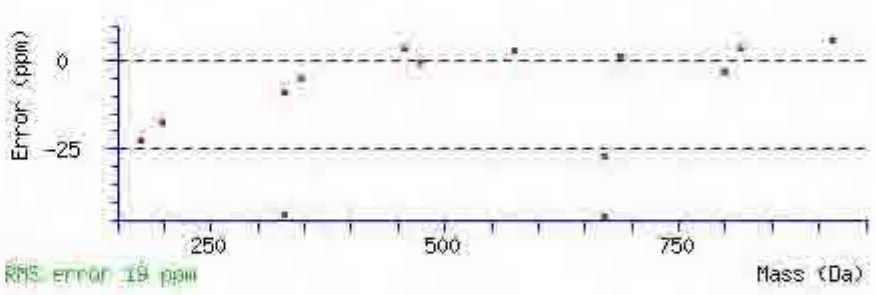
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1013.586945
Ions Score: 45 **Expect:** 0.0014
Matches : 14/74 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	**199.144104**	100.075690					V	*915.525808*	458.266542	898.499259	449.753268	897.515243	449.261260	8
3	**328.186697**	164.596987			310.176132	155.591704	E	*816.457394*	408.732335	799.430845	400.219061	798.446829	399.727053	7
4	441.270761	221.139019			423.260196	212.133736	L	*687.414801*	344.211039	670.388252	335.697764	669.404236	335.205756	6
5	542.318440	271.662858			524.307875	262.657576	T	*574.330737*	287.669007	557.304188	279.155732	556.320172	278.663724	5
6	**670.377018**	335.692147	653.350469	327.178873	652.366453	326.686865	Q	*473.283058*	237.145167	456.256509	228.631892			4
7	727.398482	364.202879	710.371933	355.689605	709.387917	355.197597	G	*345.224480*	173.115878	328.197931	164.602603			3
8	840.482546	420.744911	823.455997	412.231637	822.471981	411.739629	L	288.203016	144.605146	271.176467	136.091871			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VVELTQGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.2	1013.586945	0.000803	VVELTQGLR
14.0	1013.586929	0.000819	TPELLTRGK
13.9	1013.586929	0.000819	VDLPIKSAR
13.6	1013.586929	0.000819	VVENGGLKAK
13.1	1013.586929	0.000819	VLDLTRNAL
12.6	1013.583099	0.004649	VLDIMPLTL
8.8	1013.586929	0.000819	LVEPSKLGR
8.3	1013.586929	0.000819	VIDLRTNAI
7.7	1013.586945	0.000803	LLTLTGQPR
7.0	1013.586945	0.000803	TILQVVARD

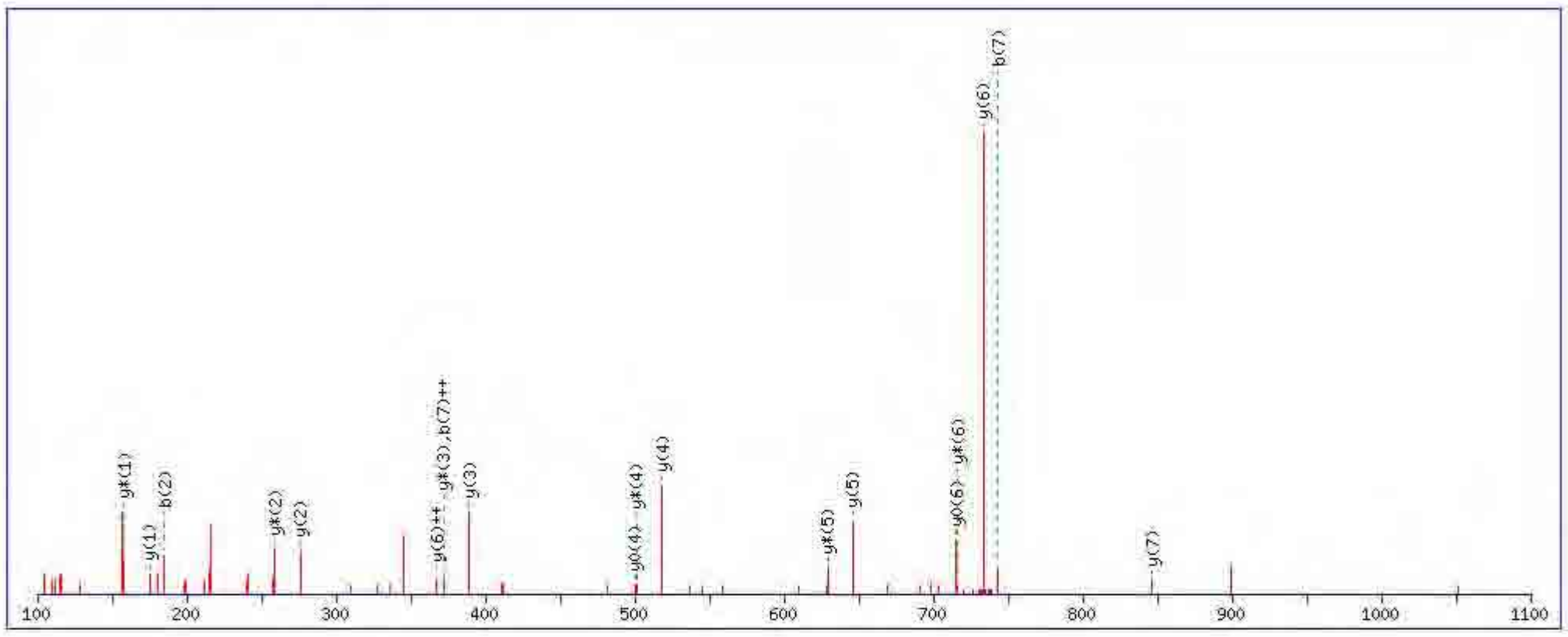
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALSQEITR**
Found in **CYTL1_HUMAN**, Cytokine-like protein 1 OS=Homo sapiens GN=CYTL1 PE=1 SV=1

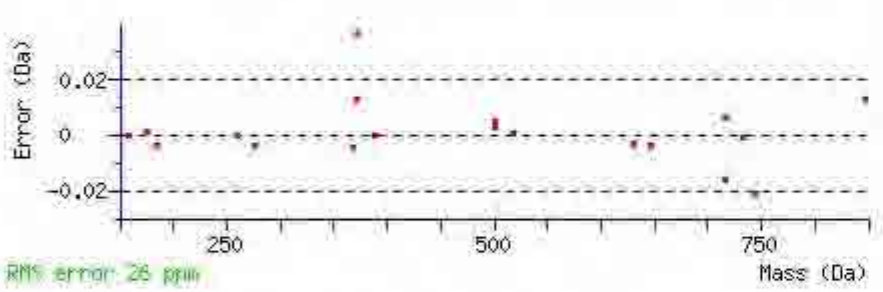
Match to Query 3510: 916.494988 from(459.254770,2+) rtinseconds(798) index(2875)
Title: Locus:1.1.1.1261.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

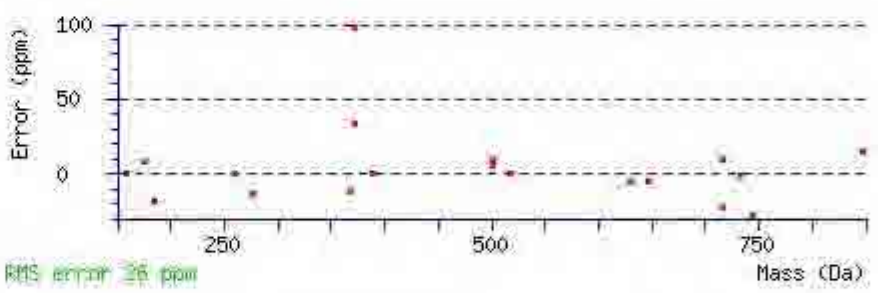
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 916.497772
Ions Score: 45 **Expect:** 0.0078
Matches : 19/72 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	185.128454	93.067865					L	846.467958	423.737617	829.441409	415.224343	828.457393	414.732335	7
3	272.160482	136.583879			254.149917	127.578596	S	733.383894	367.195585	716.357345	358.682311	715.373329	358.190303	6
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	Q	646.351866	323.679571	629.325317	315.166297	628.341301	314.674289	5
5	529.261653	265.134465	512.235104	256.621190	511.251088	256.129182	E	518.293288	259.650282	501.266739	251.137008	500.282723	250.645000	4
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	I	389.250695	195.128986	372.224146	186.615711	371.240130	186.123703	3
7	743.393396	372.200336	726.366847	363.687062	725.382831	363.195054	T	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
8							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALSQEITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	916.497772	-0.002784	ALSQEITR
30.3	916.486526	0.008462	ALSKEELQ
23.9	916.486526	0.008462	ALNTEIEK
20.8	916.486557	0.008431	APSKVTDAL
20.7	916.497772	-0.002784	AINTLETR
20.6	916.497772	-0.002784	ALSLQETR
19.2	916.497772	-0.002784	APSSAISLR
19.1	916.497787	-0.002799	ALSKGQNVT
18.2	916.497787	-0.002799	ALSAGNGVTK
18.1	916.497787	-0.002799	AISSPTVSR

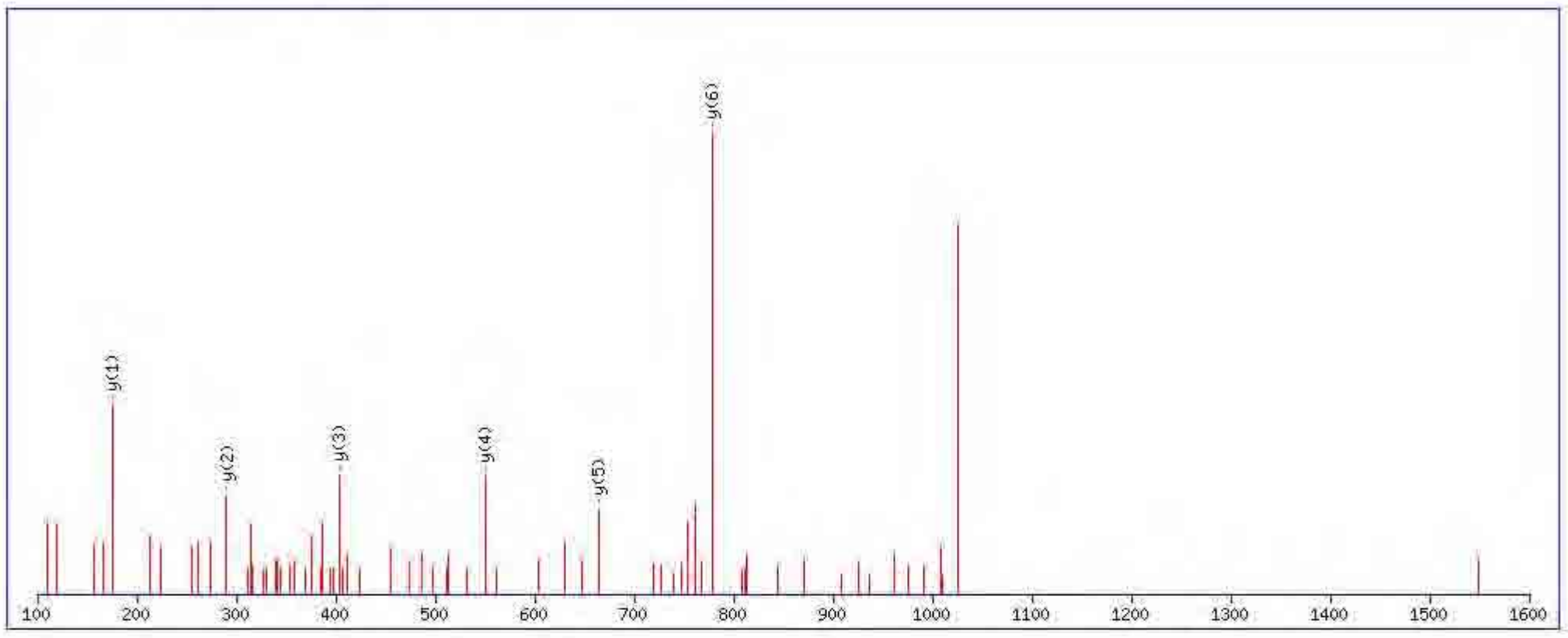
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMNNFLDR**
Found in **DSG1_HUMAN**, Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2

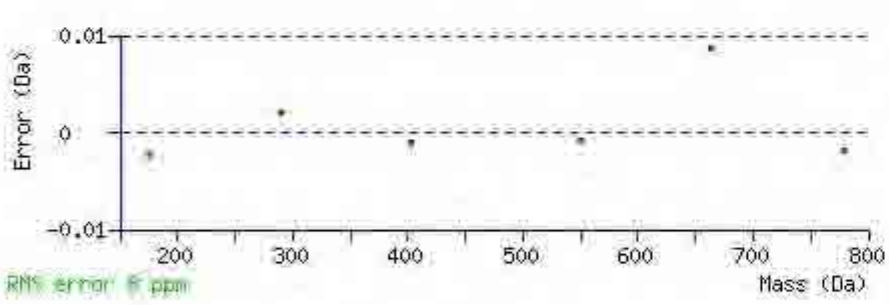
Match to Query 5758: 1025.465608 from(513.740080,2+) rtinseconds(972) index(4635)
Title: Locus:1.1.1.1359.18
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

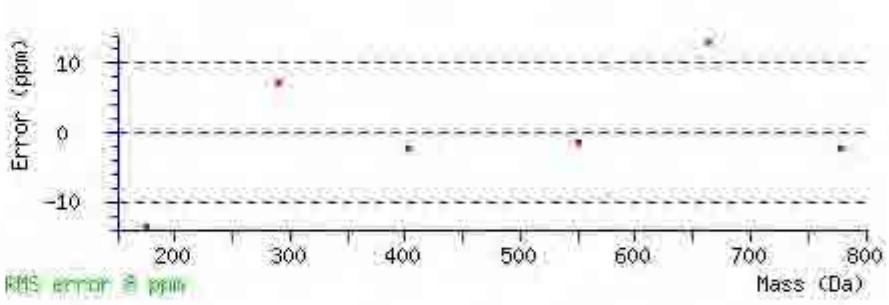
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1025.460022
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 52 **Expect:** 0.00016
Matches : 6/118 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	249.090355	125.048815			231.079790	116.043533	M	925.419627	463.213452	908.393078	454.700177	907.409062	454.208169	7
3	363.133282	182.070279	346.106733	173.557005	345.122717	173.064997	N	*778.384227*	389.695752	761.357678	381.182477	760.373662	380.690469	6
4	477.176209	239.091743	460.149660	230.578468	459.165644	230.086460	N	*664.341300*	332.674288	647.314751	324.161014	646.330735	323.669006	5
5	624.244623	312.625950	607.218074	304.112675	606.234058	303.620667	F	*550.298373*	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	737.328687	369.167982	720.302138	360.654707	719.318122	360.162699	L	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
7	852.355630	426.681453	835.329081	418.168179	834.345065	417.676171	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TMNNFLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	1025.460022	0.005586	TMNNFLDR
10.8	1025.471268	-0.005660	PCHQTGLDR
8.6	1025.456665	0.008943	EPHPFDPR
8.6	1025.456665	0.008943	EPHPFDPR
7.6	1025.467880	-0.002272	RGSSYWDR
6.3	1025.460022	0.005586	NSMFQEVR
5.8	1025.460022	0.005586	IFMQTNER
2.1	1025.471252	-0.005644	HKMDDPQR
0.3	1025.464249	0.001359	CKMVQMMR
0.3	1025.460022	0.005586	MNTSAFPSR

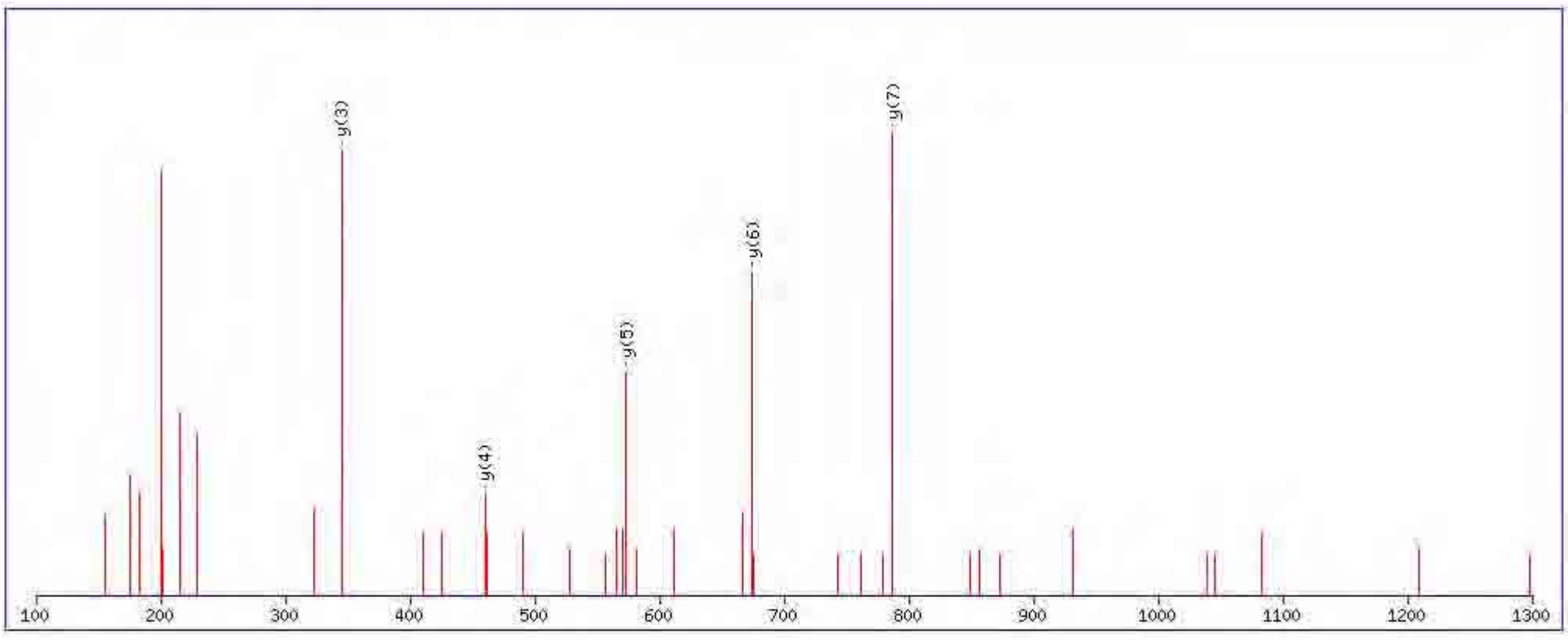
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILTIDIGR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

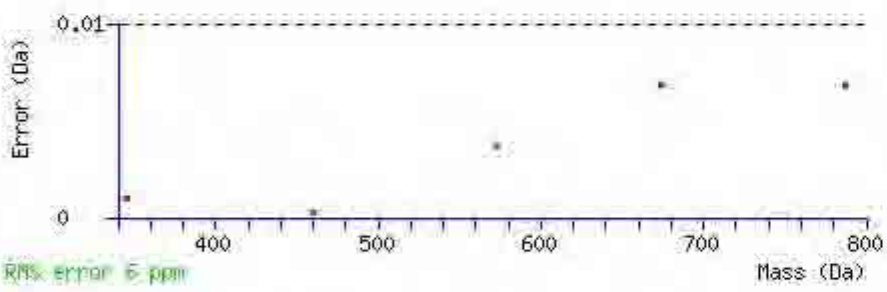
Match to Query 5571: 1014.575948 from(508.295250,2+) rtinseconds(1905) index(15099)
Title: Locus:1.1.1.1877.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

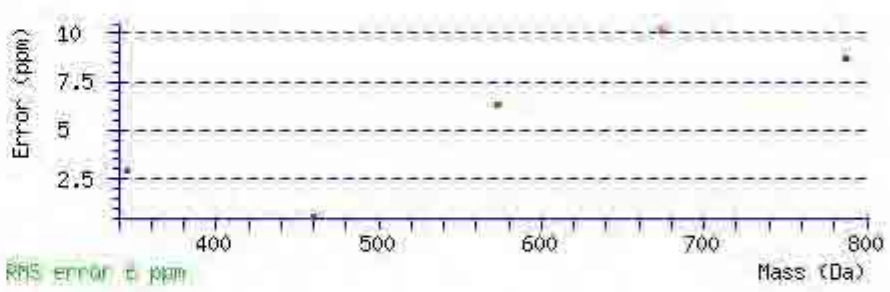
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1014.570953
Ions Score: 36 **Expect:** 0.0043
Matches : 5/74 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	229.118283	115.062779	211.107718	106.057497	I	900.551294	450.779285	883.524745	442.266011	882.540729	441.774003	8
3	342.202347	171.604811	324.191782	162.599529	L	*787.467230*	394.237253	770.440681	385.723979	769.456665	385.231971	7
4	443.250026	222.128651	425.239461	213.123369	T	*674.383166*	337.695221	657.356617	329.181947	656.372601	328.689939	6
5	556.334090	278.670683	538.323525	269.665401	I	*573.335487*	287.171382	556.308938	278.658107	555.324922	278.166099	5
6	671.361033	336.184155	653.350468	327.178872	D	*460.251423*	230.629350	443.224874	222.116075	442.240858	221.624067	4
7	784.445097	392.726187	766.434532	383.720904	I	*345.224480*	173.115878	328.197931	164.602604			3
8	841.466561	421.236919	823.455996	412.231636	G	232.140416	116.573846	215.113867	108.060572			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DILTIDIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1014.570953	0.004995	DILTIDIGR
10.4	1014.582169	-0.006221	DILTRIER
10.4	1014.570938	0.005010	VELTKLQAN
9.8	1014.570953	0.004995	DILVDGKAGK
9.8	1014.578339	-0.002391	DLLLTPKCL
9.3	1014.582169	-0.006221	NNTLLGQKK
9.3	1014.570938	0.005010	NNTPLLSLK
2.5	1014.575012	0.000936	VFVPLPGSTV
2.0	1014.578354	-0.002406	IPMDLTVVK
2.0	1014.570923	0.005025	DLLAANKASL

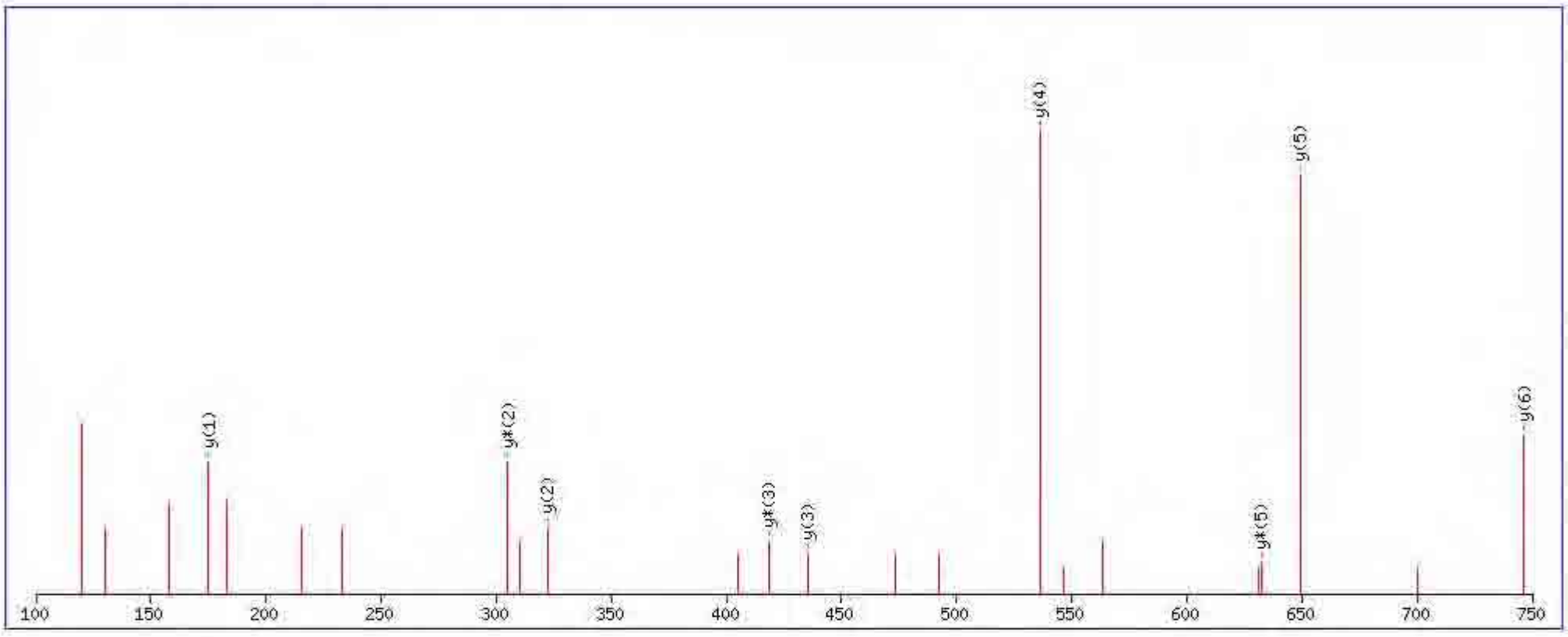
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPITLFR**
Found in **FBLN7_HUMAN**, Fibulin-7 OS=Homo sapiens GN=FBLN7 PE=2 SV=1

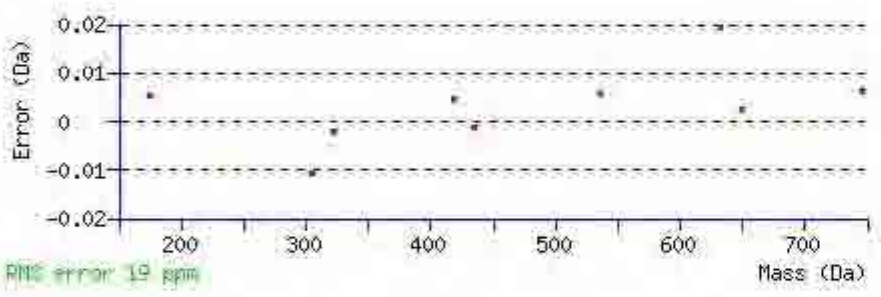
Match to Query 1964: 846.489408 from(424.251980,2+) rtinseconds(1564) index(10806)
Title: Locus:1.1.1.1691.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

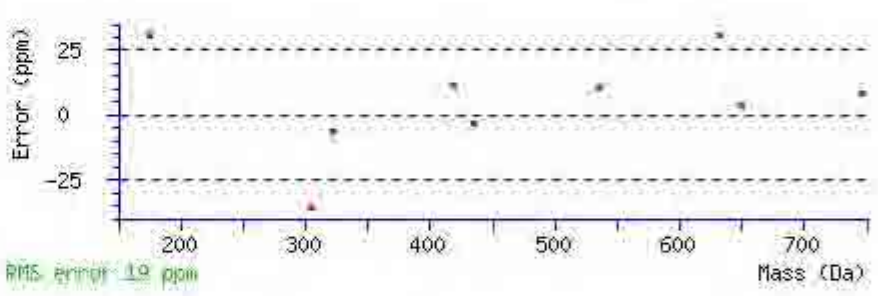
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 846.496338
Ions Score: 53 **Expect:** 0.00052
Matches : 9/54 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							7
2	199.107719	100.057497	181.097154	91.052215	P	*746.455937*	373.731607	729.429388	365.218332	728.445372	364.726324	6
3	312.191783	156.599529	294.181218	147.594247	I	*649.403173*	325.205224	632.376624	316.691950	631.392608	316.199942	5
4	413.239462	207.123369	395.228897	198.118087	T	*536.319109*	268.663193	519.292560	260.149918	518.308544	259.657910	4
5	526.323526	263.665401	508.312961	254.660119	L	*435.271430*	218.139353	418.244881	209.626078			3
6	673.391940	337.199608	655.381375	328.194325	F	*322.187366*	161.597321	305.160817	153.084046			2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TPITLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	846.496338	-0.006930	TPITLFR
20.1	846.496338	-0.006930	TPIFTLR
20.1	846.496338	-0.006930	TPLFLTR
20.1	846.496338	-0.006930	TPLFTLR
19.1	846.496338	-0.006930	TLPITFR
19.1	846.496353	-0.006945	TVIVPFR
18.2	846.482407	0.007001	ARGQLFR
18.2	846.482407	0.007001	GRAKPFR
15.2	846.485092	0.004316	TPLLPYK
13.8	846.485123	0.004285	TPFLLVGT

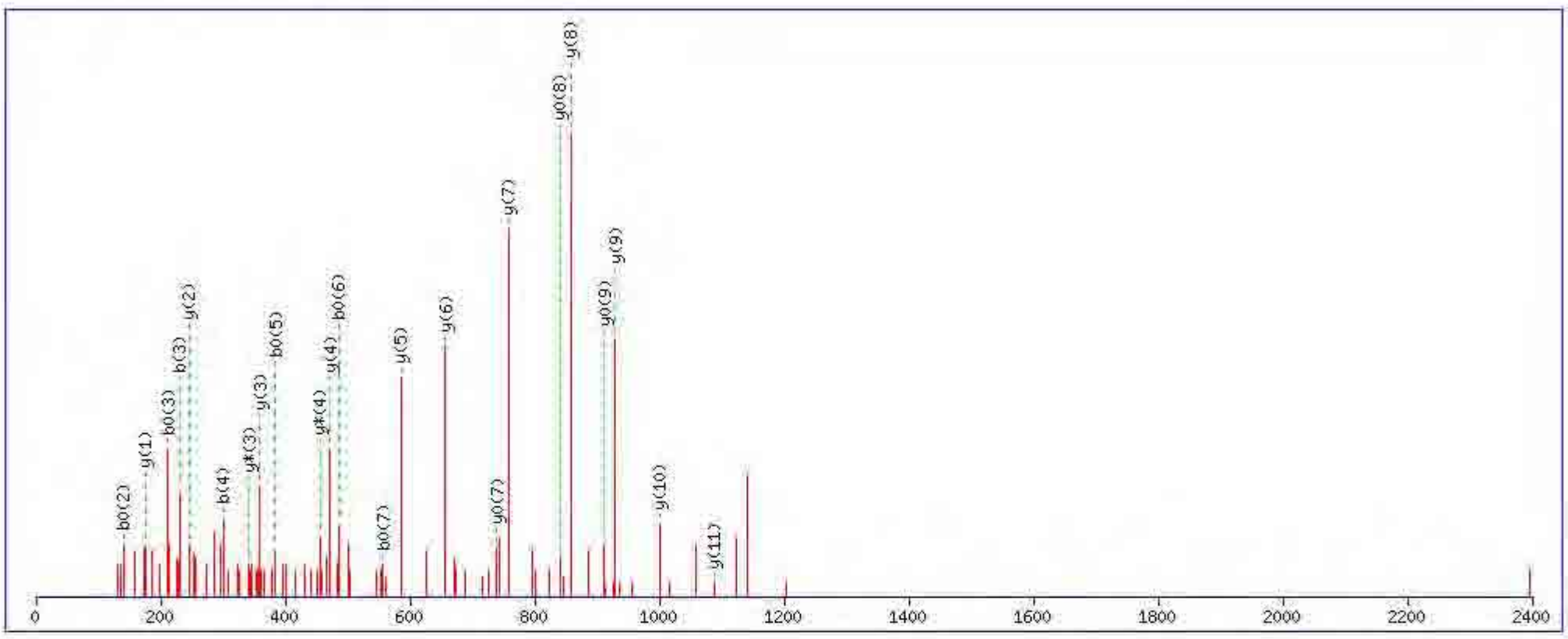
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAATTAILIAR**
Found in **GDN_HUMAN**, Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1

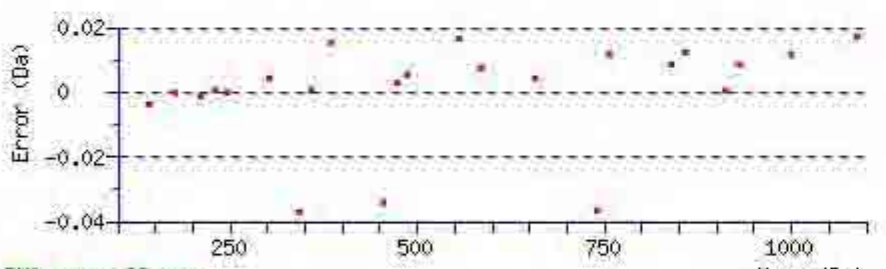
Match to Query 8998: 1157.680448 from(579.847500,2+) rtinseconds(1427) index(9149)
Title: Locus:1.1.1.1616.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

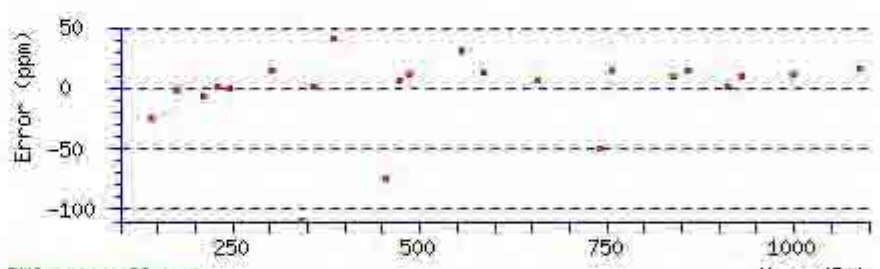
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1157.676788
Ions Score: 80 Expect: 4.1e-007
Matches : 23/96 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	159.076418	80.041847	141.065853	71.036564	S	*1087.646986*	544.327131	1070.620437	535.813857	1069.636421	535.321849	11
3	**230.113532**	115.560404	212.102967	106.555121	A	*1000.614958*	500.811117	983.588409	492.297843	982.604393	491.805835	10
4	**301.150646**	151.078961	283.140081	142.073679	A	*929.577844*	465.292560	912.551295	456.779286	911.567279	456.287278	9
5	402.198325	201.602801	384.187760	192.597518	T	*858.540730*	429.774003	841.514181	421.260729	840.530165	420.768721	8
6	503.246004	252.126640	485.235439	243.121358	T	*757.493051*	379.250164	740.466502	370.736889	739.482486	370.244881	7
7	574.283118	287.645197	556.272553	278.639915	A	*656.445372*	328.726324	639.418823	320.213050			6
8	687.367182	344.187229	669.356617	335.181947	I	*585.408258*	293.207767	568.381709	284.694493			5
9	800.451246	400.729261	782.440681	391.723979	L	*472.324194*	236.665735	455.297645	228.152461			4
10	913.535310	457.271293	895.524745	448.266011	I	*359.240130*	180.123703	342.213581	171.610429			3
11	984.572424	492.789850	966.561859	483.784568	A	*246.156066*	123.581671	229.129517	115.068397			2
12					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ASAATTAILIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.2	1157.676788	0.003660	ASAATTAILIAR
17.8	1157.676804	0.003644	TSIGILAAAVSR
15.5	1157.680817	-0.000369	GTAALPYPLKK
9.4	1157.688049	-0.007601	TGSRIVIGISR
8.3	1157.676804	0.003644	VTNSTLAAIIR
8.1	1157.680832	-0.000384	FPVKPADLKK
8.1	1157.676788	0.003660	LKETLAQLSR
8.0	1157.676804	0.003644	KTAGSQVINLK
5.3	1157.669601	0.010847	APFIELLPVK
5.3	1157.669617	0.010831	EFPTVPLVKL

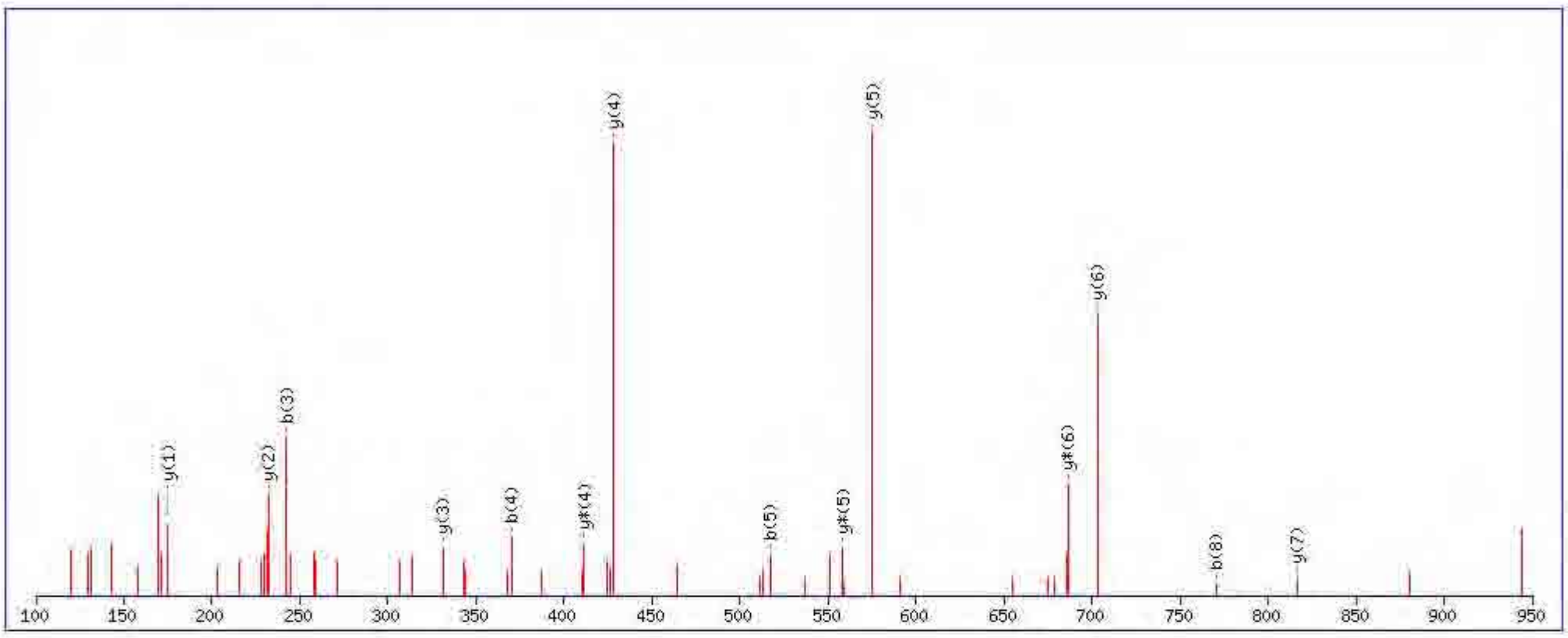
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

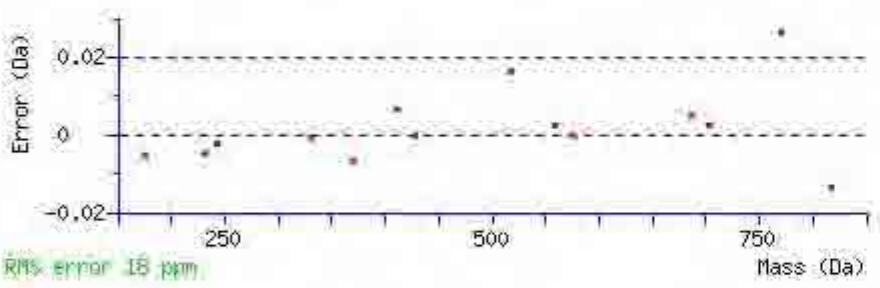
Match to Query 4071: 943.521728 from(472.768140,2+) rtinseconds(1486) index(9928)
Title: Locus:1.1.1.1648.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

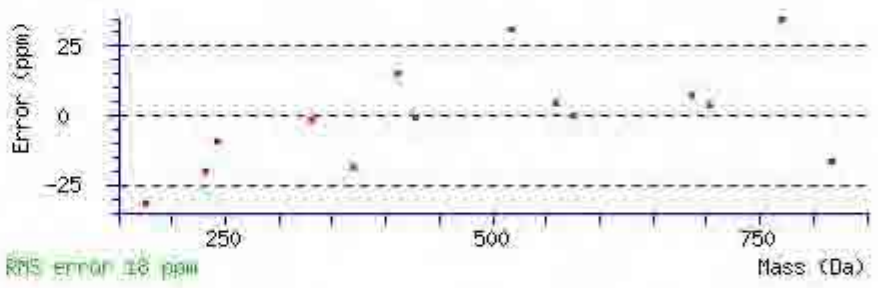
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Ions Score: 58 **Expect:** 0.00023
Matches : 14/58 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	873.494114	437.250695	856.467565	428.737421	8
3	**242.149918**	121.578597			L	***816.472650***	408.739963	799.446101	400.226689	7
4	**370.208496**	185.607886	353.181947	177.094612	Q	***703.388586***	352.197931	686.362037	343.684657	6
5	**517.276910**	259.142093	500.250361	250.628819	F	***575.330008***	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	***428.261594***	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	***331.208830***	166.108053	314.182281	157.594778	3
8	**770.419552**	385.713414	753.393003	377.200140	G	***232.140416***	116.573846	215.113867	108.060571	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	943.523956	-0.002228	AGLQFPVGR
22.9	943.519928	0.001800	QLDRTVGR
22.8	943.527298	-0.005570	QIQACLLR
22.8	943.519897	0.001831	QLKAQNSR
21.0	943.527313	-0.005585	GLAKGMPVR
17.2	943.523941	-0.002213	KISPWTGR
17.2	943.519913	0.001815	QLSRDIGR
16.1	943.523926	-0.002198	KIQNQWK
16.1	943.512695	0.009033	QIQKEIW
16.1	943.512695	0.009033	QLKKPEW

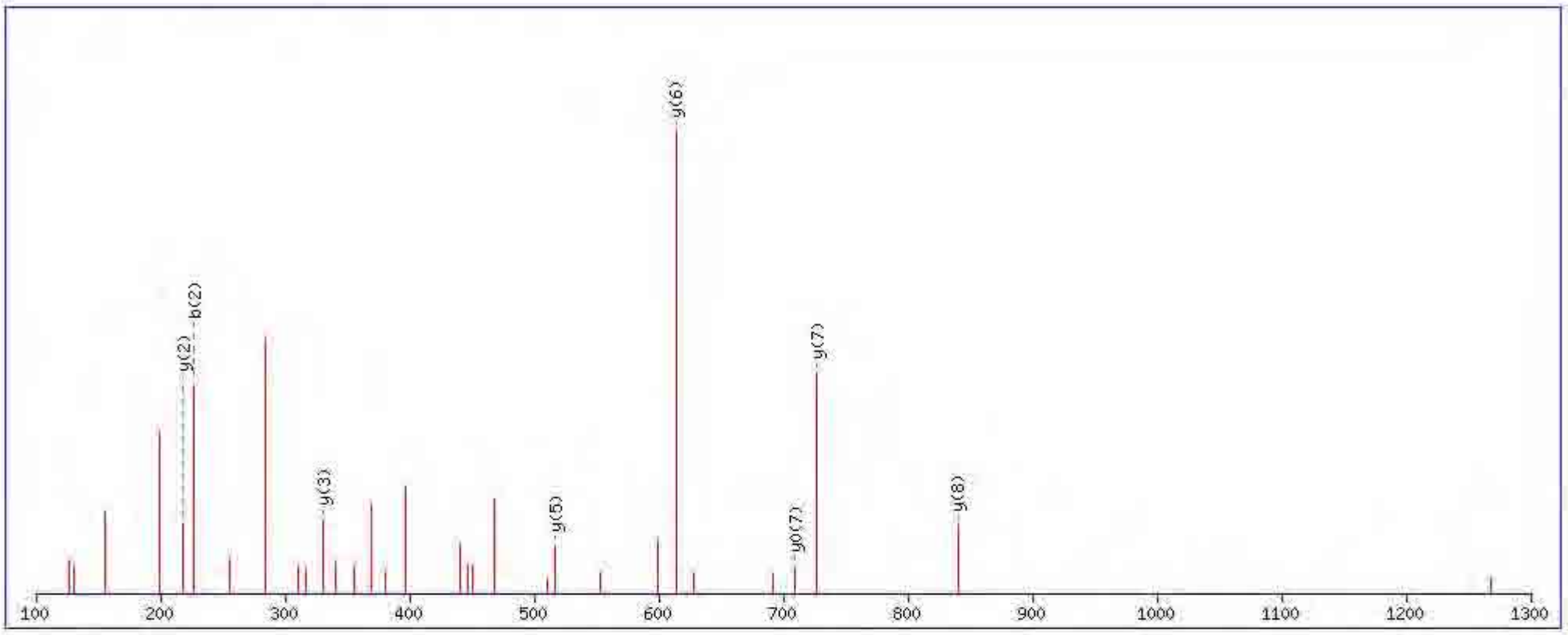
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLPGELAK**
Found in **H2B1A_HUMAN**, Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

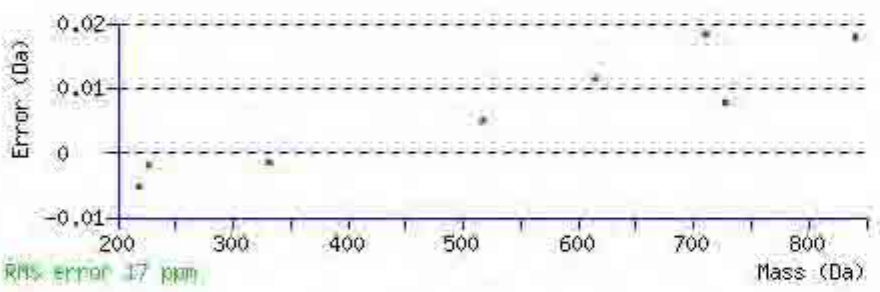
Match to Query 4263: 952.593248 from(477.303900,2+) rtinseconds(1642) index(11814)
Title: Locus:1.1.1.1734.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

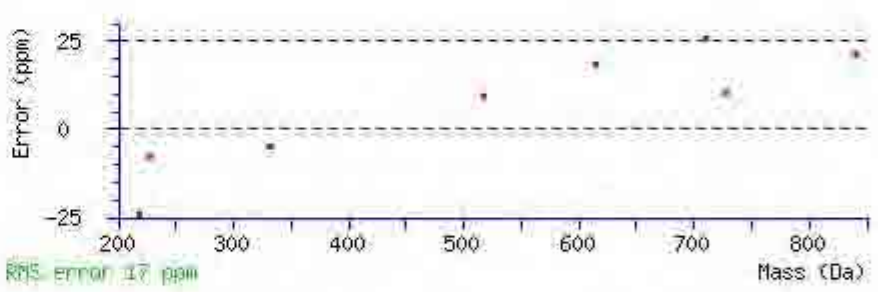
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 952.595688
Ions Score: 34 **Expect:** 0.0054
Matches : 8/64 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*840.518931*	420.763104	823.492382	412.249829	822.508366	411.757821	8
3	340.259468	170.633372			L	*727.434867*	364.221072	710.408318	355.707797	709.424302	355.215789	7
4	437.312232	219.159754			P	*614.350803*	307.679040	597.324254	299.165765	596.340238	298.673757	6
5	494.333696	247.670486			G	*517.298039*	259.152658	500.271490	250.639383	499.287474	250.147375	5
6	623.376289	312.191783	605.365724	303.186500	E	460.276575	230.641926	443.250026	222.128651	442.266010	221.636643	4
7	736.460353	368.733815	718.449788	359.728532	L	*331.233982*	166.120629	314.207433	157.607354			3
8	807.497467	404.252372	789.486902	395.247089	A	*218.149918*	109.578597	201.123369	101.065322			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLLPGELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	952.595688	-0.002440	LLLPGELAK
20.2	952.595688	-0.002440	ILLLEAGPK
20.2	952.595703	-0.002455	ILLTLVANP
18.0	952.595703	-0.002455	ILGILPPSK
17.4	952.595703	-0.002455	ILGILPPSK
16.7	952.595688	-0.002440	IIIPEIQK
16.7	952.595703	-0.002455	ILPPKSLGI
16.7	952.595703	-0.002455	IPLVLPASK
16.7	952.595688	-0.002440	LILPKPEK
16.7	952.595688	-0.002440	LILPKPEK

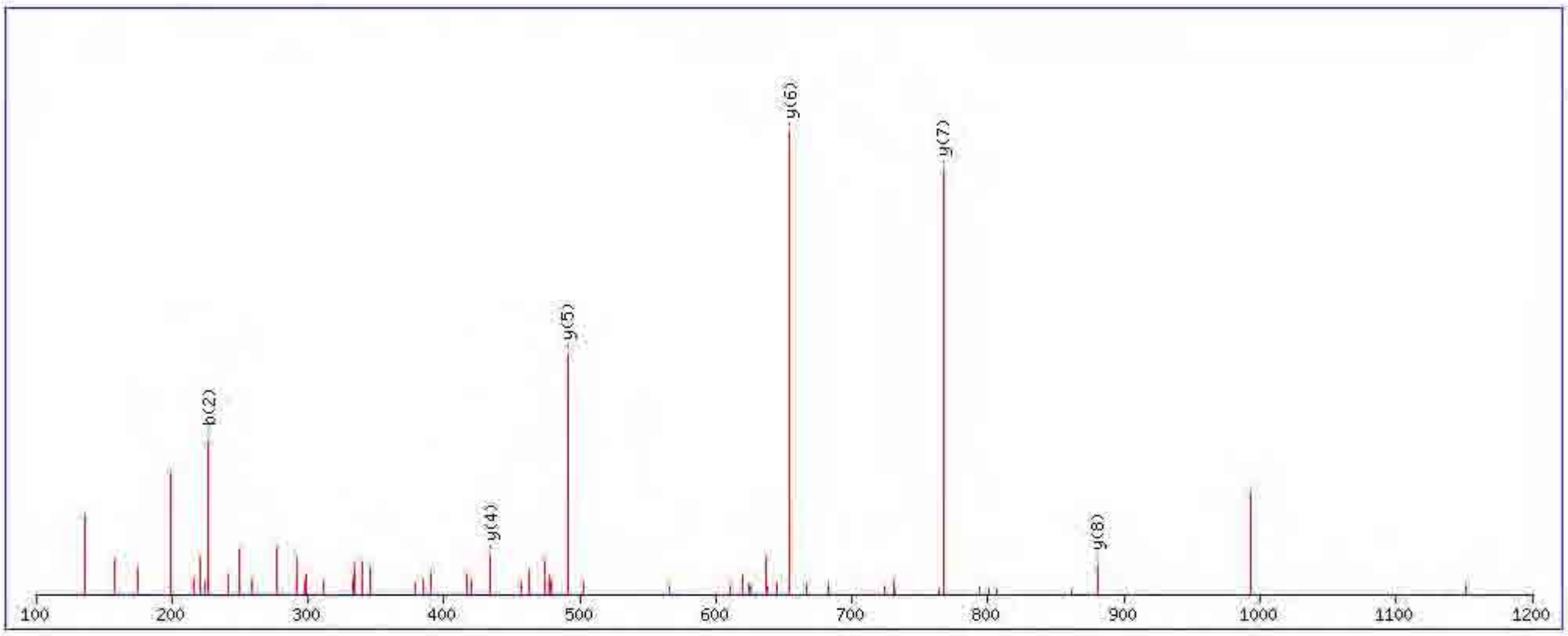
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

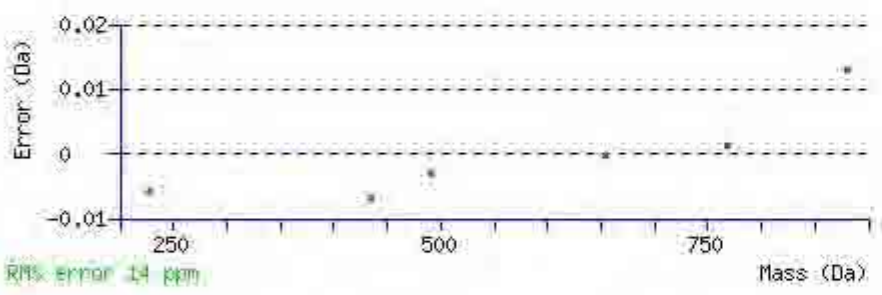
Match to Query 5095: 992.563728 from(497.289140,2+) rtinseconds(1299) index(7607)
Title: Locus:1.1.1.1545.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

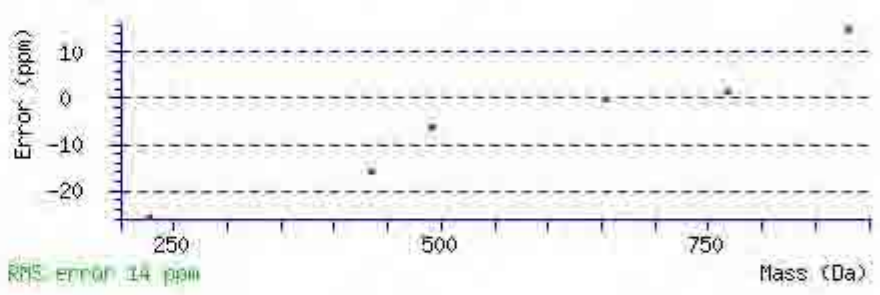
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 39 **Expect:** 0.0089
Matches : 6/66 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	363.198659	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	992.565460	-0.001732	LLIYGASTR
39.1	992.565460	-0.001732	LLIYGATSR
16.2	992.565460	-0.001732	LITYLNTR
15.5	992.554245	0.009483	ILPPLSPPQ
15.4	992.554245	0.009483	ILPPLSPPQ
15.4	992.565475	-0.001747	ILPSVSHKP
15.4	992.565475	-0.001747	LLPHVSSPK
13.4	992.569504	-0.005776	IILNAVFGF
13.2	992.554245	0.009483	ILPPLSPPQ
13.1	992.566803	-0.003075	ILPHWRR

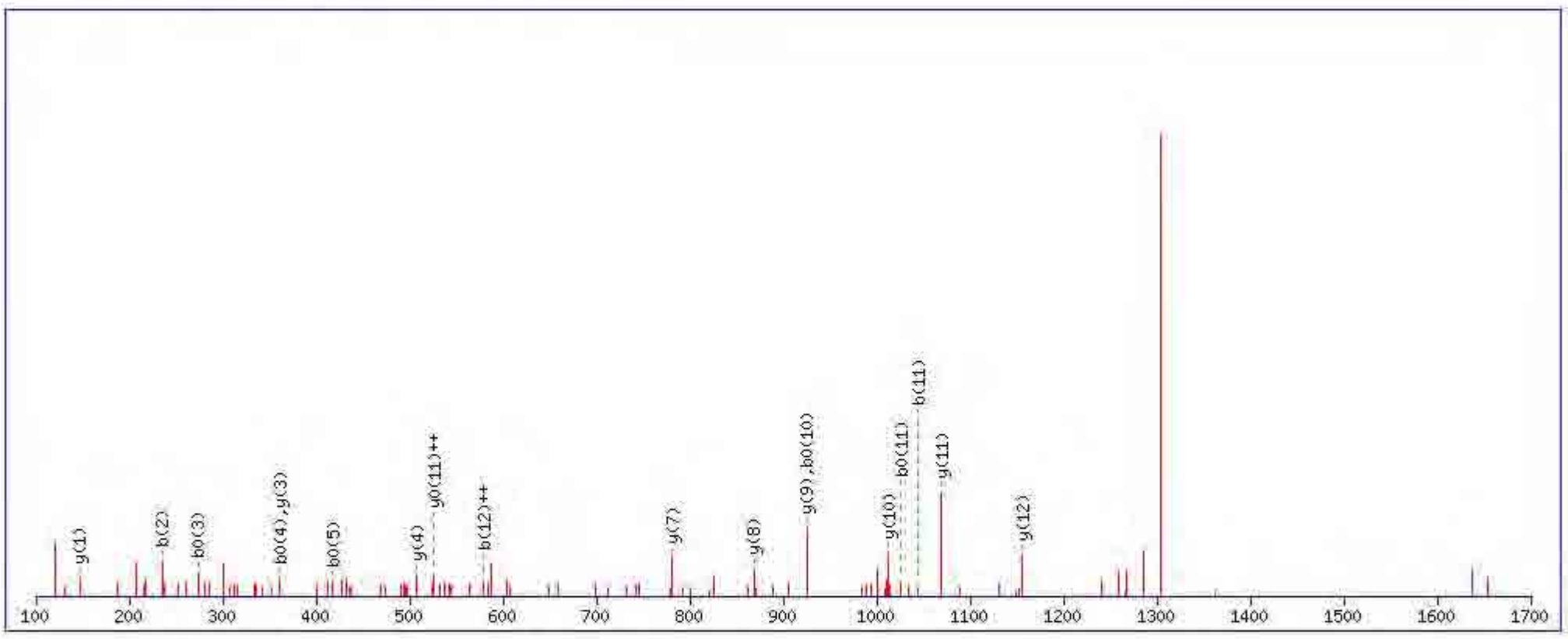
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSGSGTDFTLK**
Found in **KV201_HUMAN**, Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1

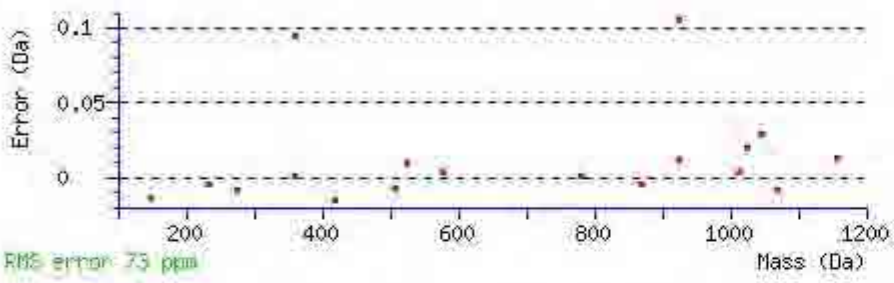
Match to Query 12683: 1302.601368 from(652.307960,2+) rtinseconds(1347) index(8090)
Title: Locus:1.1.1.1572.20
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

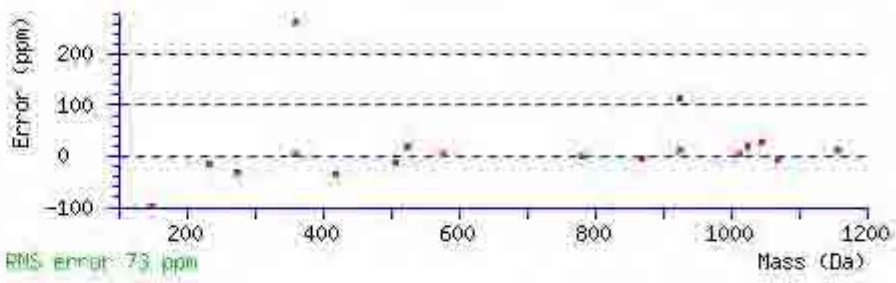
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1302.609222
Ions Score: 53 Expect: 0.0001
Matches : 18/114 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							13
2	235.107718	118.057497	217.097153	109.052214	S	*1156.548059*	578.777667	1139.521510	570.264393	1138.537494	569.772385	12
3	292.129182	146.568229	274.118617	137.562946	G	*1069.516031*	535.261653	1052.489482	526.748379	1051.505466	526.256371	11
4	379.161210	190.084243	361.150645	181.078960	S	*1012.494567*	506.750921	995.468018	498.237647	994.484002	497.745639	10
5	436.182674	218.594975	418.172109	209.589692	G	*925.462539*	463.234907	908.435990	454.721633	907.451974	454.229625	9
6	523.214702	262.110989	505.204137	253.105707	S	*868.441075*	434.724176	851.414526	426.210901	850.430510	425.718893	8
7	580.236166	290.621721	562.225601	281.616439	G	*781.409047*	391.208161	764.382498	382.694887	763.398482	382.202879	7
8	681.283845	341.145561	663.273280	332.140278	T	724.387583	362.697429	707.361034	354.184155	706.377018	353.692147	6
9	796.310788	398.659032	778.300223	389.653750	D	623.339904	312.173590	606.313355	303.660315	605.329339	303.168307	5
10	943.379202	472.193239	925.368637	463.187956	F	*508.312961*	254.660118	491.286412	246.146844	490.302396	245.654836	4
11	1044.426881	522.717078	1026.416316	513.711796	T	*361.244547*	181.125911	344.217998	172.612637	343.233982	172.120629	3
12	1157.510945	579.259110	1139.500380	570.253828	L	260.196868	130.602072	243.170319	122.088797			2
13					K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FSGSGSGTDFTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	1302.609222	-0.007854	FSGSGSGTDFTLK
52.7	1302.609222	-0.007854	FSGSGSGTBFTLK
9.4	1302.594803	0.006565	MCLGSKASTFAST
9.2	1302.597977	0.003391	FTAESYTVLGDT
8.0	1302.591431	0.009937	FSAKMPNASFST
8.0	1302.593948	0.007420	DGTSLPETPNPK
7.2	1302.606689	-0.005321	FSLGYMPYPGR
6.8	1302.591446	0.009922	FLVPDHVNMSE
6.8	1302.591431	0.009937	FSAKMPNASFST
6.8	1302.609192	-0.007824	SFSGFSISQSKE

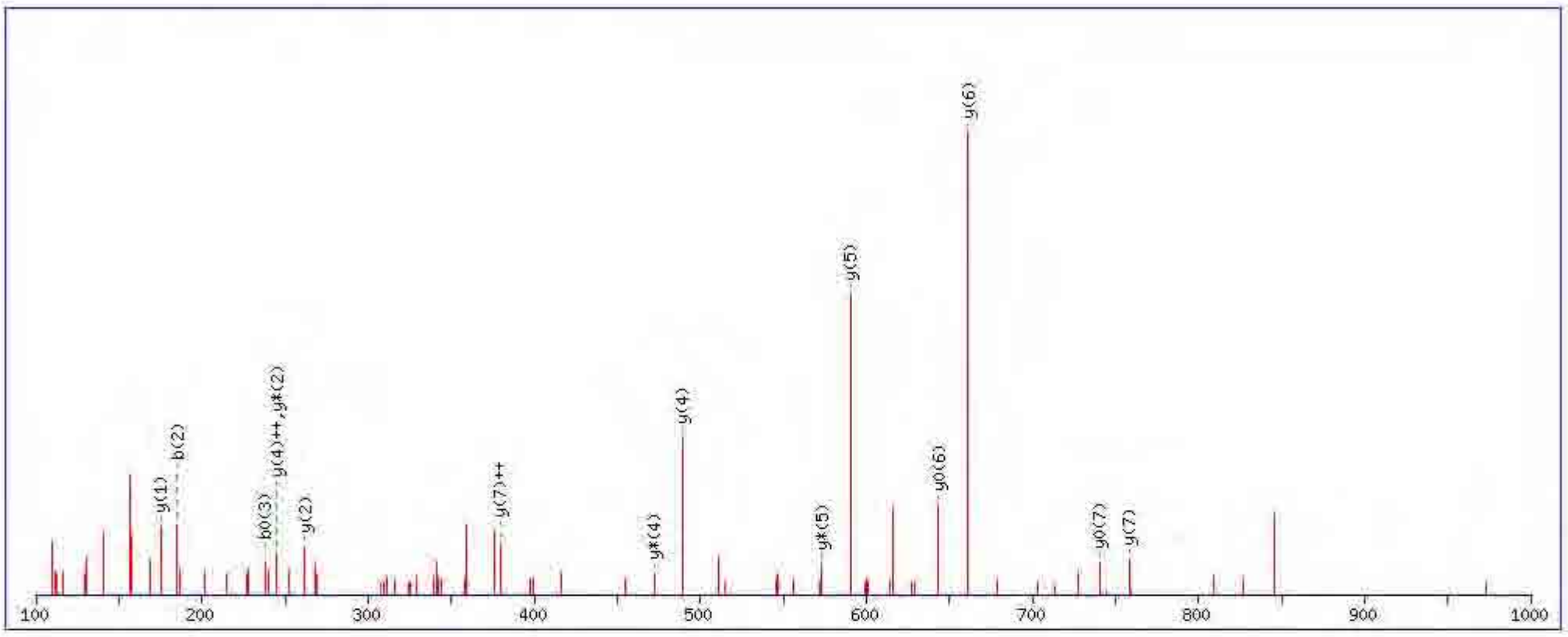
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPATVQSR**
Found in **K1C23_HUMAN**, Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2

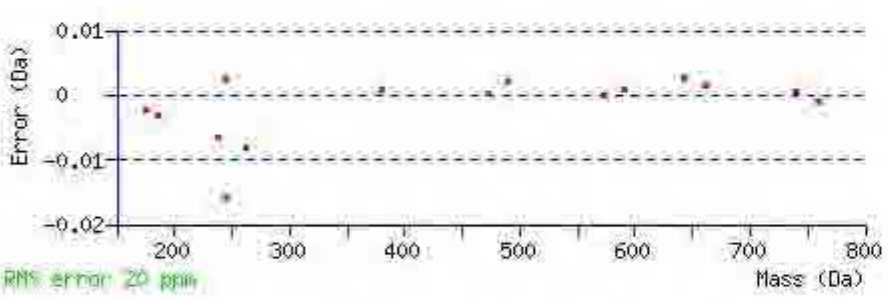
Match to Query 1916: 844.438288 from(423.226420,2+) rtinseconds(392) index(330)
Title: Locus:1.1.1.1036.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

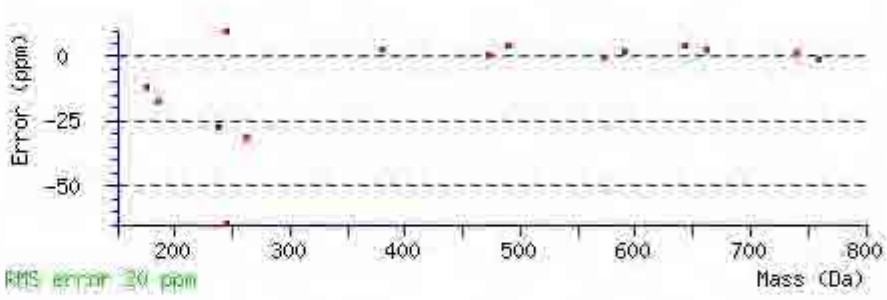
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 844.440277
Ions Score: 44 **Expect:** 0.008
Matches : 15/72 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	185.092068	93.049672			167.081503	84.044389	P	*758.415529*	379.711403	741.388980	371.198128	740.404964	370.706120	7
3	256.129182	128.568229			238.118617	119.562947	A	*661.362765*	331.185021	644.336216	322.671746	643.352200	322.179738	6
4	357.176861	179.092068			339.166296	170.086786	T	*590.325651*	295.666464	573.299102	287.153189	572.315086	286.661181	5
5	456.245275	228.626275			438.234710	219.620993	V	*489.277972*	245.142624	472.251423	236.629350	471.267407	236.137342	4
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	Q	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
7	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPATVQSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.8	844.440277	-0.001989	SPATVQSR
30.9	844.440262	-0.001974	SPATADKR
30.1	844.440277	-0.001989	SVIGPNSR
25.4	844.440262	-0.001974	SPASSLQR
20.9	844.440277	-0.001989	TKSPGPSR
20.4	844.440262	-0.001974	SPSSKRPS
13.9	844.440262	-0.001974	APASSPKR
13.5	844.440262	-0.001974	APSLTNSR
13.4	844.440262	-0.001974	SAPPSKSR
13.1	844.433731	0.004557	MARGARPS

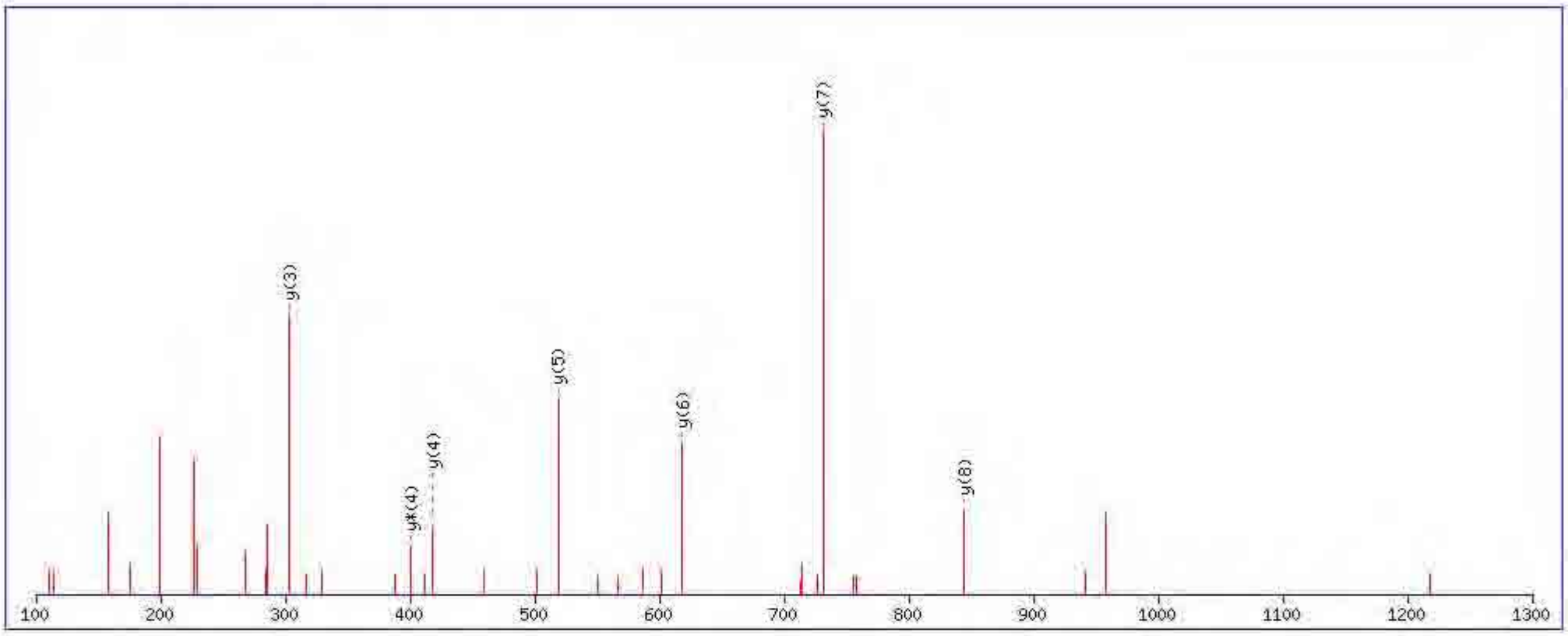
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLVTDGAR**
Found in **LAMA5_HUMAN**, Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8

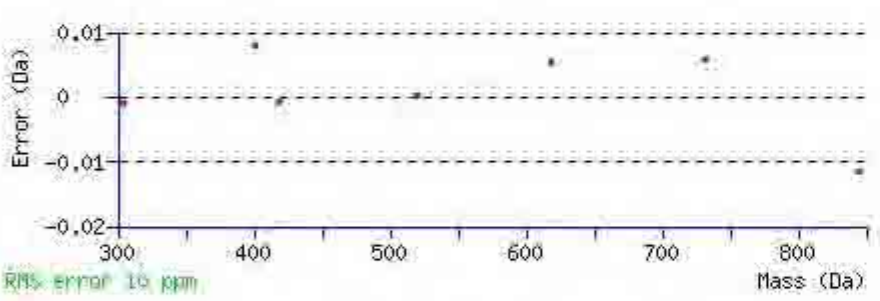
Match to Query 4343: 956.562608 from(479.288580,2+) rtinseconds(1305) index(7688)
Title: Locus:1.1.1.1548.12
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

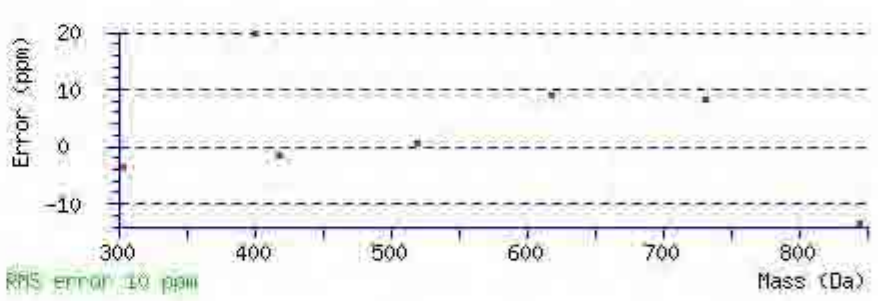
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 956.565475
Ions Score: 56 **Expect:** 0.00033
Matches : 7/66 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	227.175404	114.091340			L	*844.488694*	422.747985	827.462145	414.234711	826.478129	413.742703	8
3	340.259468	170.633372			L	*731.404630*	366.205953	714.378081	357.692679	713.394065	357.200671	7
4	439.327882	220.167579			V	*618.320566*	309.663921	601.294017	301.150647	600.310001	300.658639	6
5	540.375561	270.691419	522.364996	261.686136	T	*519.252152*	260.129714	502.225603	251.616440	501.241587	251.124432	5
6	655.402504	328.204890	637.391939	319.199608	D	*418.204473*	209.605874	401.177924	201.092600	400.193908	200.600592	4
7	712.423968	356.715622	694.413403	347.710340	G	*303.177530*	152.092403	286.150981	143.579128			3
8	783.461082	392.234179	765.450517	383.228897	A	246.156066	123.581671	229.129517	115.068396			2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILLVTDGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	956.565475	-0.002867	ILLVTDGAR
39.0	956.554230	0.008378	ILLSLDGNL
24.5	956.565460	-0.002852	LLPSDLKR
24.5	956.565460	-0.002852	LPLDSLKR
24.1	956.565445	-0.002837	LLELGEKR
24.1	956.565460	-0.002852	ILLLSQDR
24.1	956.565475	-0.002867	IPITVKDR
24.1	956.565460	-0.002852	LLPSLKDR
24.1	956.554245	0.008363	PIISLTGPK
22.0	956.554230	0.008378	IILDEAGVK

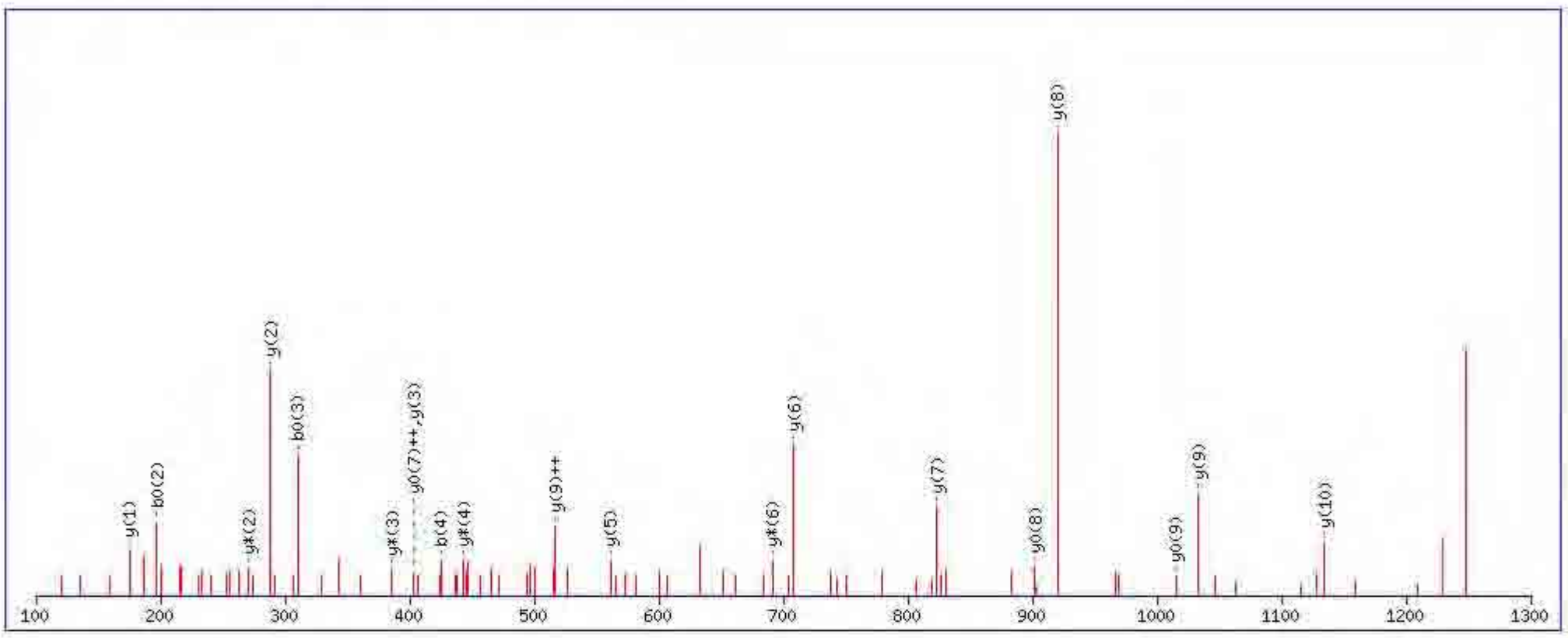
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLPDFTGDLR**
Found in **LBP_HUMAN**, Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3

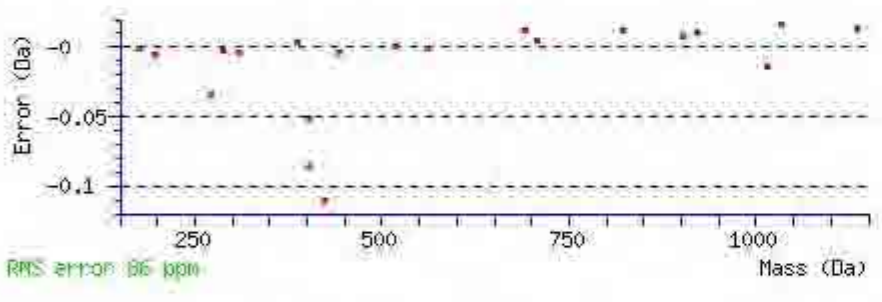
Match to Query 11426: 1246.664008 from(624.339280,2+) rtinseconds(2094) index(17465)
Title: Locus:1.1.1.1981.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

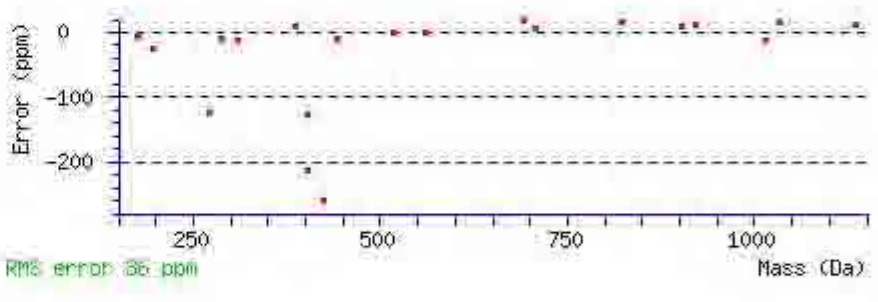
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1246.655762
Ions Score: 57 **Expect:** 0.00018
Matches : 20/94 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	*1134.578966*	567.793121	1117.552417	559.279847	1116.568401	558.787839	10
3	328.223083	164.615179	310.212518	155.609897	L	*1033.531287*	517.269282	1016.504738	508.756007	1015.520722	508.263999	9
4	425.275847	213.141561	407.265282	204.136279	P	*920.447223*	460.727249	903.420674	452.213975	902.436658	451.721967	8
5	540.302790	270.655033	522.292225	261.649750	D	*823.394459*	412.200868	806.367910	403.687593	805.383894	403.195585	7
6	687.371204	344.189240	669.360639	335.183957	F	*708.367516*	354.687396	691.340967	346.174122	690.356951	345.682114	6
7	788.418883	394.713079	770.408318	385.707797	T	*561.299102*	281.153189	544.272553	272.639915	543.288537	272.147907	5
8	845.440347	423.223812	827.429782	414.218529	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	960.467290	480.737283	942.456725	471.732000	D	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1073.551354	537.279315	1055.540789	528.274032	L	*288.203016*	144.605146	271.176467	136.091871			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLPDFTGDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	1246.655762	0.008246	ITLPDFTGDLR
15.6	1246.655762	0.008246	PTPPGQPPISPK
12.5	1246.659103	0.004905	LSLECSLVDIR
10.9	1246.659103	0.004905	LTPEIMKEVR
10.8	1246.674362	-0.010354	PVMYAVALDLR
8.5	1246.653076	0.010932	PTPGQRLHPGR
7.9	1246.670349	-0.006341	IPTQMQRLTK
7.9	1246.659119	0.004889	VDILGLVSEMR
7.8	1246.655731	0.008277	LTIIQDPEYR
7.5	1246.659134	0.004874	TLPIVRDVAMT

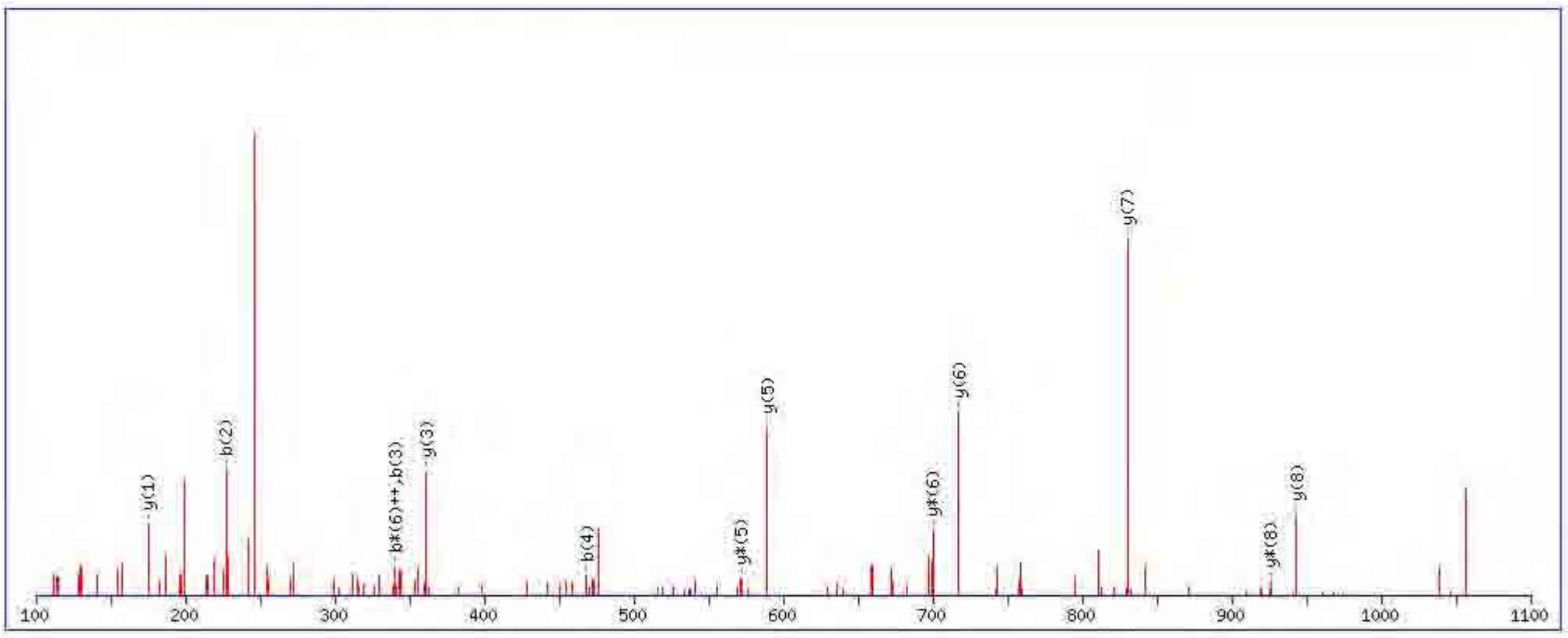
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLIKVEEGR**
Found in **NR4A3_HUMAN**, Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=2 SV=3

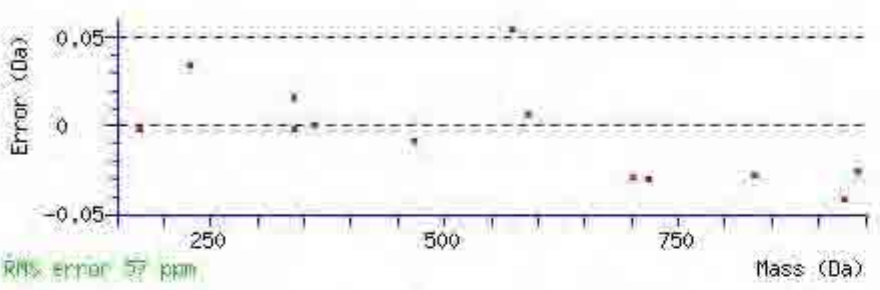
Match to Query 6432: 1055.602088 from(528.808320,2+) rtinseconds(1553) index(10722)
Title: Locus:1.1.1.1685.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

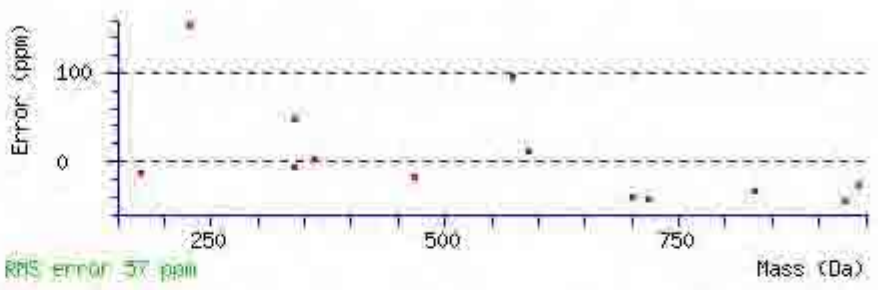
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597488
Variable modifications:
P1 : Oxidation (P)
Ions Score: 42 **Expect:** 0.0073
Matches : 13/76 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.054955	57.531116					P							9
2	227.139019	114.073147					L	*943.557107*	472.282192	926.530558	463.768917	925.546542	463.276909	8
3	340.223083	170.615179					I	*830.473043*	415.740160	813.446494	407.226885	812.462478	406.734877	7
4	468.318046	234.662661	451.291497	226.149386			K	*717.388979*	359.198128	700.362430	350.684853	699.378414	350.192845	6
5	567.386460	284.196868	550.359911	275.683594			V	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	E	490.225602	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	825.471646	413.239461	808.445097	404.726187	807.461081	404.234179	E	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	882.493110	441.750193	865.466561	433.236919	864.482545	432.744911	G	232.140416	116.573846	215.113867	108.060571			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PLIKVEEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1055.597488	0.004600	PLIKVEEGR
41.8	1055.597504	0.004584	LLPQLTSPR
27.0	1055.597488	0.004600	LLKLDPADR
25.5	1055.608704	-0.006616	ILLREAEGR
25.5	1055.608704	-0.006616	LLLRAEGER
23.0	1055.601532	0.000556	ILLGLWVQD
22.1	1055.604874	-0.002786	ILLIKNMDP
21.9	1055.597488	0.004600	LGPLALETAR
19.8	1055.597488	0.004600	PEDKVILAR
16.3	1055.597488	0.004600	LPASLSLPAR

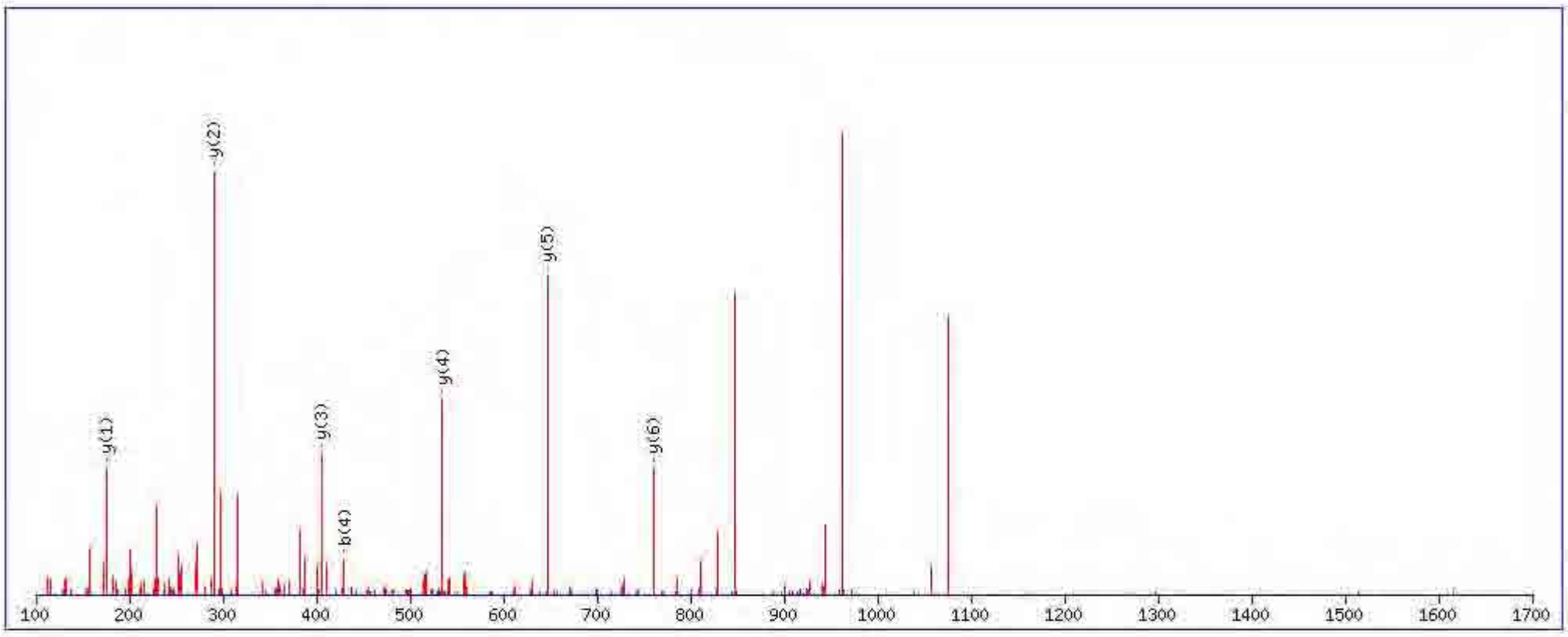
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTVIIEDDR**
Found in **PARD3_HUMAN**, Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2

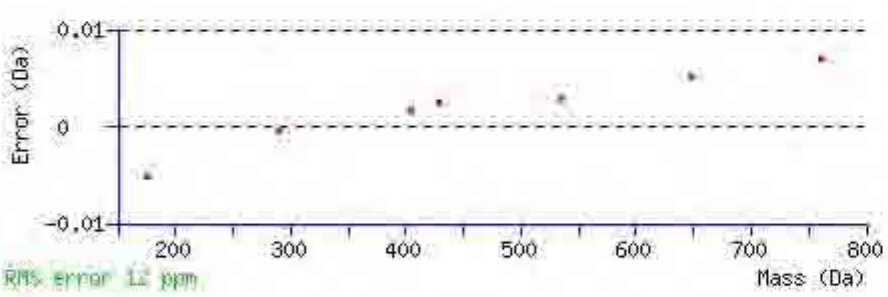
Match to Query 6925: 1074.520268 from(538.267410,2+) rtinseconds(1274) index(7319)
Title: Locus:1.1.1.1531.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

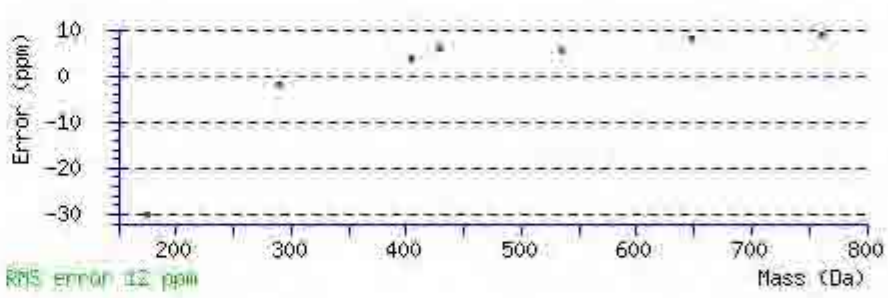
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.519318
Ions Score: 49 **Expect:** 0.003
Matches : 7/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	217.081898	109.044587	199.071333	100.039304	T	960.499652	480.753464	943.473103	472.240190	942.489087	471.748182	8
3	316.150312	158.578794	298.139747	149.573512	V	859.451973	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	429.234376	215.120826	411.223811	206.115544	I	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
5	542.318440	271.662858	524.307875	262.657576	I	*647.299495*	324.153386	630.272946	315.640111	629.288930	315.148103	5
6	671.361033	336.184155	653.350468	327.178872	E	*534.215431*	267.611354	517.188882	259.098079	516.204866	258.606071	4
7	786.387976	393.697626	768.377411	384.692343	D	*405.172838*	203.090057	388.146289	194.576782	387.162273	194.084774	3
8	901.414919	451.211097	883.404354	442.205815	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DTVIIEDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.7	1074.519318	0.000950	DTVIIEDDR
33.7	1074.519287	0.000981	LEEGLEETR
29.2	1074.523331	-0.003063	EKLYPPSPP
28.8	1074.526688	-0.006420	LDSMAIEALP
21.8	1074.512772	0.007496	NSLNPEVMR
21.7	1074.526703	-0.006435	GSPMEISLPI
21.7	1074.530548	-0.010280	LTTPPSSNSR
21.4	1074.519333	0.000935	VTDPQGKSDI
20.7	1074.520645	-0.000377	LWTRNDDR
20.7	1074.513443	0.006825	PEWLDFPR

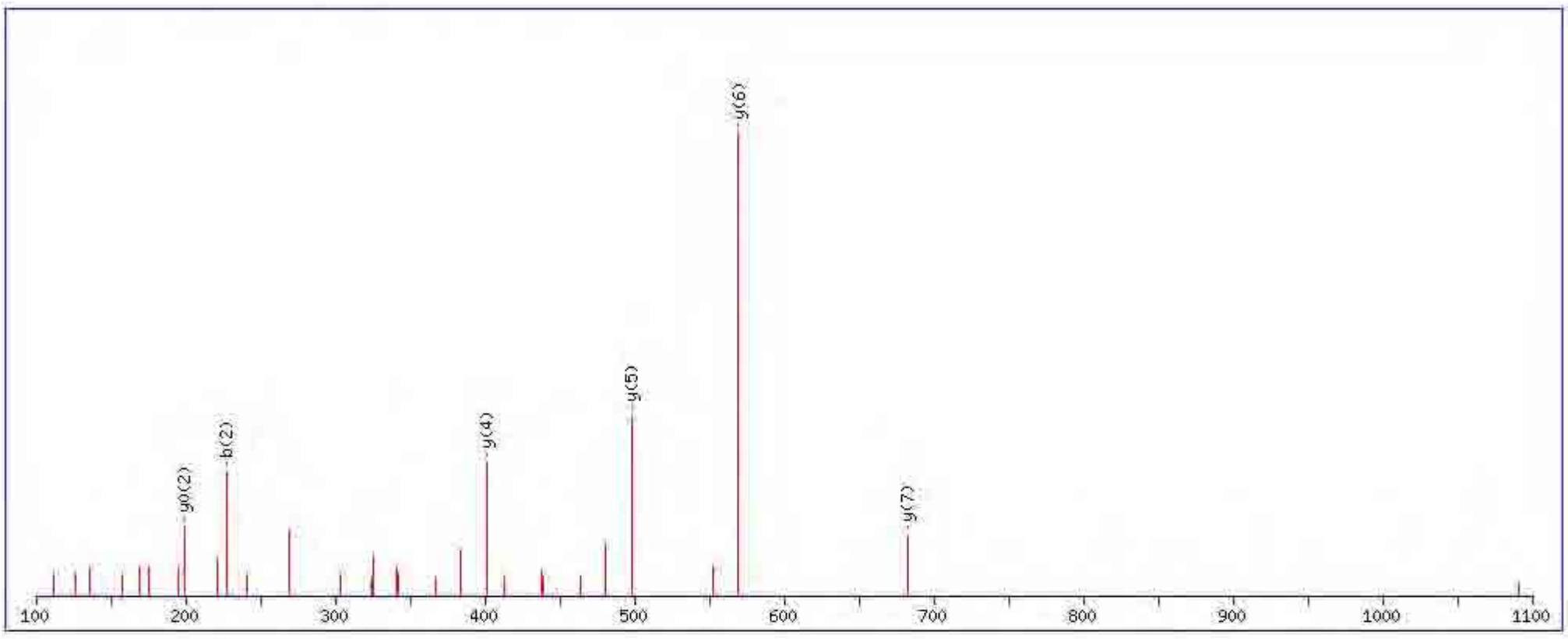
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLAPPSTP**
Found in **F110D_HUMAN**, Protein FAM110D OS=Homo sapiens GN=FAM110D PE=2 SV=1

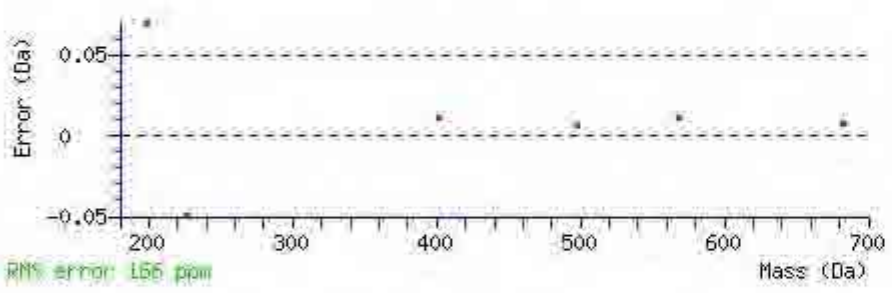
Match to Query 987: 794.455088 from(398.234820,2+) rtinseconds(804) index(2924)
Title: Locus:1.1.1.1264.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

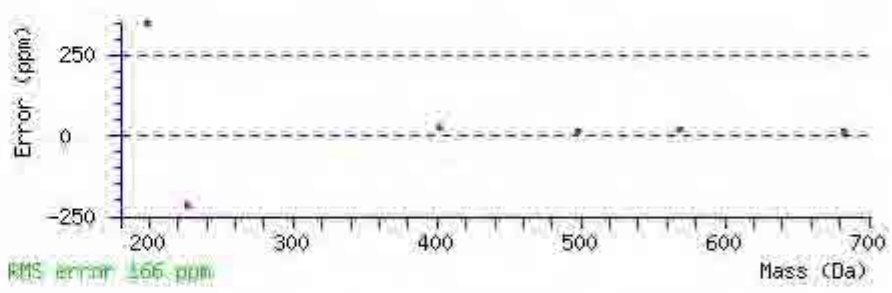
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 794.453796
Ions Score: 41 **Expect:** 0.0036
Matches : 6/44 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L					8
2	227.175404	114.091340			L	*682.377018*	341.692147	664.366453	332.686865	7
3	298.212518	149.609897			A	*569.292954*	285.150115	551.282389	276.144833	6
4	395.265282	198.136279			P	*498.255840*	249.631558	480.245275	240.626276	5
5	492.318046	246.662661			P	*401.203076*	201.105176	383.192511	192.099894	4
6	579.350074	290.178675	561.339509	281.173393	S	304.150312	152.578794	286.139747	143.573512	3
7	680.397753	340.702515	662.387188	331.697232	T	217.118284	109.062780	199.107719	100.057498	2
8					P	116.070605	58.538941			1





NCBI **BLAST** search of LLAPPSTP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	794.453796	0.001292	LLAPPSTP
20.5	794.453796	0.001292	LLAEPVPG
15.0	794.453796	0.001292	LISSTFK
14.1	794.453812	0.001276	IAPPPVVS
11.8	794.447250	0.007838	IIKCYR
11.8	794.447250	0.007838	ILYCKR
11.8	794.447266	0.007822	LIPCPPR
11.8	794.447266	0.007822	LLCPPPR
11.8	794.455124	-0.000036	LLHWAR
11.8	794.447250	0.007838	LLYCKR

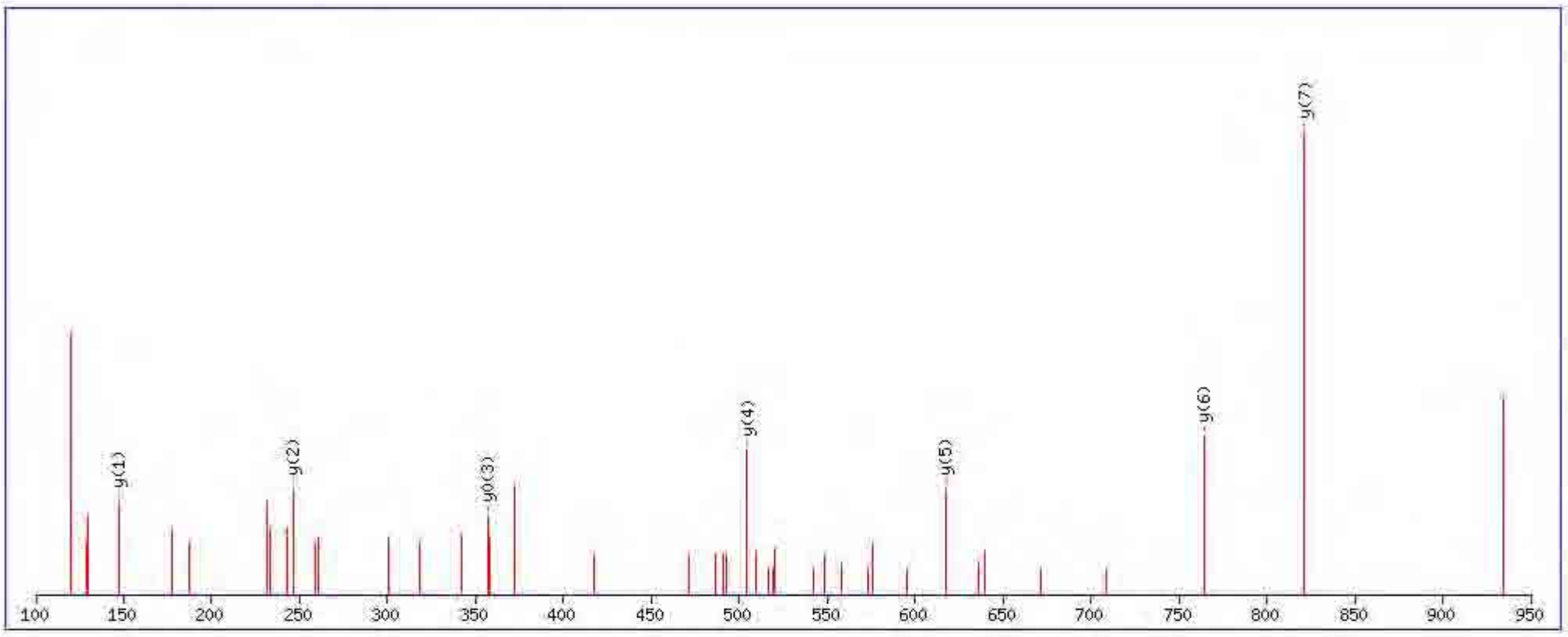
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGFIEEVK**
Found in **SPB12_HUMAN**, Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1

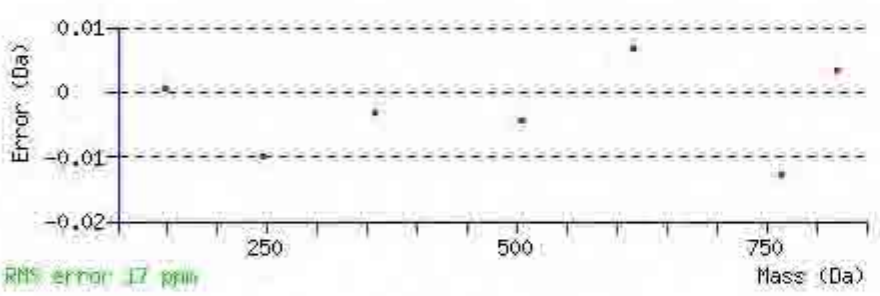
Match to Query 3865: 933.518168 from(467.766360,2+) rtinseconds(1509) index(10180)
Title: Locus:1.1.1.1661.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

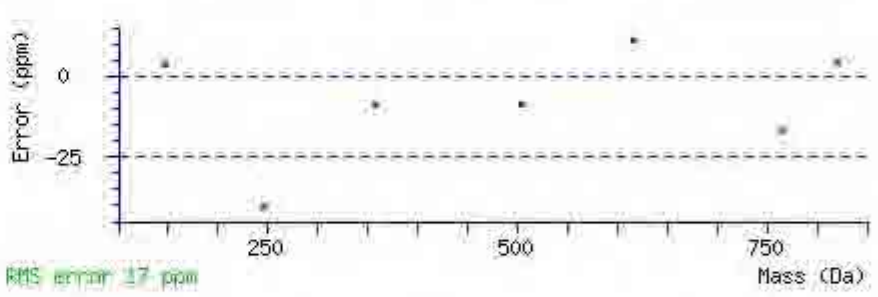
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 933.517120
Ions Score: 40 **Expect:** 0.0072
Matches : 7/58 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							8
2	171.112804	86.060040			G	*821.440346*	411.223811	804.413797	402.710537	803.429781	402.218529	7
3	318.181218	159.594247			F	*764.418882*	382.713079	747.392333	374.199805	746.408317	373.707797	6
4	431.265282	216.136279			I	*617.350468*	309.178872	600.323919	300.665598	599.339903	300.173590	5
5	560.307875	280.657576	542.297310	271.652293	E	*504.266404*	252.636840	487.239855	244.123565	486.255839	243.631557	4
6	689.350468	345.178872	671.339903	336.173590	E	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
7	788.418882	394.713079	770.408317	385.707797	V	*246.181218*	123.594247	229.154669	115.080972			2
8					K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IGFIEEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	933.517120	0.001048	IGFIEEVK
37.3	933.517120	0.001048	LGFLAEALT
15.6	933.517120	0.001048	IGFELVEK
15.2	933.513092	0.005076	LGKSSSLDK
12.5	933.513107	0.005061	LGSSVTDKK
11.3	933.517151	0.001017	IGSVVVYPT
11.0	933.517151	0.001017	IFGVLAVDT
10.9	933.517120	0.001048	VAFLLDEK
10.9	933.514435	0.003733	IGRHPNPK
10.6	933.520493	-0.002325	LLDMSLVK

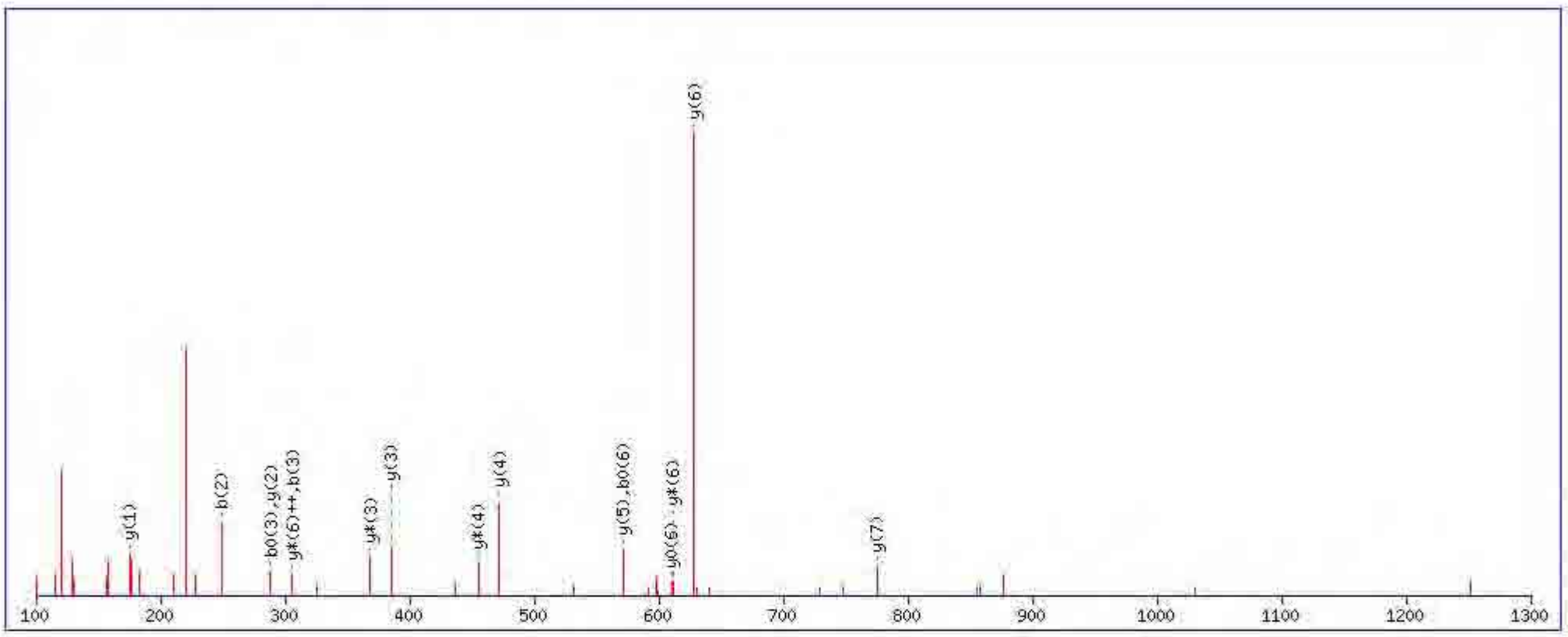
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFGVSPLR**
Found in **XP32_HUMAN**, Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1

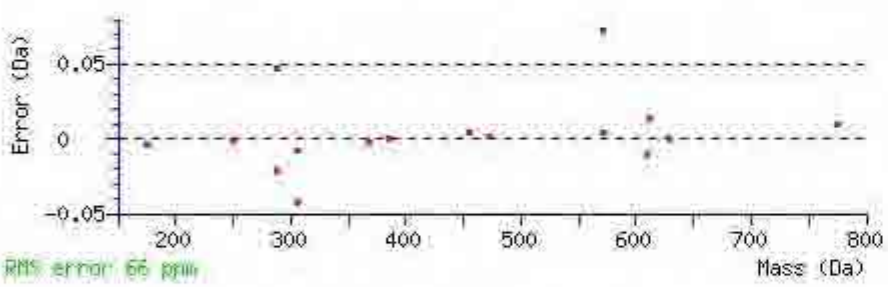
Match to Query 2598: 875.484628 from(438.749590,2+) rtinseconds(1303) index(7659)
Title: Locus:1.1.1.1547.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

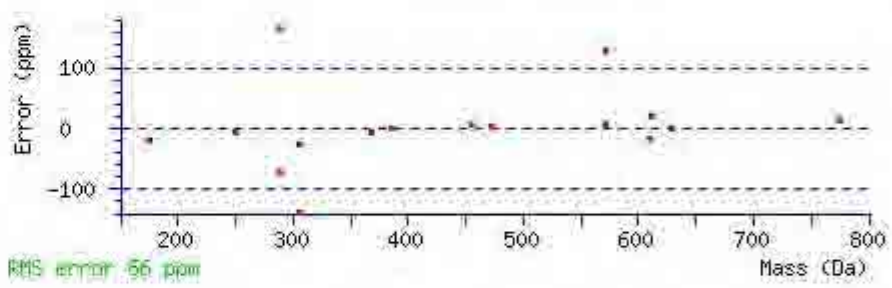
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 875.486511
Ions Score: 57 **Expect:** 0.00027
Matches : 16/64 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	**249.123369**	125.065322	231.112804	116.060040	F	*775.446100*	388.226688	758.419551	379.713414	757.435535	379.221406	7
3	**306.144833**	153.576054	288.134268	144.570772	G	*628.377686*	314.692481	611.351137	306.179207	610.367121	305.687199	6
4	405.213247	203.110261	387.202682	194.104979	V	*571.356222*	286.181749	554.329673	277.668475	553.345657	277.176467	5
5	492.245275	246.626275	474.234710	237.620993	S	*472.287808*	236.647542	455.261259	228.134268	454.277243	227.642260	4
6	589.298039	295.152658	571.287474	286.147375	P	*385.255780*	193.131528	368.229231	184.618254			3
7	702.382103	351.694690	684.371538	342.689407	L	*288.203016*	144.605146	271.176467	136.091872			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TFGVSPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	875.486511	-0.001883	TFGVSPLR
18.8	875.486481	-0.001853	FEKSPLR
15.3	875.486481	-0.001853	KEFSIPR
15.0	875.486481	-0.001853	KSEFPIR
14.6	875.486496	-0.001868	FTAPTAIR
10.2	875.486511	-0.001883	FTLGPVSR
9.9	875.486496	-0.001868	TFIPDKR
9.6	875.486496	-0.001868	PPPLSPPR
9.6	875.486496	-0.001868	SGLFSPIR
9.1	875.478653	0.005975	KPVMVIGT

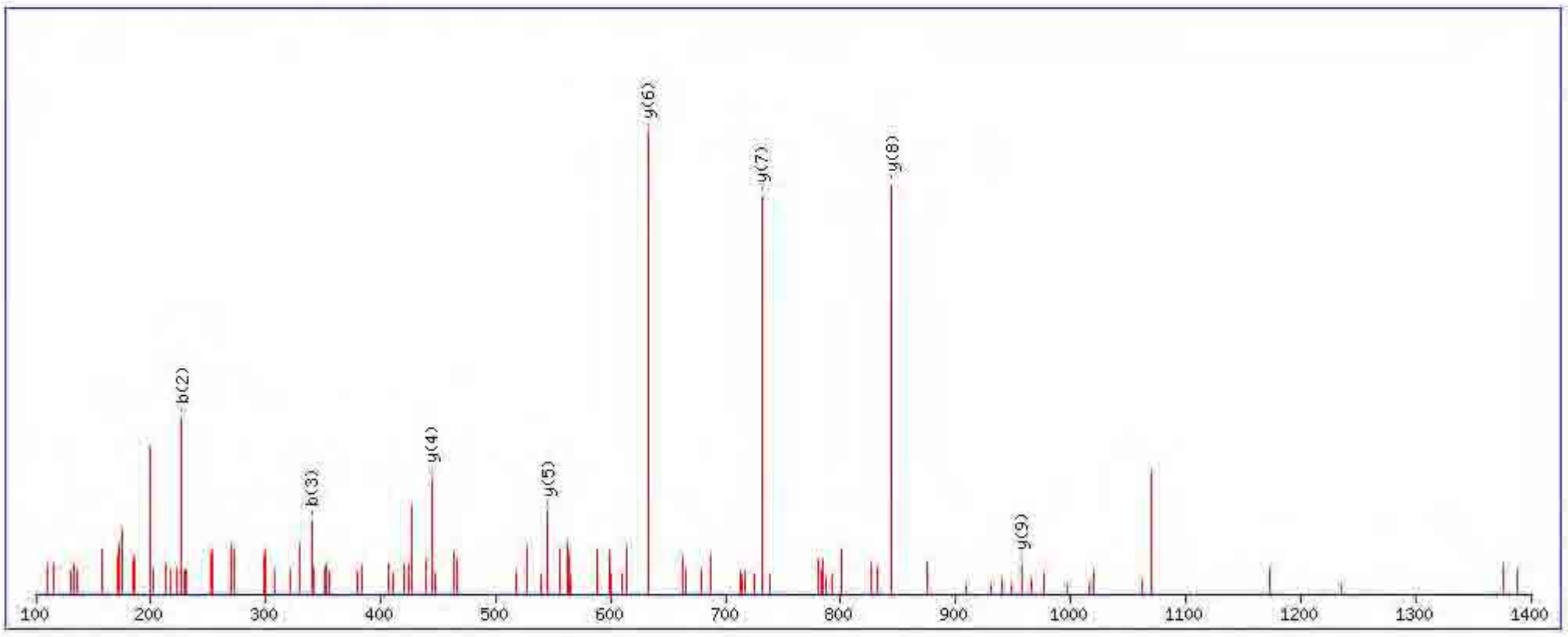
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

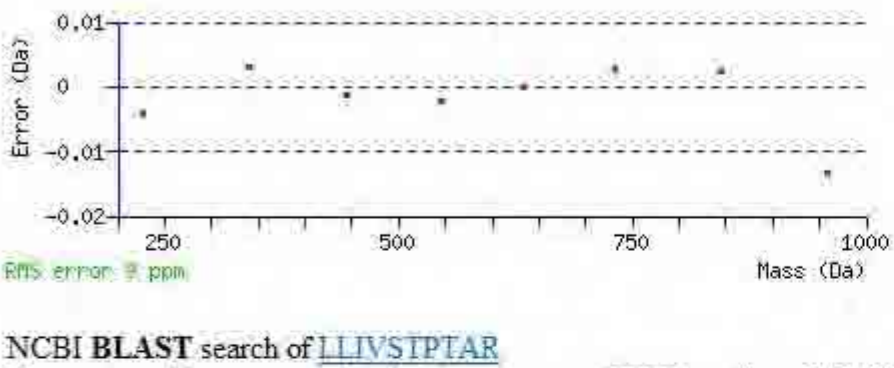
Match to Query 6791: 1069.646548 from(535.830550,2+) rtinseconds(1394) index(8728)
Title: Locus:1.1.1.1598.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

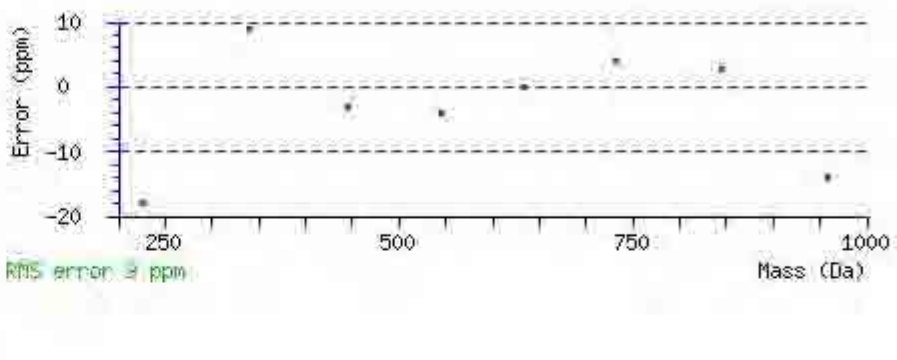
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 53 **Expect:** 0.00026
Matches : 8/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	844.488694	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	731.404630	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	632.336216	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	444.256509	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	1069.649536	-0.002988	LLIVSTPTAR
23.9	1069.638321	0.008227	IPLVPSKVSV
23.9	1069.638306	0.008242	LLPVLLSTAQ
22.6	1069.649506	-0.002958	LLLDALREK
22.6	1069.653564	-0.007016	LLLWVSVVAA
22.6	1069.649521	-0.002973	PLLSVKELR
16.7	1069.639633	0.006915	LLWPTRLR
13.8	1069.649521	-0.002973	LLIIRSAPAT
11.6	1069.638290	0.008258	IIIDGIDIAK
11.6	1069.649521	-0.002973	IIIQLLSDR

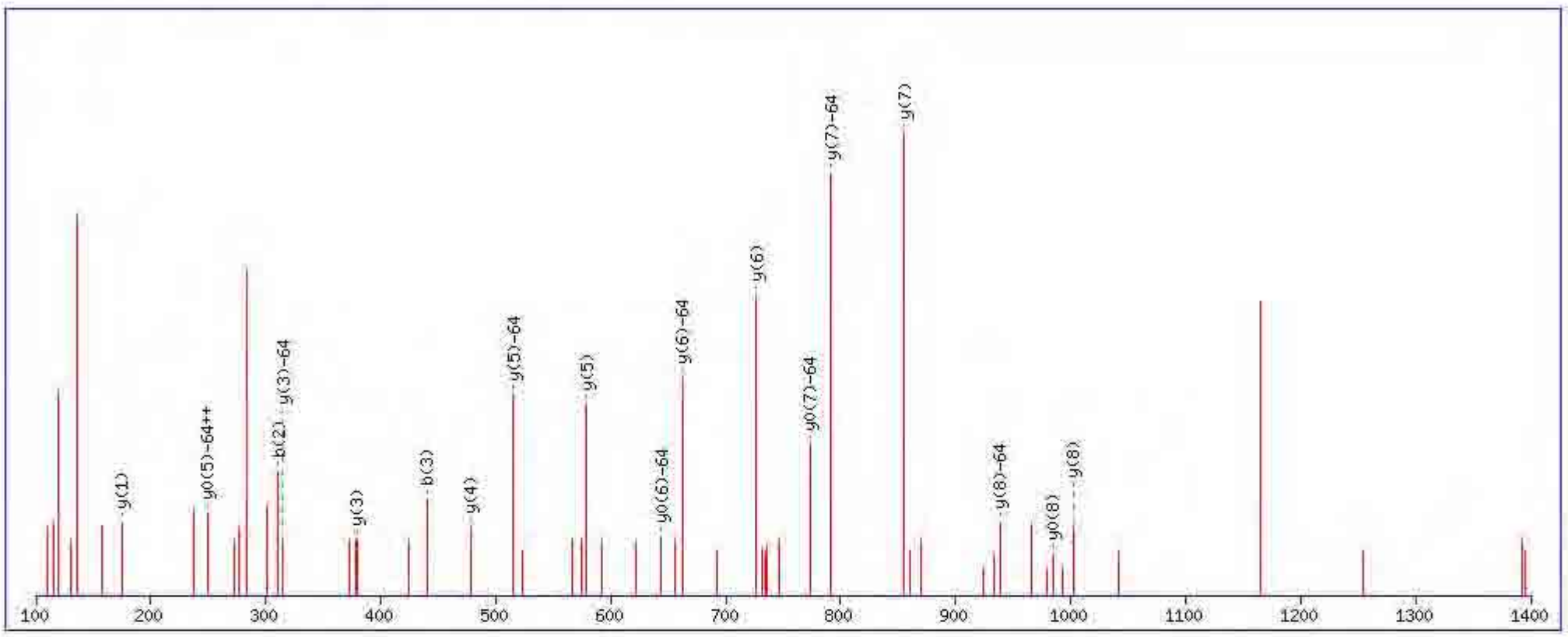
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFEFTVMGR**
Found in **TSP4_HUMAN**, Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2

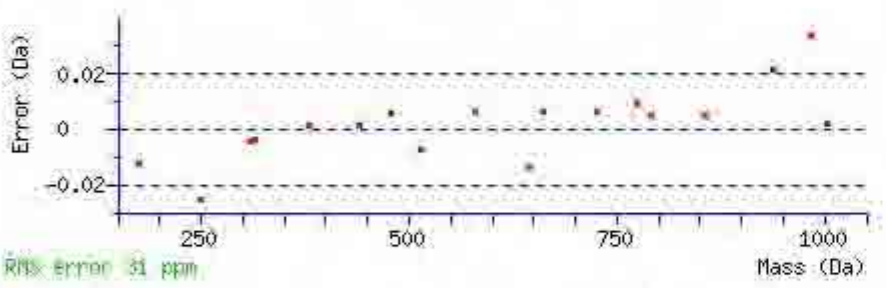
Match to Query 9142: 1164.515828 from(583.265190,2+) rtinseconds(1655) index(11985)
Title: Locus:1.1.1.1741.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

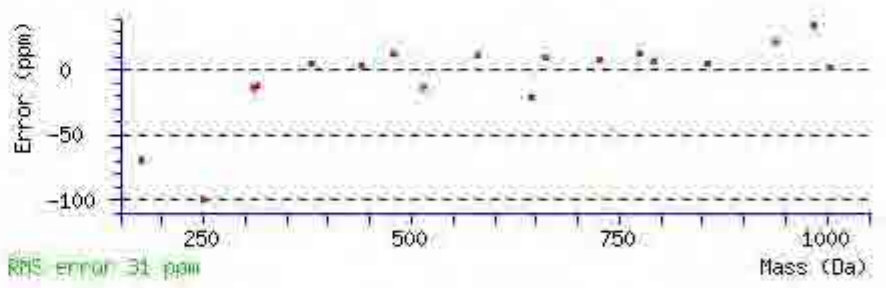
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1164.527390
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 31 **Expect:** 0.0036
Matches : 18/108 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	311.139019	156.073148			F	*1002.471330*	501.739303	985.444781	493.226029	984.460765	492.734021	8
3	440.181612	220.594444	422.171047	211.589162	E	*855.402916*	428.205096	838.376367	419.691822	837.392351	419.199814	7
4	587.250026	294.128651	569.239461	285.123369	F	*726.360323*	363.683800	709.333774	355.170525	708.349758	354.678517	6
5	688.297705	344.652491	670.287140	335.647208	T	*579.291909*	290.149593	562.265360	281.636318	561.281344	281.144310	5
6	787.366119	394.186698	769.355554	385.181415	V	*478.244230*	239.625753	461.217681	231.112479			4
7	934.401519	467.704398	916.390954	458.699115	M	*379.175816*	190.091546	362.149267	181.578272			3
8	991.422983	496.215130	973.412418	487.209847	G	232.140416	116.573846	215.113867	108.060572			2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YFEFTVMGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.2	1164.527390	-0.011562	YFEFTVMGR
4.9	1164.523361	-0.007533	VEQMFQDPR
3.5	1164.526733	-0.010905	LNMDPMTVGR
2.6	1164.519318	-0.003490	NPTNNSMSLR
1.8	1164.523346	-0.007518	EGQYPSICPR
1.0	1164.523361	-0.007533	FSTGPPTECAR
1.0	1164.508072	0.007756	GALSEEQMRE
0.3	1164.516144	-0.000316	FYETFVCEK

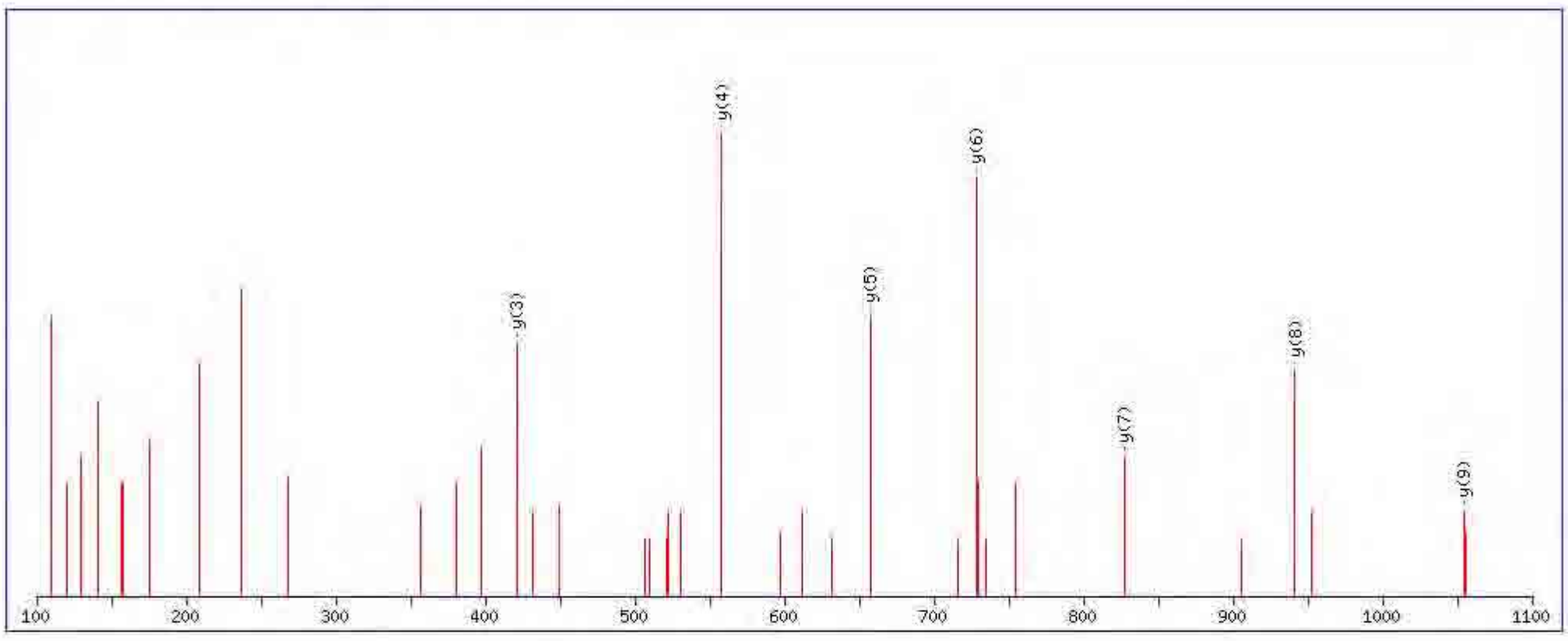
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSPAINVAVHVFR**
Found in **TTHY_HUMAN**, Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1

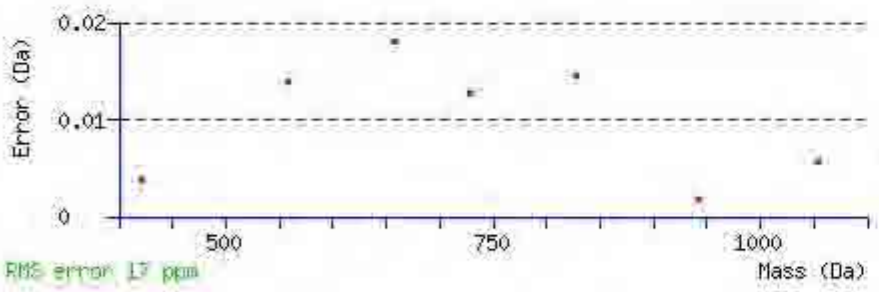
Match to Query 3390: 1365.744072 from(456.255300,3+) rtinseconds(1614) index(11481)
Title: Locus:1.1.1.1718.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_2.mgf

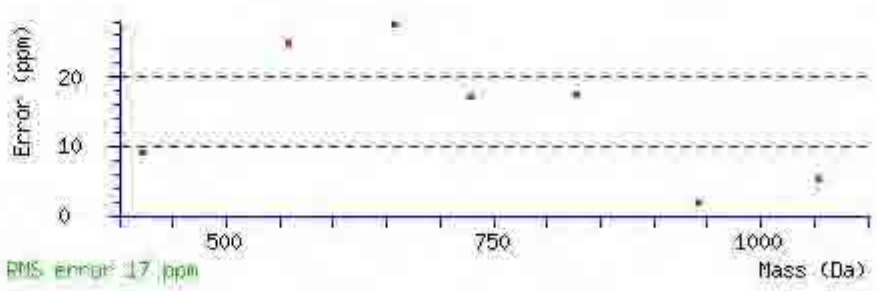
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1365.751724
Ions Score: 56 **Expect:** 3.6e-005
Matches : 7/110 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	145.060768	73.034022			127.050203	64.028740	S	1309.737531	655.372404	1292.710982	646.859129	1291.726966	646.367121	12
3	242.113532	121.560404			224.102967	112.555121	P	1222.705503	611.856389	1205.678954	603.343115			11
4	313.150646	157.078961			295.140081	148.073679	A	1125.652739	563.330007	1108.626190	554.816733			10
5	426.234710	213.620993			408.224145	204.615711	I	*1054.615625*	527.811450	1037.589076	519.298176			9
6	540.277637	270.642457	523.251088	262.129182	522.267072	261.637174	N	*941.531561*	471.269418	924.505012	462.756144			8
7	639.346051	320.176664	622.319502	311.663389	621.335486	311.171381	V	*827.488634*	414.247955	810.462085	405.734680			7
8	710.383165	355.695221	693.356616	347.181946	692.372600	346.689938	A	*728.420220*	364.713748	711.393671	356.200473			6
9	809.451579	405.229427	792.425030	396.716153	791.441014	396.224145	V	*657.383106*	329.195191	640.356557	320.681917			5
10	946.510491	473.758883	929.483942	465.245609	928.499926	464.753601	H	*558.314692*	279.660984	541.288143	271.147710			4
11	1045.578905	523.293090	1028.552356	514.779816	1027.568340	514.287808	V	*421.255780*	211.131528	404.229231	202.618253			3
12	1192.647319	596.827297	1175.620770	588.314023	1174.636754	587.822015	F	322.187366	161.597321	305.160817	153.084047			2
13							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GSPAINVAVHVFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1365.751724	-0.007652	GSPAINVAVHVFR
4.8	1365.736465	0.007607	RPAIPVPVAPSSR
1.5	1365.736450	0.007622	VNVPQPAAAAIQR

Sibling 1 – technical replicate # 3

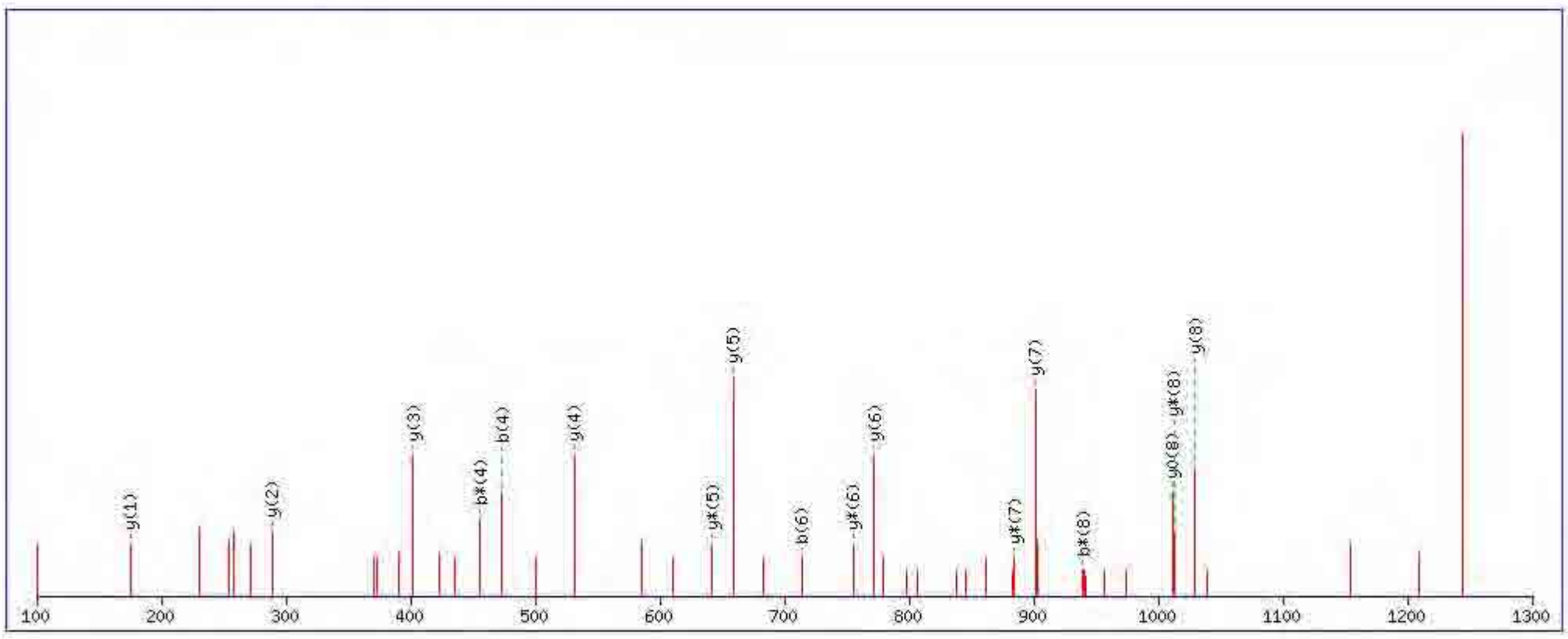
Mascot Search Results

Peptide View

MS/MS Fragmentation of TNQELQEINR
Found in ANXA2_HUMAN, Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

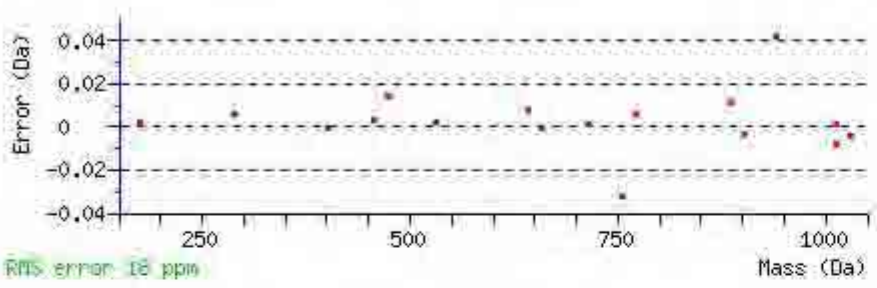
Match to Query 10603: 1243.619708 from(622.817130,2+) rtinseconds(913) index(3057)
Title: Locus:1.1.1.1623.23
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

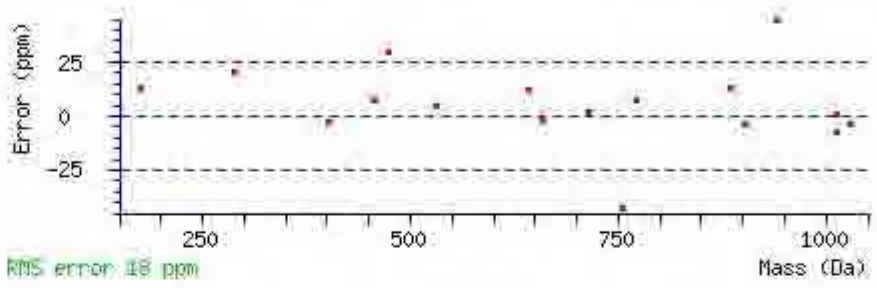
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1243.615646
Ions Score: 56 **Expect:** 0.00016
Matches : 17/100 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	N	1143.575276	572.291276	1126.548727	563.778002	1125.564711	563.285994	9
3	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	*1029.532349*	515.269813	1012.505800	506.756538	1011.521784	506.264530	8
4	**473.199053**	237.103164	456.172504	228.589890	455.188488	228.097882	E	*901.473771*	451.240524	884.447222	442.727249	883.463206	442.235241	7
5	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	L	*772.431178*	386.719227	755.404629	378.205953	754.420613	377.713945	6
6	**714.341695**	357.674486	697.315146	349.161211	696.331130	348.669203	Q	*659.347114*	330.177195	642.320565	321.663921	641.336549	321.171913	5
7	843.384288	422.195782	826.357739	413.682508	825.373723	413.190500	E	*531.288536*	266.147906	514.261987	257.634632	513.277971	257.142624	4
8	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	I	*402.245943*	201.626609	385.219394	193.113335			3
9	1070.511279	535.759278	1053.484730	527.246003	1052.500714	526.753995	N	*289.161879*	145.084577	272.135330	136.571303			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNQELQEINR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	1243.615646	0.004062	TNQELQEINR
14.6	1243.626892	-0.007184	QTDGEQAARIR
11.3	1243.615677	0.004031	GKTGQPGLEGER
10.8	1243.623077	-0.003369	IVMEVPPGNTR
9.6	1243.630905	-0.011197	KESQPAIWNR
9.4	1243.630905	-0.011197	HYSPTKELNR
7.4	1243.615662	0.004046	AKGSEGEQGPLR
7.3	1243.626923	-0.007215	GSPPRSGTAQVR
6.8	1243.629578	-0.009870	GKDASISLEPDL
6.2	1243.626892	-0.007184	SRTIQQENPR

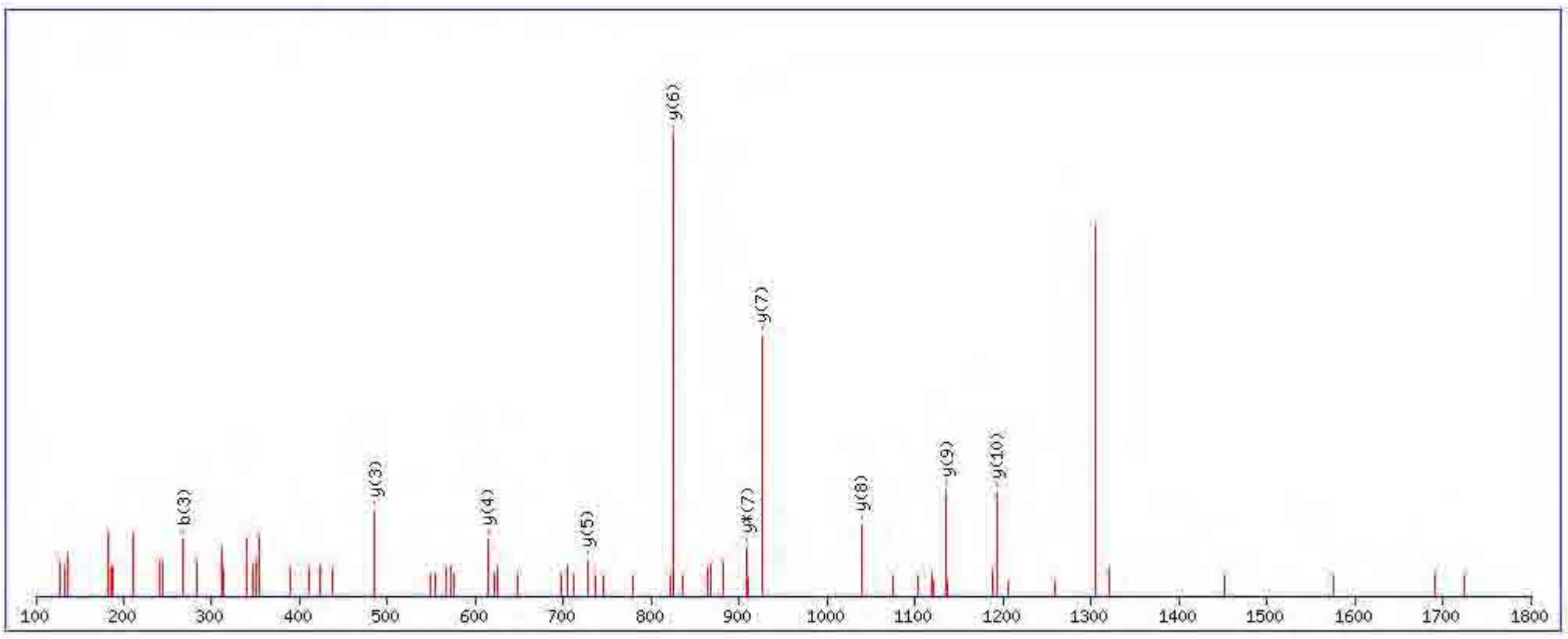
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPITPLEFYR**
Found in **BLMH_HUMAN**, Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1

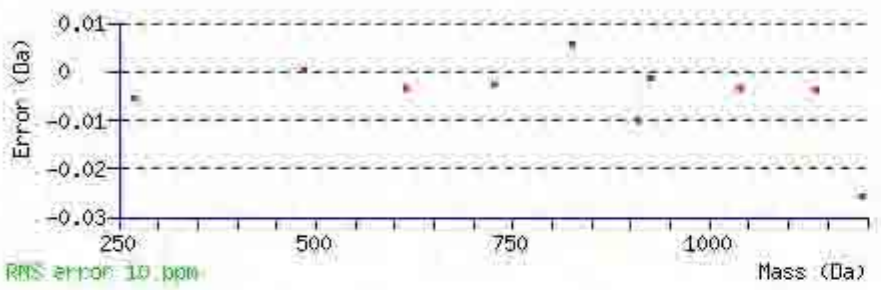
Match to Query 11915: 1304.712208 from(653.363380,2+) rtinseconds(2101) index(16668)
Title: Locus:1.1.1.2285.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

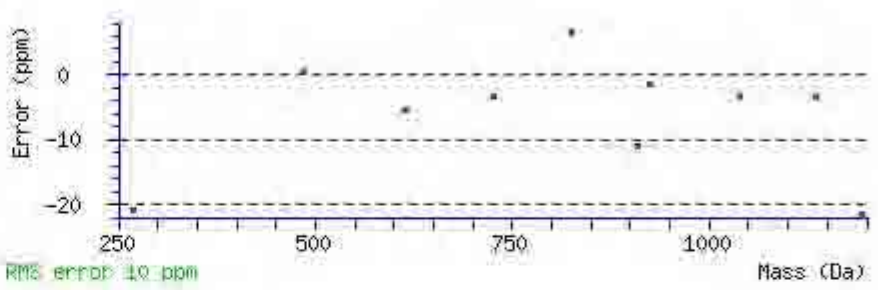
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1304.712860
Ions Score: 49 **Expect:** 8.8e-005
Matches : 10/86 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	*1192.636087*	596.821682	1175.609538	588.308407	1174.625522	587.816399	10
3	268.165568	134.586422			P	*1135.614623*	568.310949	1118.588074	559.797675	1117.604058	559.305667	9
4	381.249632	191.128454			I	*1038.561859*	519.784568	1021.535310	511.271293	1020.551294	510.779285	8
5	482.297311	241.652293	464.286746	232.647011	T	*925.477795*	463.242536	908.451246	454.729261	907.467230	454.237253	7
6	579.350075	290.178676	561.339510	281.173393	P	*824.430116*	412.718696	807.403567	404.205422	806.419551	403.713414	6
7	692.434139	346.720708	674.423574	337.715425	L	*727.377352*	364.192314	710.350803	355.679039	709.366787	355.187031	5
8	821.476732	411.242004	803.466167	402.236722	E	*614.293288*	307.650282	597.266739	299.137007	596.282723	298.644999	4
9	968.545146	484.776211	950.534581	475.770929	F	*485.250695*	243.128985	468.224146	234.615711			3
10	1131.608475	566.307876	1113.597910	557.302593	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGPITPLEFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	1304.712860	-0.000652	IGPITPLEFYR
5.6	1304.720078	-0.007870	LGPVESLQGHLR
3.7	1304.708832	0.003376	PLGPGLKPPEER
3.4	1304.720062	-0.007854	LSLPAPEPPGRR
0.9	1304.724106	-0.011898	WPPTLQPPTLR
0.8	1304.708847	0.003361	IPAVGGKELDLHG
0.6	1304.708862	0.003346	LGPGPPPLGPLAR
0.2	1304.708832	0.003376	NASPVQVKTAYK
0.0	1304.720062	-0.007854	LSLPAPEPPGRR

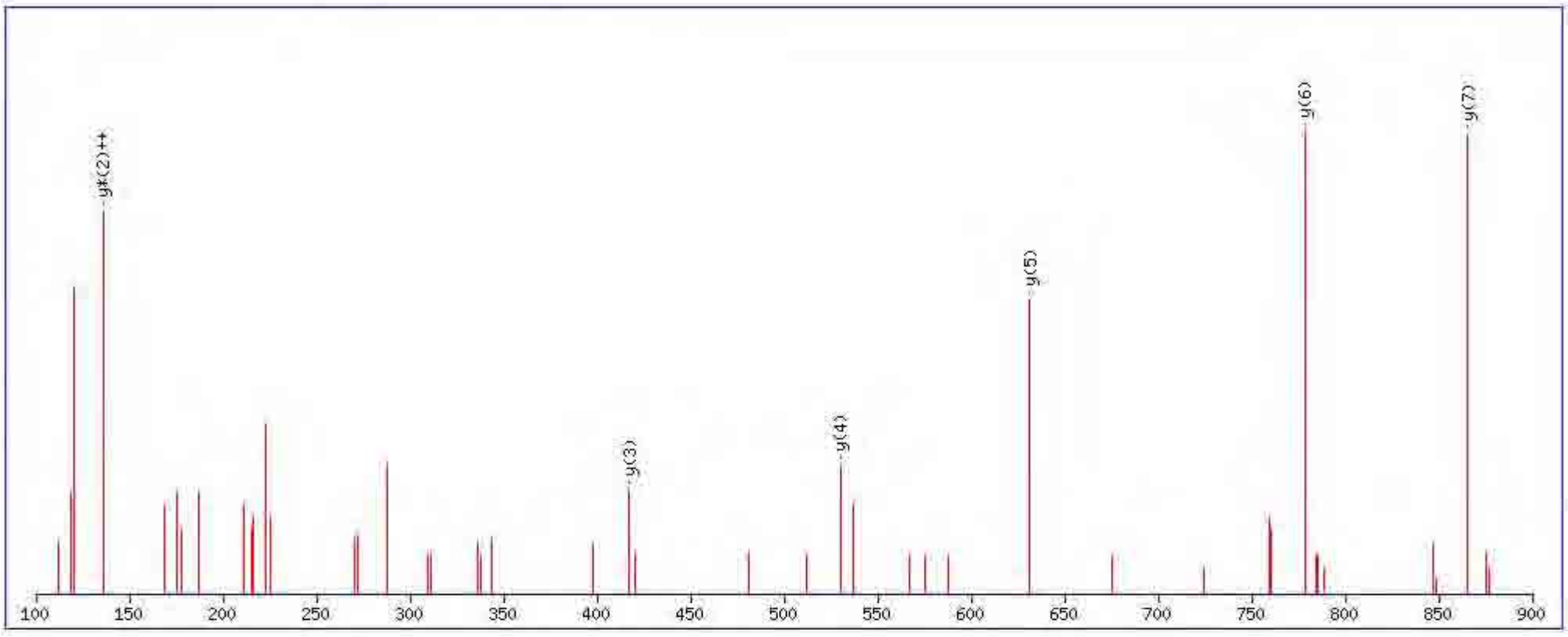
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFTIELR**
Found in **CBPB2_HUMAN**, Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

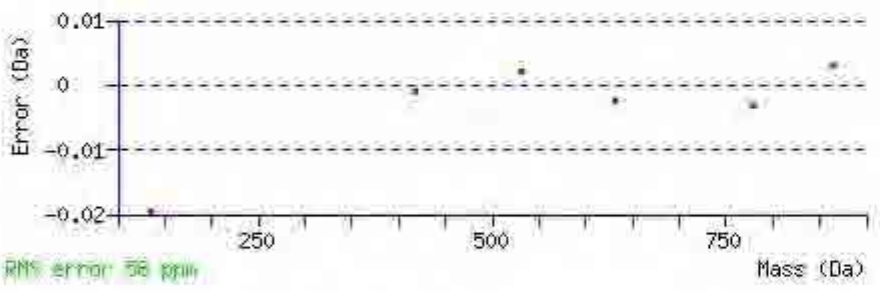
Match to Query 5121: 1027.532048 from(514.773300,2+) rtinseconds(1841) index(13338)
Title: Locus:1.1.1.2142.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

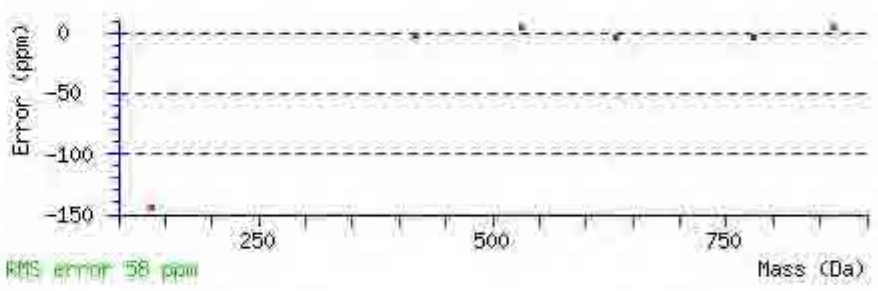
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1027.533829
Ions Score: 40 **Expect:** 0.0031
Matches : 6/64 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							8
2	251.102633	126.054954	233.092068	117.049672	S	*865.477794*	433.242535	848.451245	424.729261	847.467229	424.237253	7
3	398.171047	199.589161	380.160482	190.583879	F	*778.445766*	389.726521	761.419217	381.213247	760.435201	380.721239	6
4	499.218726	250.113001	481.208161	241.107719	T	*631.377352*	316.192314	614.350803	307.679040	613.366787	307.187032	5
5	612.302790	306.655033	594.292225	297.649751	I	*530.329673*	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	741.345383	371.176330	723.334818	362.171047	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
7	854.429447	427.718362	836.418882	418.713079	L	288.203016	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YSFTIELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.2	1027.533829	-0.001781	YSFTIELR
12.7	1027.541031	-0.008983	RIASAPEPR
11.8	1027.541031	-0.008983	KSSNLTNHK
11.7	1027.529800	0.002248	DNAPTIEIR
6.3	1027.531143	0.000905	LHSHHELR
3.9	1027.541031	-0.008983	NLRDPELR
3.4	1027.525986	0.006062	YTALVTLMT
3.0	1027.529800	0.002248	AEAGGLPELR
3.0	1027.529800	0.002248	AQLGEPELR
2.1	1027.522614	0.009434	YSVAEVFIT

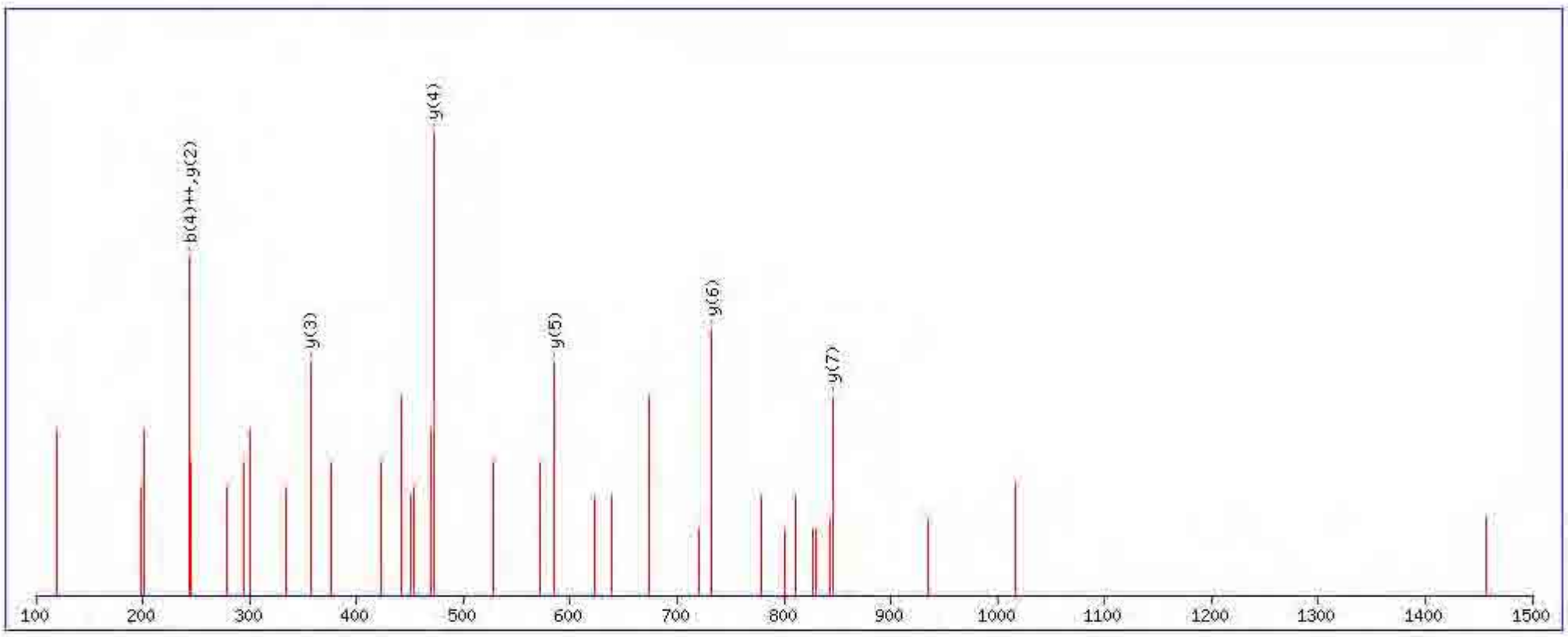
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPLFLDLPK**
Found in **CATL2_HUMAN**, Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2

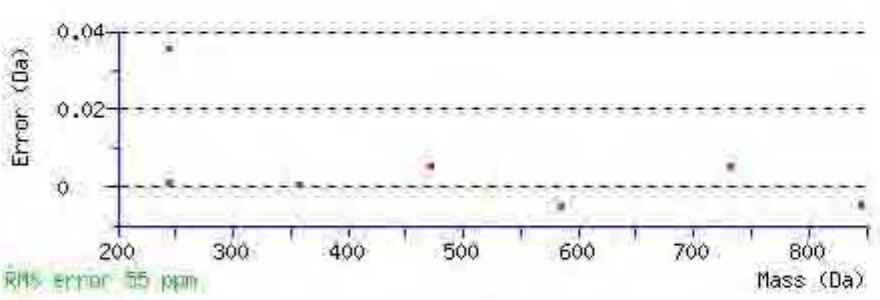
Match to Query 6101: 1070.608308 from(536.311430,2+) rtinseconds(2036) index(15788)
Title: Locus:1.1.1.2250.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

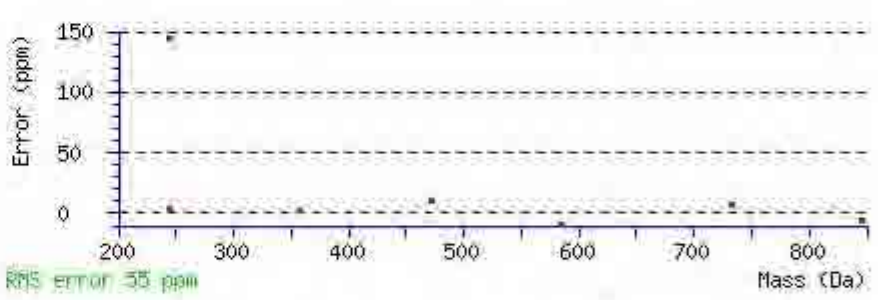
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1070.601181
Ions Score: 48 **Expect:** 0.001
Matches : 7/74 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							9
2	227.102633	114.054954	209.092068	105.049672	P	942.565881	471.786579	925.539332	463.273304	924.555316	462.781296	8
3	340.186697	170.596986	322.176132	161.591704	L	*845.513117*	423.260197	828.486568	414.746922	827.502552	414.254914	7
4	487.255111	244.131193	469.244546	235.125911	F	*732.429053*	366.718165	715.402504	358.204890	714.418488	357.712882	6
5	600.339175	300.673226	582.328610	291.667943	L	*585.360639*	293.183958	568.334090	284.670683	567.350074	284.178675	5
6	715.366118	358.186697	697.355553	349.181415	D	*472.276575*	236.641925	455.250026	228.128651	454.266010	227.636643	4
7	828.450182	414.728729	810.439617	405.723447	L	*357.249632*	179.128454	340.223083	170.615180			3
8	925.502946	463.255111	907.492381	454.249829	P	*244.165568*	122.586422	227.139019	114.073148			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EPLFLDLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	1070.601181	0.007127	EPLFLDLPK
14.9	1070.608383	-0.000075	QDDLIRAIK
10.9	1070.608383	-0.000075	QLDDLRALK
8.7	1070.601212	0.007096	ILIFSPPPVG
8.0	1070.616455	-0.008147	IILFSFGFK
8.0	1070.601212	0.007096	ILIFSPPPVG
8.0	1070.601212	0.007096	ILIFSPPPVG
8.0	1070.608414	-0.000106	QDLDVVKVR
8.0	1070.612411	-0.004103	TKIAWDLPK
8.0	1070.608398	-0.000090	TLRTQDLPK

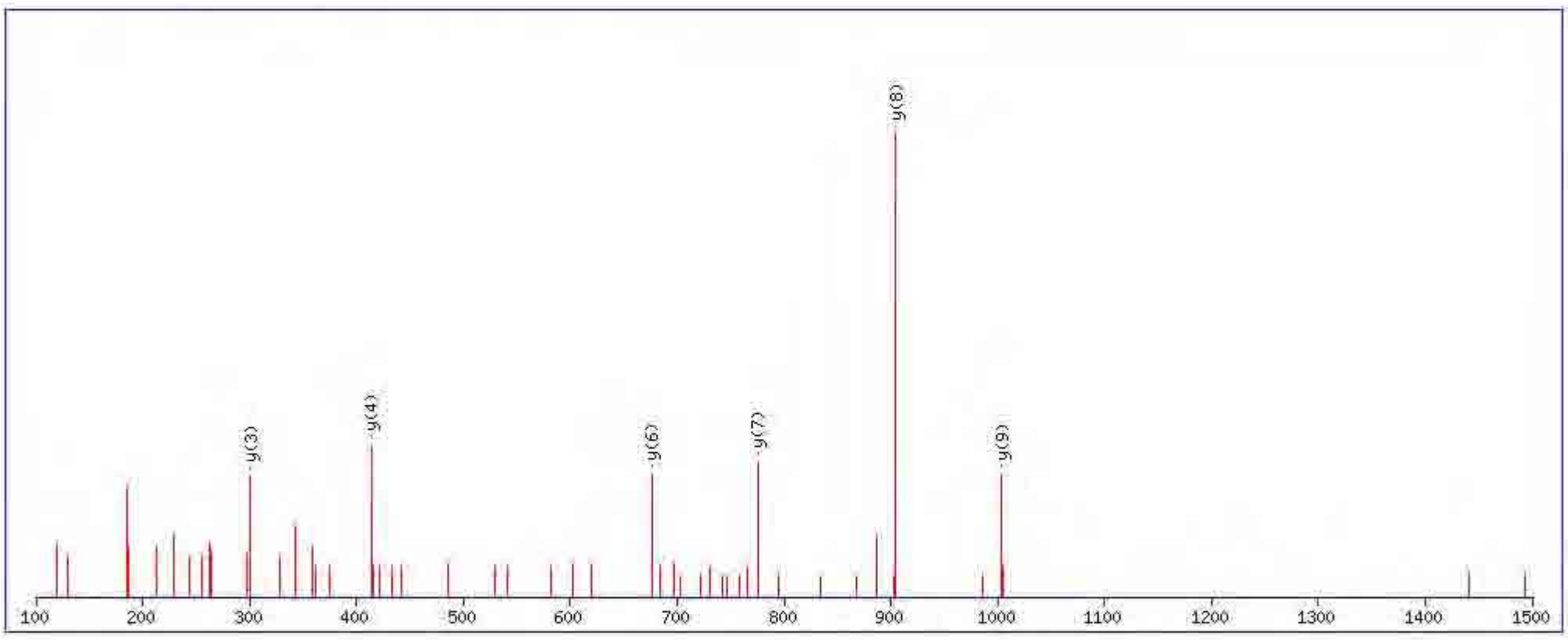
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEVFDIGPK**
Found in **COCA1_HUMAN**, Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2

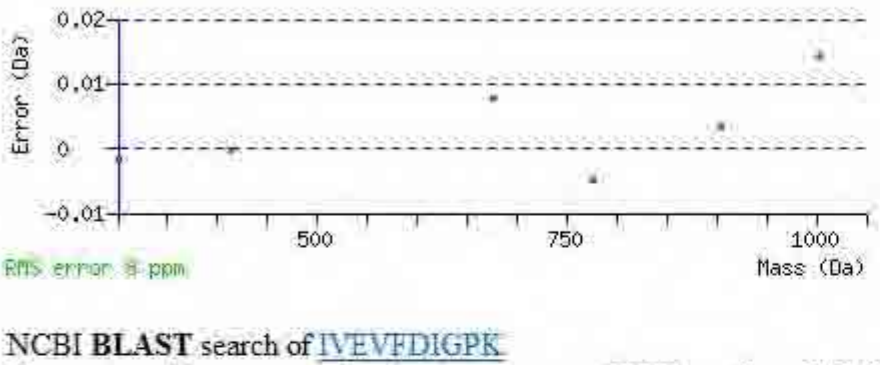
Match to Query 7162: 1115.622728 from(558.818640,2+) rtinseconds(1837) index(13291)
Title: Locus:1.1.1.2140.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

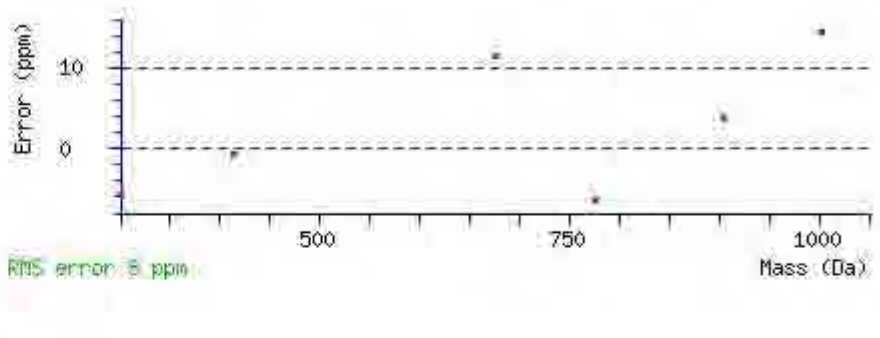
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1115.622665
Ions Score: 47 **Expect:** 0.00055
Matches : 6/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							10
2	213.159754	107.083515			V	*1003.545874*	502.276575	986.519325	493.763301	985.535309	493.271293	9
3	342.202347	171.604811	324.191782	162.599529	E	*904.477460*	452.742368	887.450911	444.229094	886.466895	443.737086	8
4	441.270761	221.139018	423.260196	212.133736	V	*775.434867*	388.221072	758.408318	379.707797	757.424302	379.215789	7
5	588.339175	294.673226	570.328610	285.667943	F	*676.366453*	338.686865	659.339904	330.173590	658.355888	329.681582	6
6	703.366118	352.186697	685.355553	343.181415	D	529.298039	265.152658	512.271490	256.639383	511.287474	256.147375	5
7	816.450182	408.728729	798.439617	399.723447	I	*414.271096*	207.639186	397.244547	199.125912			4
8	873.471646	437.239461	855.461081	428.234179	G	*301.187032*	151.097154	284.160483	142.583880			3
9	970.524410	485.765843	952.513845	476.760561	P	244.165568	122.586422	227.139019	114.073148			2
10					K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of IVEVFDIGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1115.622665	0.000063	IVEVFDIGPK
11.4	1115.633881	-0.011153	LVERILTSW
8.8	1115.622665	0.000063	IVDLNFLIGP
7.5	1115.633881	-0.011153	PDEIFRLVK
6.4	1115.622665	0.000063	ILDTFLGLPQ
5.1	1115.629852	-0.007124	AKTPTSLNIR
4.5	1115.618607	0.004121	ITLLKDEER
4.3	1115.633881	-0.011153	LDLKLFDRP
4.3	1115.618637	0.004091	LVLTNNQLTT
4.3	1115.629852	-0.007124	LVLGSARNSSI

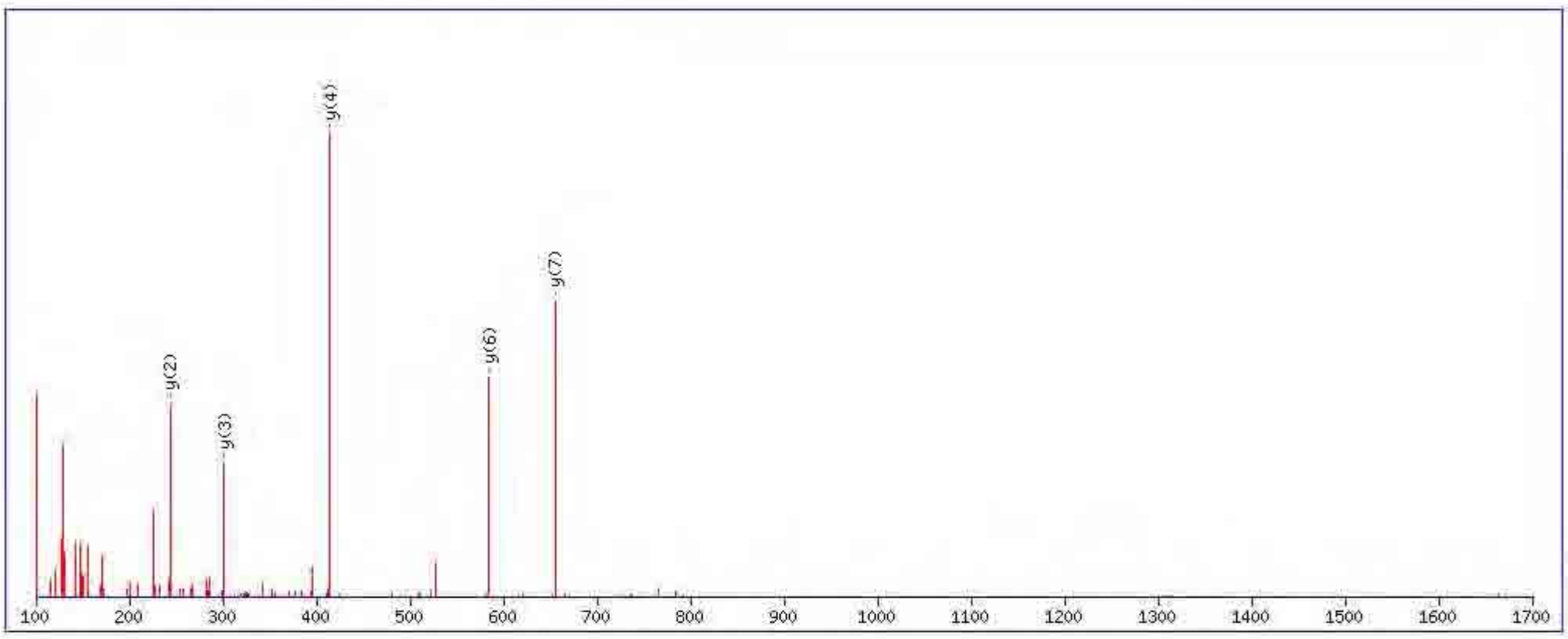
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAGPPGPK**
Found in **CO9A2_HUMAN**, Collagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2

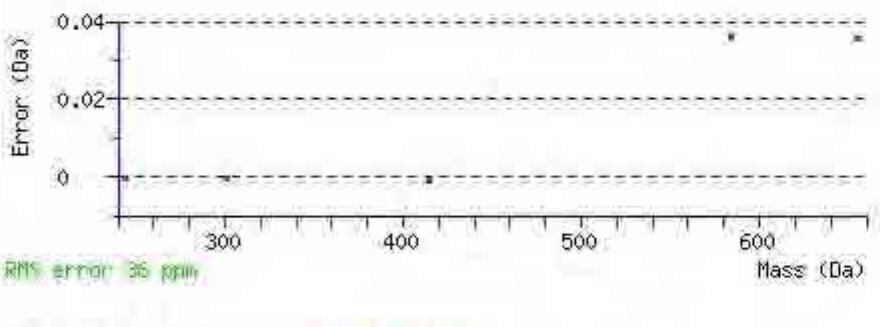
Match to Query 625: 782.427828 from(392.221190,2+) rtinseconds(582) index(323)
Title: Locus:1.1.1.1439.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

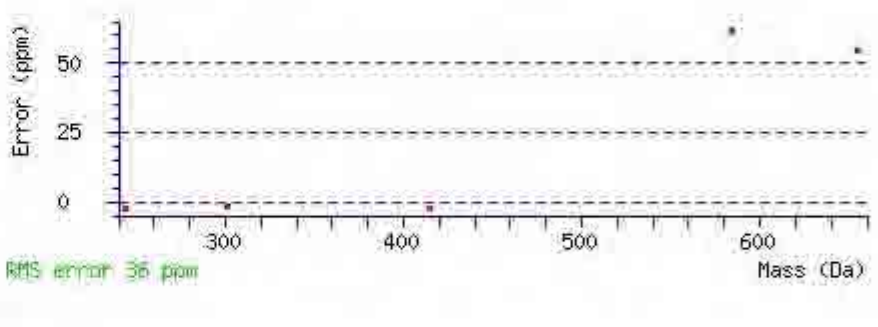
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 782.428650
Variable modifications:
P4 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 44 **Expect:** 0.0035
Matches : 5/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.102239	65.054757	112.075690	56.541483	K					8
2	200.139353	100.573315	183.112804	92.060040	A	*655.340968*	328.174122	638.314419	319.660848	7
3	257.160817	129.084047	240.134268	120.570772	G	*584.303854*	292.655565	567.277305	284.142291	6
4	370.208496	185.607886	353.181947	177.094612	P	527.282390	264.144833	510.255841	255.631559	5
5	483.256175	242.131726	466.229626	233.618451	P	*414.234711*	207.620994	397.208162	199.107719	4
6	540.277639	270.642458	523.251090	262.129183	G	*301.187032*	151.097154	284.160483	142.583880	3
7	637.330403	319.168840	620.303854	310.655565	P	*244.165568*	122.586422	227.139019	114.073148	2
8					K	147.112804	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of KAGPPGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	782.428650	-0.000822	GAAGLPGPK
44.0	782.428650	-0.000822	KAGPPGPK
27.9	782.428650	-0.000822	KPKPGPGA
27.5	782.428650	-0.000822	AKGPPGPK
22.9	782.428665	-0.000837	GAPGVTGPK
22.4	782.428650	-0.000822	GAAGLPGPK
17.5	782.428635	-0.000807	AANLPGPK
16.5	782.428650	-0.000822	KAGPPGPK
11.9	782.428650	-0.000822	QPGSPGLK
11.1	782.432678	-0.004850	QKIFTF

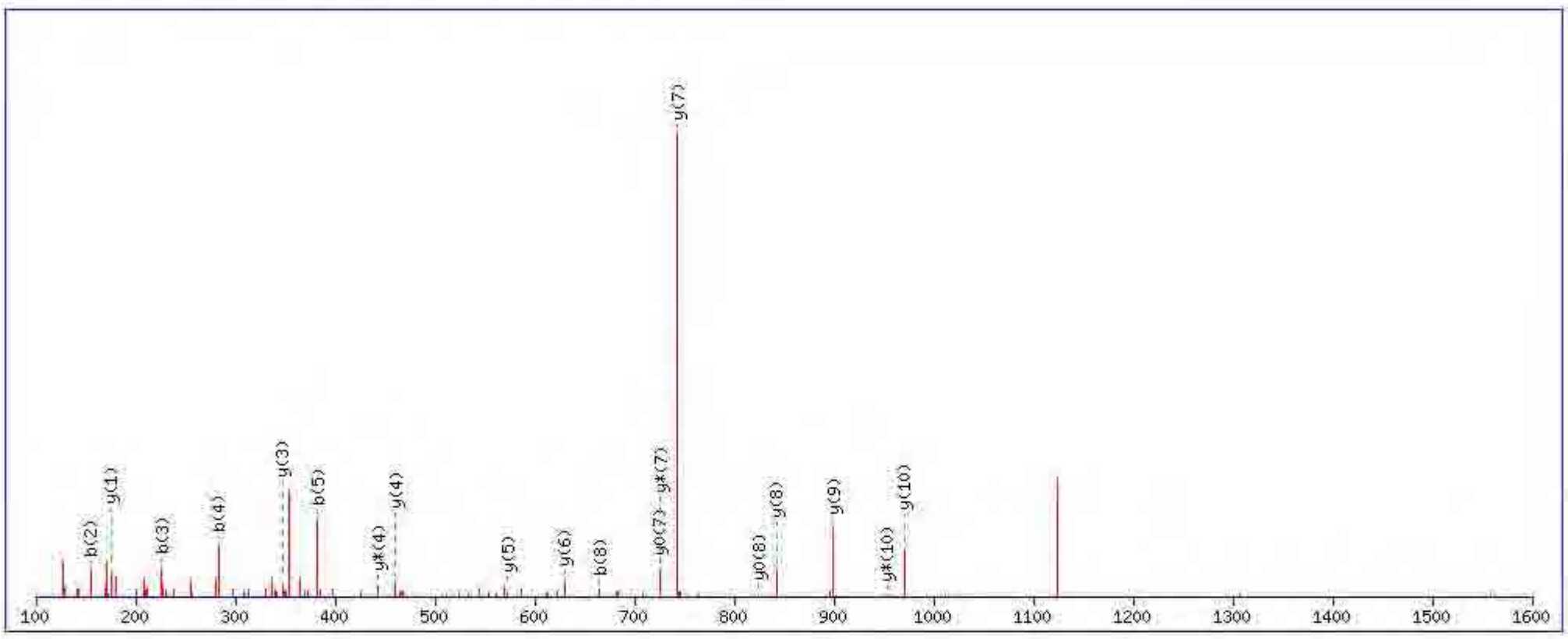
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPAGVPGLLGDR**
Found in **CO8A2_HUMAN**, Collagen alpha-2(VIII) chain OS=Homo sapiens GN=COL8A2 PE=1 SV=2

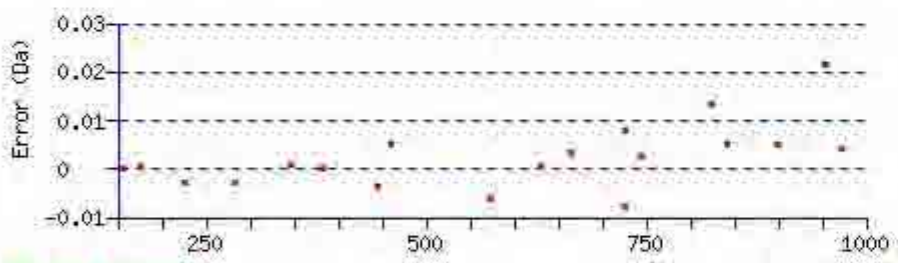
Match to Query 7379: 1123.601188 from(562.807870,2+) rtinseconds(1414) index(8131)
Title: Locus:1.1.1.1907.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

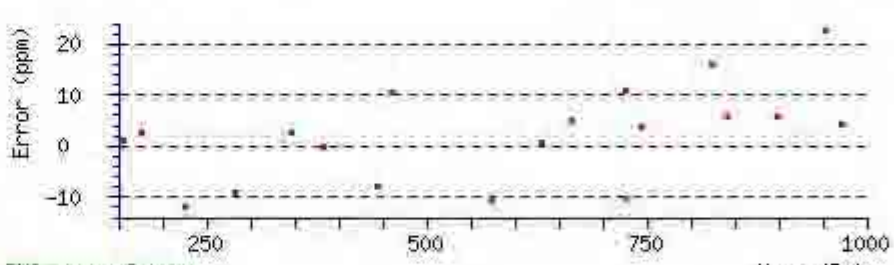
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1123.598587
Variable modifications:
P6 : Oxidation (P)
Ions Score: 53 **Expect:** 0.0001
Matches : 19/88 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							12
2	155.081504	78.044390			P	1067.584386	534.295831	1050.557837	525.782557	1049.573821	525.290549	11
3	226.118618	113.562947			A	970.531622	485.769449	953.505073	477.256175	952.521057	476.764167	10
4	283.140082	142.073679			G	899.494508	450.250892	882.467959	441.737618	881.483943	441.245610	9
5	382.208496	191.607886			V	842.473044	421.740160	825.446495	413.226886	824.462479	412.734878	8
6	495.256175	248.131726			P	743.404630	372.205953	726.378081	363.692679	725.394065	363.200671	7
7	552.277639	276.642458			G	630.356951	315.682114	613.330402	307.168839	612.346386	306.676831	6
8	665.361703	333.184490			L	573.335487	287.171382	556.308938	278.658107	555.324922	278.166099	5
9	778.445767	389.726522			L	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
10	835.467231	418.237254			G	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
11	950.494174	475.750725	932.483609	466.745443	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GPAGVPGLLGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	1123.598587	0.002601	GPAGVPGLLGDR
9.8	1123.609802	-0.008614	GPQVQLVNNR
9.1	1123.594742	0.006446	VLVCSKPVTY
7.7	1123.609818	-0.008630	GPGLGTPTPRR
7.5	1123.609787	-0.008599	QPRPALSPSR
6.7	1123.598587	0.002601	GGGLPIQVPDR
6.4	1123.592026	0.009162	PLHMAVERR
6.0	1123.598541	0.002647	KPRGIPEAQE
5.7	1123.598557	0.002631	PGAQPDLALAR
5.5	1123.598572	0.002616	QPGQPSLLPR

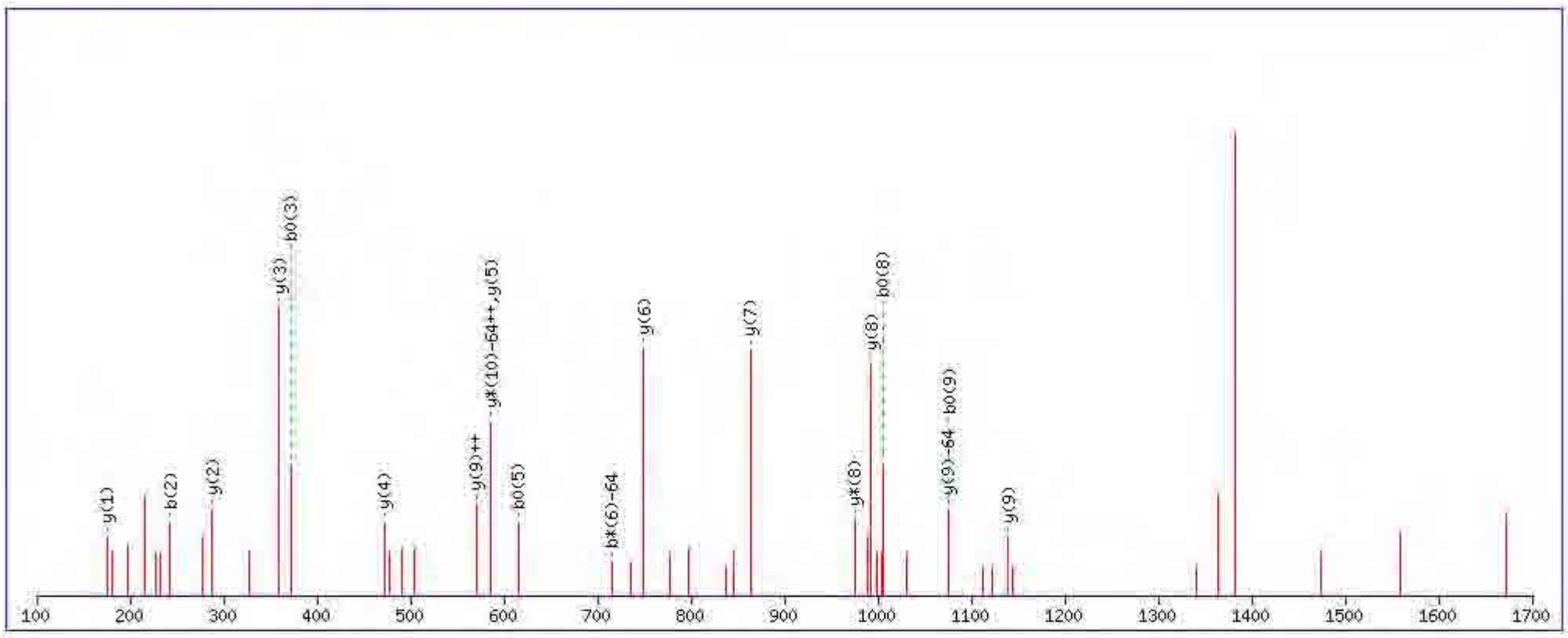
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

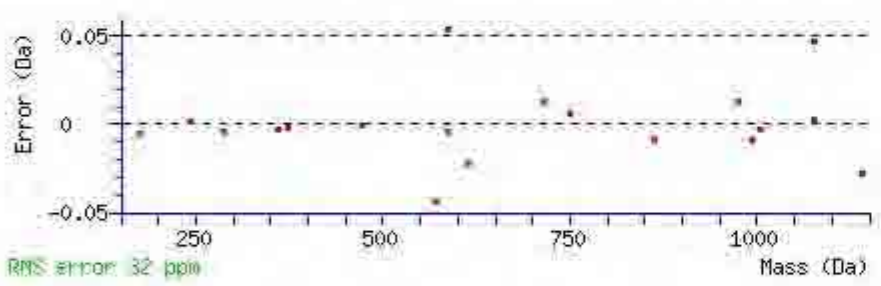
Match to Query 13347: 1380.680368 from(691.347460,2+) rtinseconds(1473) index(8905)
Title: Locus:1.1.1.1939.22
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

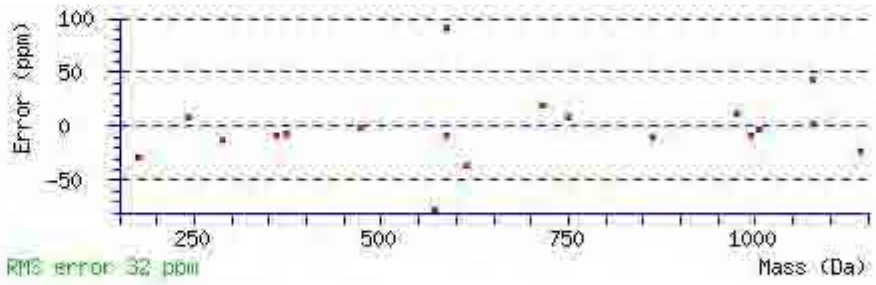
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 58 **Expect:** 0.00015
Matches : 19/154 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1252.635434	626.821355	1235.608885	618.308081	1234.624869	617.816073	10
3	390.169333	195.588304			372.158768	186.583022	M	*1139.551370*	570.279323	1122.524821	561.766049	1121.540805	561.274040	9
4	519.211926	260.109601			501.201361	251.104319	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	633.254853	317.131065	616.228304	308.617790	615.244288	308.125782	N	*863.473377*	432.240326	846.446828	423.727052			7
6	796.318182	398.662729	779.291633	390.149454	778.307617	389.657446	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	910.361109	455.684192	893.334560	447.170918	892.350544	446.678910	N	*586.367121*	293.687199	569.340572	285.173924			5
8	1023.445173	512.226224	1006.418624	503.712950	1005.434608	503.220942	I	*472.324194*	236.665735	455.297645	228.152460			4
9	1094.482287	547.744782	1077.455738	539.231507	1076.471722	538.739499	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1207.566351	604.286813	1190.539802	595.773539	1189.555786	595.281531	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	1380.670700	0.009668	EIMENYNIALR
15.9	1380.688492	-0.008124	YIPENVSSSTLR
10.2	1380.688477	-0.008109	PEPLEAAGEPALR
10.1	1380.677261	0.003107	ITEEDKVNSSL
9.6	1380.681961	-0.001593	SDRNIVLYDMR
9.3	1380.688477	-0.008109	PEPLEAAGEPALR
8.4	1380.667389	0.012979	PFNVQYPGQTSK
7.5	1380.670731	0.009637	ITNLQYEVDMR
7.0	1380.686005	-0.005637	VDPRFGAYVACAL
6.9	1380.674103	0.006265	TLGSLMNIKNMSG

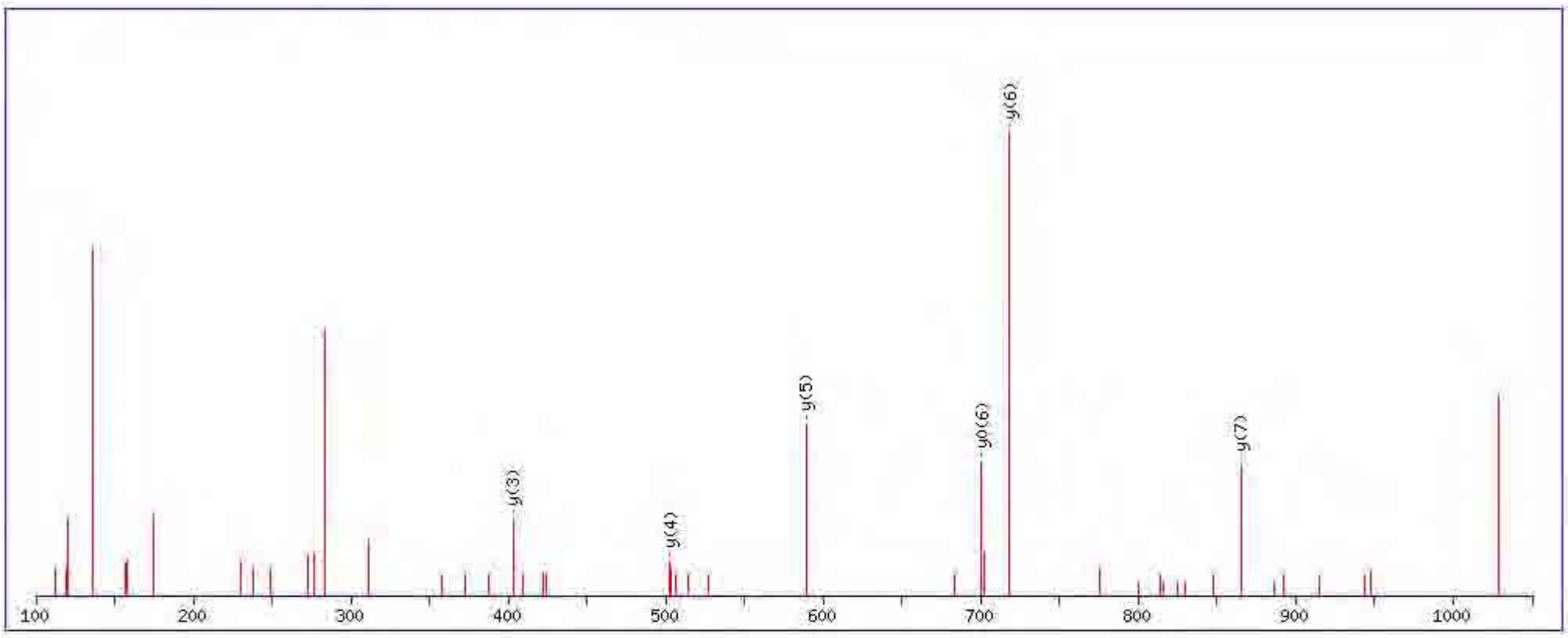
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFESVLDR**
Found in **DERM_HUMAN**, Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2

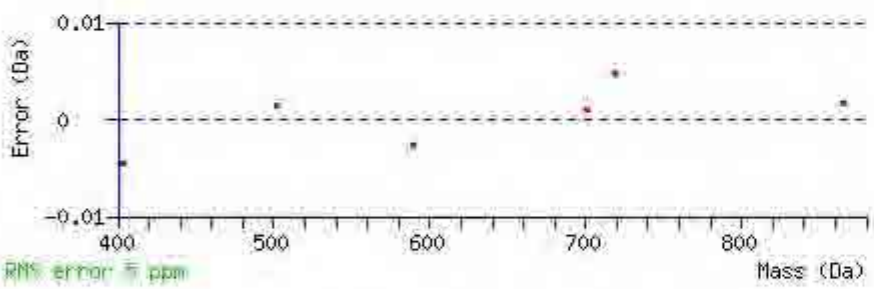
Match to Query 5114: 1027.502948 from(514.758750,2+) rtinseconds(1539) index(9748)
Title: Locus:1.1.1.1976.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

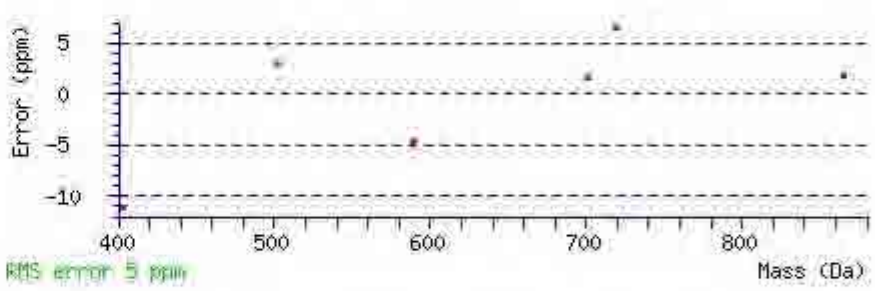
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1027.497452
Ions Score: 37 **Expect:** 0.0079
Matches : 6/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940			Y							8
2	311.139019	156.073148			F	*865.441408*	433.224342	848.414859	424.711067	847.430843	424.219059	7
3	440.181612	220.594444	422.171047	211.589162	E	*718.372994*	359.690135	701.346445	351.176860	700.362429	350.684852	6
4	527.213640	264.110458	509.203075	255.105176	S	*589.330401*	295.168838	572.303852	286.655564	571.319836	286.163556	5
5	626.282054	313.644665	608.271489	304.639383	V	*502.298373*	251.652824	485.271824	243.139550	484.287808	242.647542	4
6	739.366118	370.186697	721.355553	361.181415	L	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
7	854.393061	427.700169	836.382496	418.694886	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YFESVLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	1027.497452	0.005496	YFESVLDR
12.2	1027.497452	0.005496	YFEAVQGSK
7.6	1027.504684	-0.001736	RPGPSPVDR
6.8	1027.508652	-0.005704	YYIREER
6.2	1027.508698	-0.005750	VNLPWPDR
6.0	1027.508698	-0.005750	NLPVWDPR
5.9	1027.512070	-0.009122	VFSSKGMTR
5.9	1027.500793	0.002155	YMKSINEK
2.2	1027.508698	-0.005750	GPGVEDLWR
2.2	1027.504700	-0.001752	GPVGPSGGGSTR

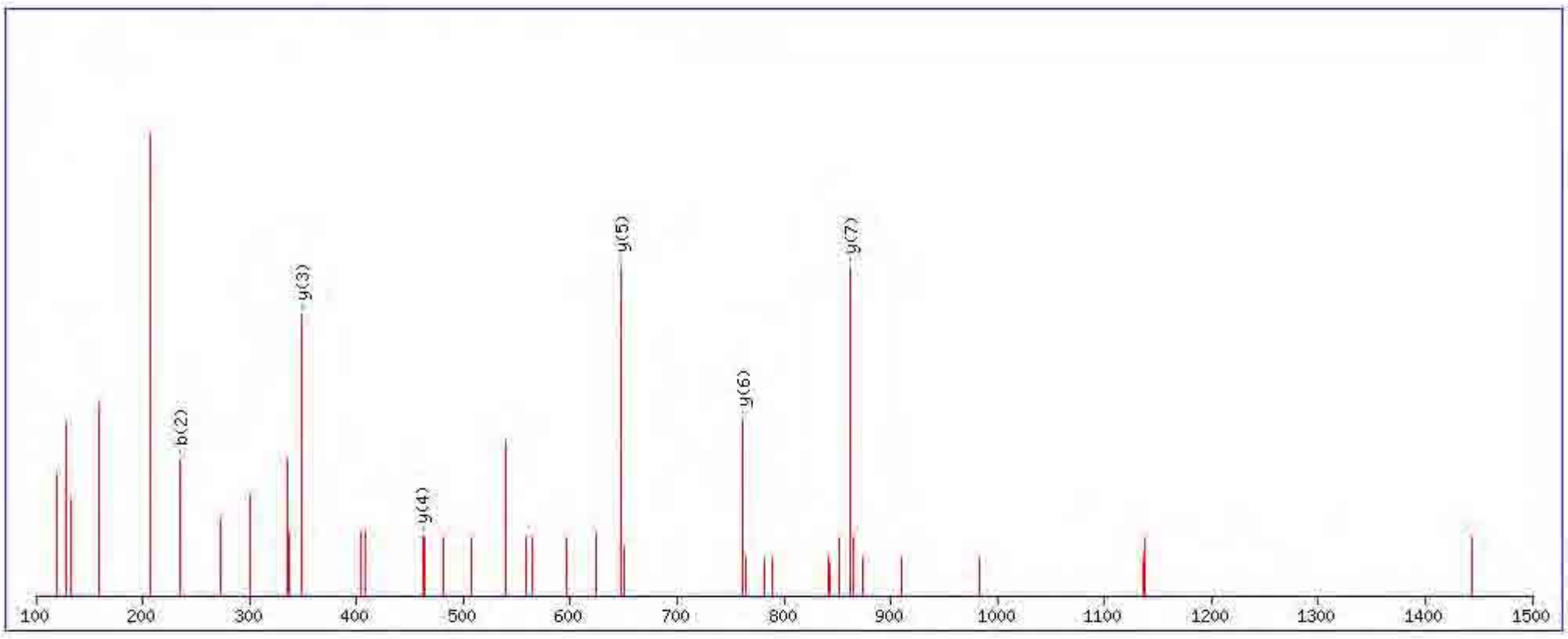
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFTIWLSDK**
Found in **DSC3_HUMAN**, Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3

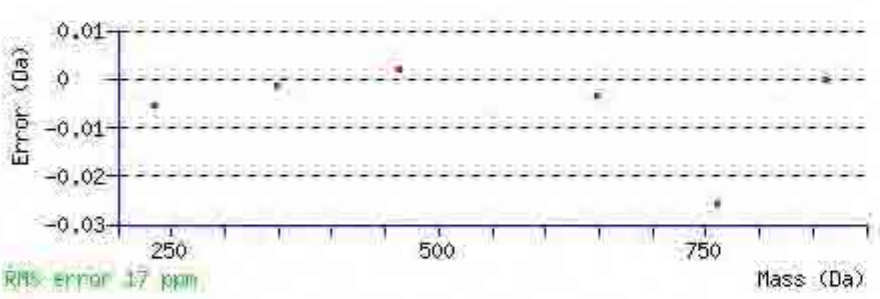
Match to Query 6668: 1095.567948 from(548.791250,2+) rtinseconds(1984) index(15113)
Title: Locus:1.1.1.2221.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

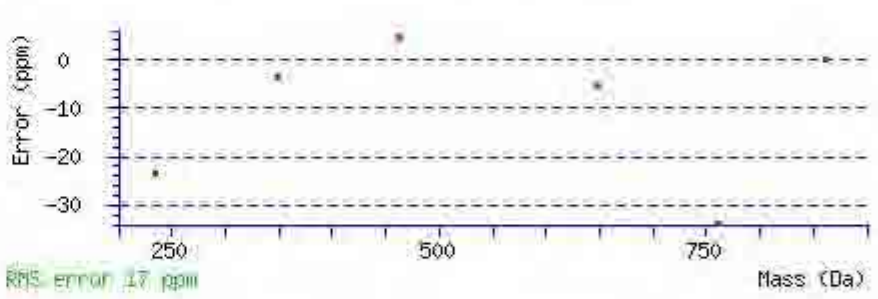
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1095.560059
Ions Score: 37 **Expect:** 0.0044
Matches : 6/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							9
2	235.107718	118.057497	217.097153	109.052214	F	1009.535309	505.271293	992.508760	496.758018	991.524744	496.266010	8
3	336.155397	168.581336	318.144832	159.576054	T	*862.466895*	431.737086	845.440346	423.223811	844.456330	422.731803	7
4	449.239461	225.123369	431.228896	216.118086	I	*761.419216*	381.213246	744.392667	372.699972	743.408651	372.207964	6
5	635.318774	318.163025	617.308209	309.157743	W	*648.335152*	324.671214	631.308603	316.157940	630.324587	315.665932	5
6	748.402838	374.705057	730.392273	365.699775	L	*462.255839*	231.631558	445.229290	223.118283	444.245274	222.626275	4
7	835.434866	418.221071	817.424301	409.215789	S	*349.171775*	175.089526	332.145226	166.576251	331.161210	166.084243	3
8	950.461809	475.734543	932.451244	466.729260	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
9					K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of SFTIWLSDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	1095.560059	0.007889	SFTIWLSDK
10.8	1095.557373	0.010575	HPRPFPSSR
9.0	1095.563446	0.004502	MSVQSVAIVF
8.8	1095.571274	-0.003326	FSNPRALYL
8.8	1095.574646	-0.006698	MSNLFSILR
8.2	1095.563416	0.004532	LMNIFLKDS
8.0	1095.563431	0.004517	KSFLTALCDV
6.5	1095.560074	0.007874	SFTTTLPWK
5.4	1095.571289	-0.003341	FSTAFLASPR
4.4	1095.559418	0.008530	SMTAGKTGTVK

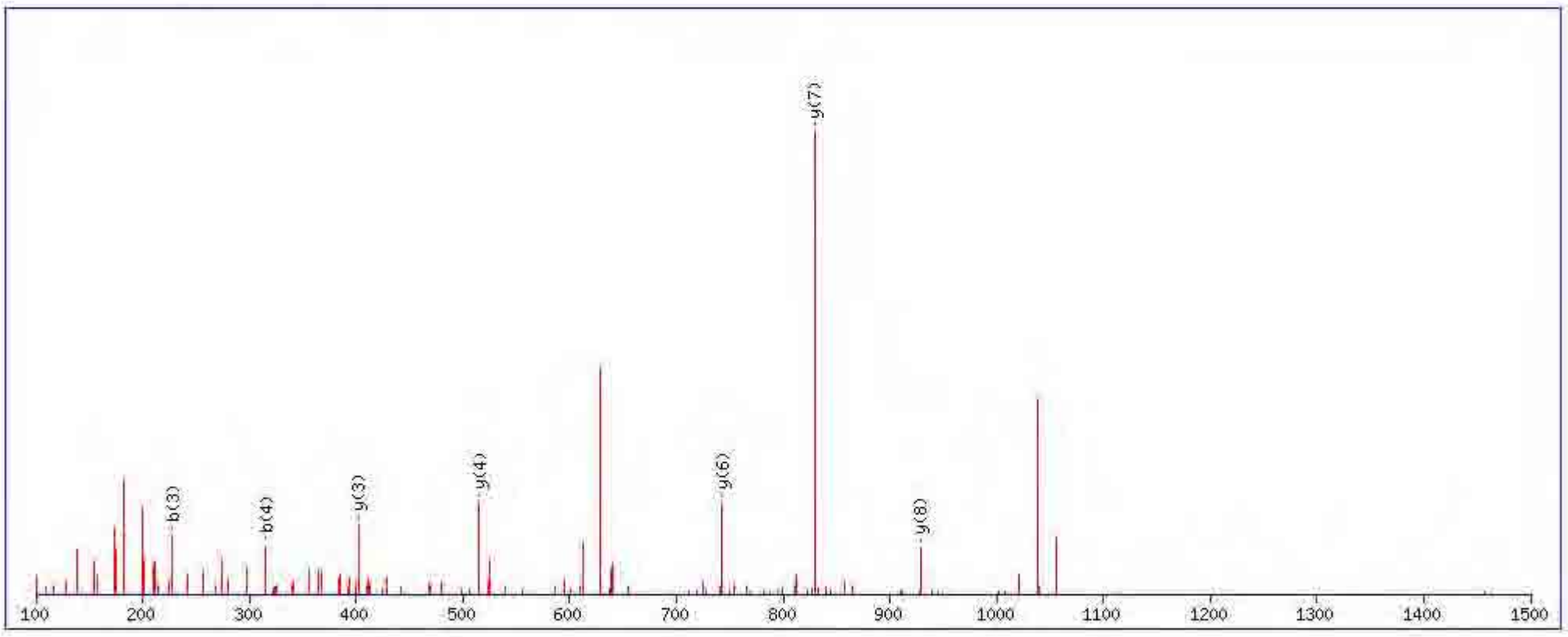
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVSQVLNRL**
Found in **RPB2_HUMAN**, DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1

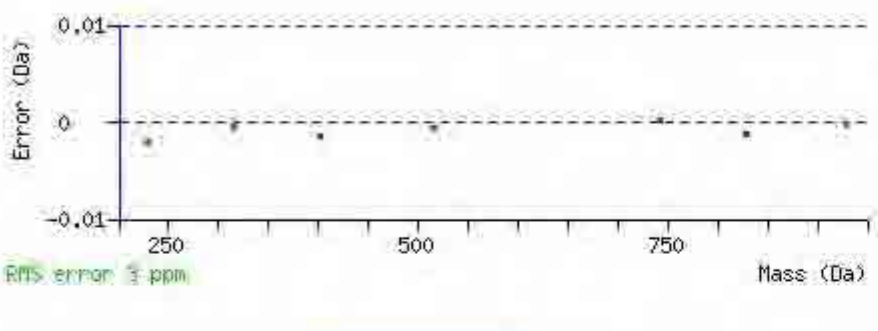
Match to Query 5762: 1055.610688 from(528.812620,2+) rtinseconds(1410) index(8079)
Title: Locus:1.1.1.1905.12
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

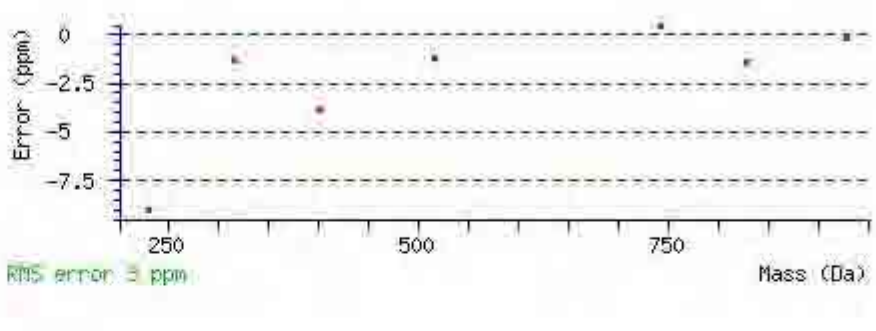
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.608734
Ions Score: 41 **Expect:** 0.0068
Matches : 7/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							10
2	129.065854	65.036565					G	985.578905	493.293091	968.552356	484.779816	967.568340	484.287808	9
3	**228.134268**	114.570772					V	***928.557441***	464.782359	911.530892	456.269084	910.546876	455.777076	8
4	**315.166296**	158.086786			297.155731	149.081504	S	***829.489027***	415.248152	812.462478	406.734877	811.478462	406.242869	7
5	443.224874	222.116075	426.198325	213.602801	425.214309	213.110793	Q	***742.456999***	371.732138	725.430450	363.218863			6
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	V	614.398421	307.702849	597.371872	299.189574			5
7	655.377352	328.192314	638.350803	319.679040	637.366787	319.187032	L	***515.330007***	258.168642	498.303458	249.655367			4
8	769.420279	385.213778	752.393730	376.700503	751.409714	376.208495	N	***402.245943***	201.626609	385.219394	193.113335			3
9	925.521390	463.264333	908.494841	454.751059	907.510825	454.259051	R	288.203016	144.605146	271.176467	136.091871			2
10							L	132.101905	66.554590					1





NCBI **BLAST** search of AGVSQVLNRL
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.6	1055.608734	0.001954	AGVSQVLNRL
26.3	1055.608734	0.001954	QVSGIIGNLR
22.9	1055.608704	0.001984	KADLINNLR
20.0	1055.604874	0.005814	MPLALSLPAK
19.7	1055.608734	0.001954	SPNVGALKVR
16.2	1055.619980	-0.009292	TGRLQVAGVR
15.2	1055.608719	0.001969	RASLGPLQSK
13.4	1055.612747	-0.002059	KWLPNGTLK
13.3	1055.604874	0.005814	MPLALSLPAK
11.6	1055.608704	0.001984	LNLSNNLIR

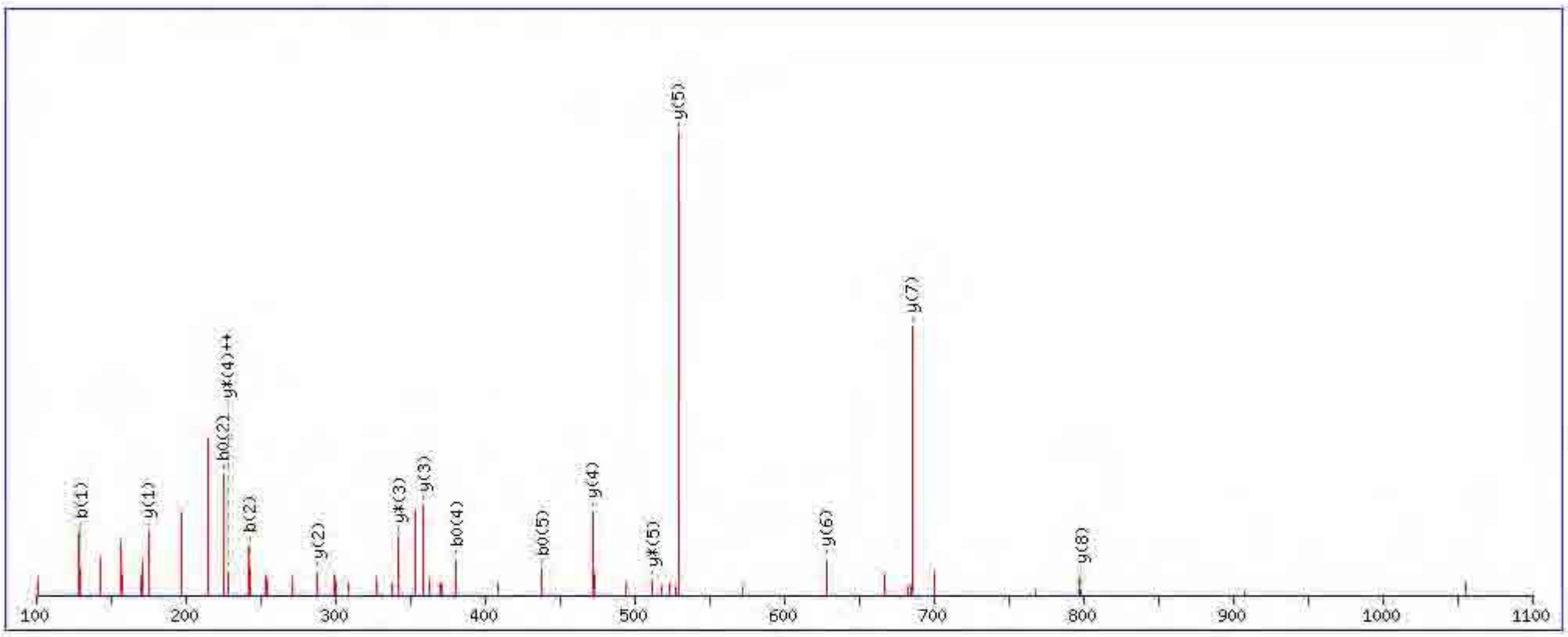
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGVGIALR**
Found in **FABP5_HUMAN**, Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3

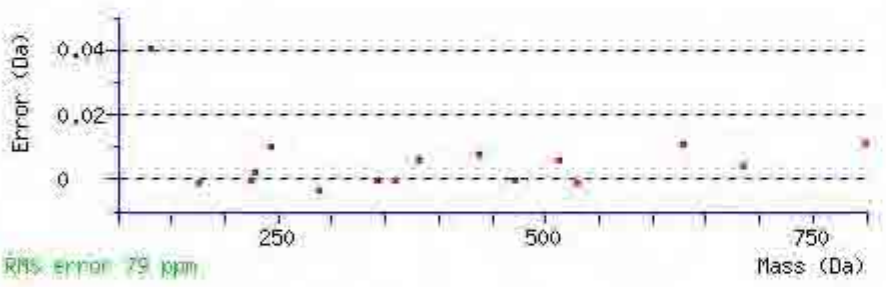
Match to Query 3180: 926.553188 from(464.283870,2+) rtinseconds(1601) index(10463)
Title: Locus:1.1.1.2010.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

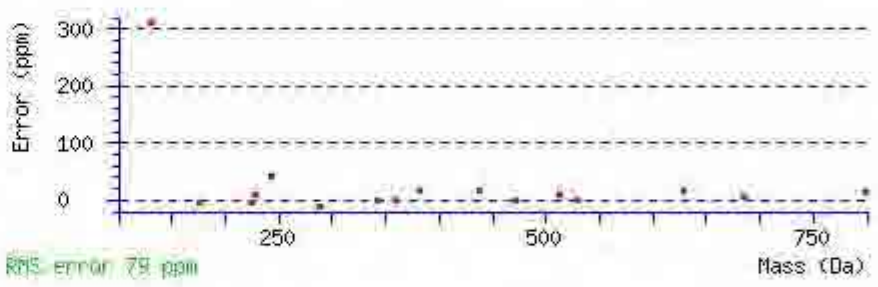
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 926.554901
Ions Score: 47 **Expect:** 0.0013
Matches : 16/64 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					9
2	243.133933	122.070605	225.123368	113.065322	L	*798.519600*	399.763438	781.493051	391.250163	8
3	300.155397	150.581336	282.144832	141.576054	G	*685.435536*	343.221406	668.408987	334.708131	7
4	399.223811	200.115544	381.213246	191.110261	V	*628.414072*	314.710674	611.387523	306.197400	6
5	456.245275	228.626275	438.234710	219.620993	G	*529.345658*	265.176467	512.319109	256.663192	5
6	569.329339	285.168308	551.318774	276.163025	I	*472.324194*	236.665735	455.297645	228.152460	4
7	640.366453	320.686865	622.355888	311.681582	A	*359.240130*	180.123703	342.213581	171.610428	3
8	753.450517	377.228897	735.439952	368.223614	L	*288.203016*	144.605146	271.176467	136.091871	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ELGVGIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	926.554901	-0.001713	ELGVGIALR
23.6	926.554901	-0.001713	ELRGLLQV
13.4	926.554901	-0.001713	LREGPVLK
12.5	926.554901	-0.001713	EGVLGALLR
11.3	926.554886	-0.001698	INVELALR
11.1	926.554901	-0.001713	ELLGKVPR
11.0	926.554901	-0.001713	RLEGILGGL
10.2	926.554901	-0.001713	ELKGVPIR
9.6	926.554901	-0.001713	ELLVQAVR
9.3	926.554901	-0.001713	KIVDPLAR

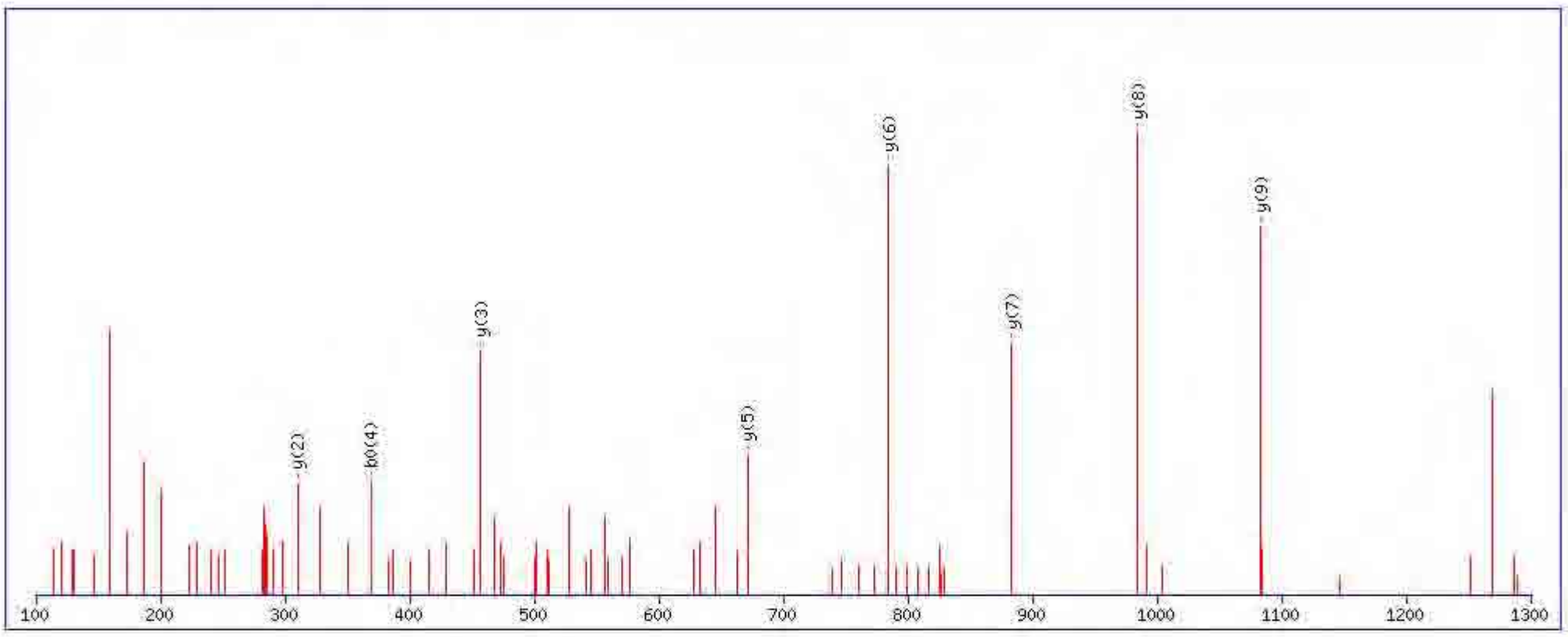
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVVTVIDVFYK**
Found in **FIL A2_HUMAN**, Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1

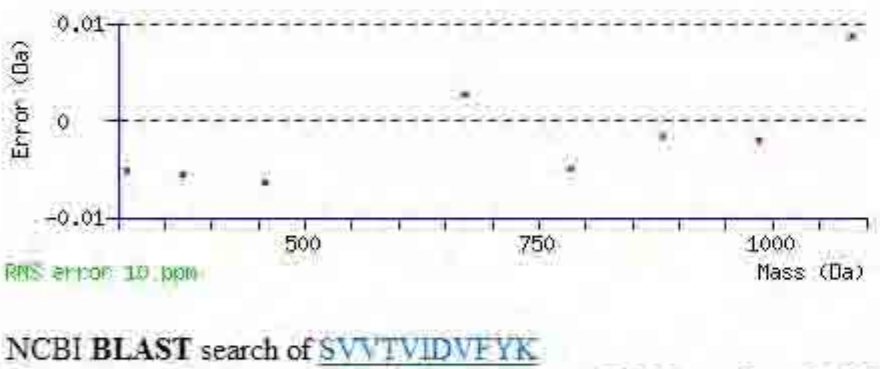
Match to Query 11131: 1268.704868 from(635.359710,2+) rtinseconds(2258) index(18587)
Title: Locus:1.1.1.2370.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

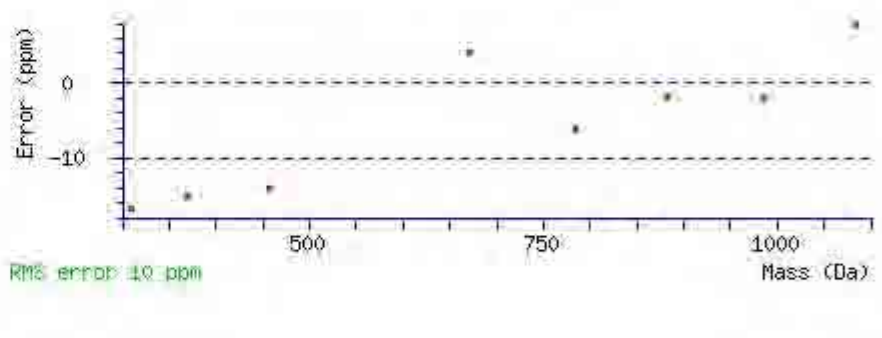
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1268.701660
Ions Score: 55 **Expect:** 4.5e-005
Matches : 8/92 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	187.107718	94.057497	169.097153	85.052214	V	1182.676889	591.842082	1165.650340	583.328808	1164.666324	582.836800	10
3	286.176132	143.591704	268.165567	134.586422	V	*1083.608475*	542.307876	1066.581926	533.794601	1065.597910	533.302593	9
4	387.223811	194.115544	369.213246	185.110261	T	*984.540061*	492.773668	967.513512	484.260394	966.529496	483.768386	8
5	486.292225	243.649751	468.281660	234.644468	V	*883.492382*	442.249829	866.465833	433.736554	865.481817	433.244546	7
6	599.376289	300.191783	581.365724	291.186500	I	*784.423968*	392.715622	767.397419	384.202347	766.413403	383.710339	6
7	714.403232	357.705254	696.392667	348.699972	D	*671.339904*	336.173590	654.313355	327.660315	653.329339	327.168307	5
8	813.471646	407.239461	795.461081	398.234178	V	556.312961	278.660119	539.286412	270.146844			4
9	960.540060	480.773668	942.529495	471.768385	F	*457.244547*	229.125911	440.217998	220.612637			3
10	1123.603389	562.305332	1105.592824	553.300050	Y	*310.176133*	155.591704	293.149584	147.078430			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVVTVIDVFYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	1268.701660	0.003208	SVVTVIDVFYK
8.1	1268.712875	-0.008007	VSLWPVPVAASK
7.5	1268.708847	-0.003979	VSLSQPRTLPAT
6.3	1268.712845	-0.007977	WVIEAKDLPAK
5.8	1268.694931	0.009937	VSSLHTSRVQR
5.8	1268.708832	-0.003964	VSGEPLLAKPAR
5.8	1268.708862	-0.003994	ESPGVPVAKVVR
5.6	1268.708847	-0.003979	LTTAVPSPSKPR
5.6	1268.708862	-0.003994	TSPLPAGQVLVR
5.0	1268.716248	-0.011380	VCAPVLAKPGVIS

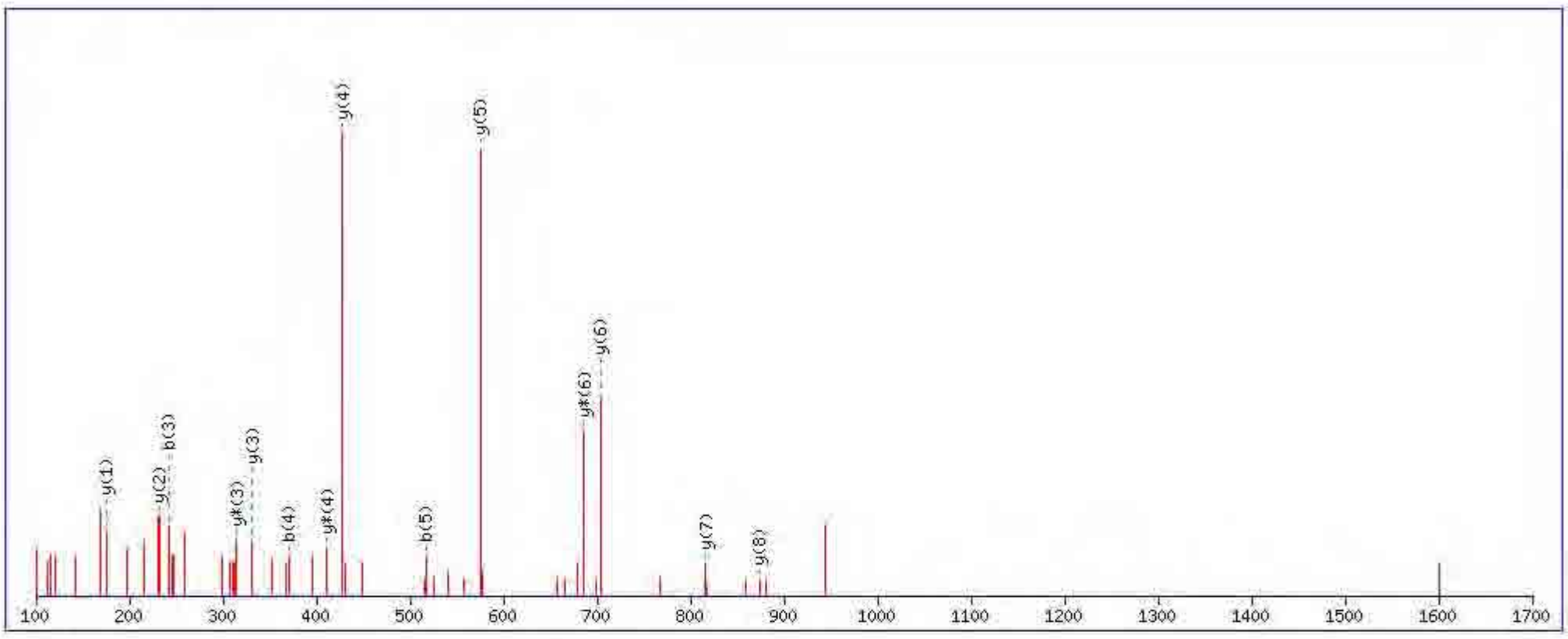
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

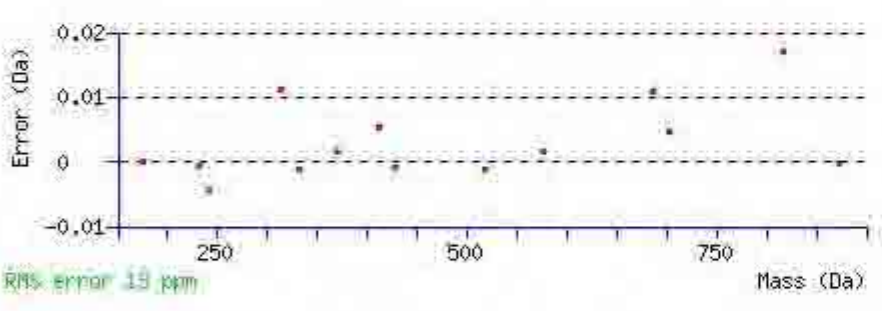
Match to Query 3534: 943.527648 from(472.771100,2+) rtinseconds(1496) index(9213)
Title: Locus:1.1.1.1952.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

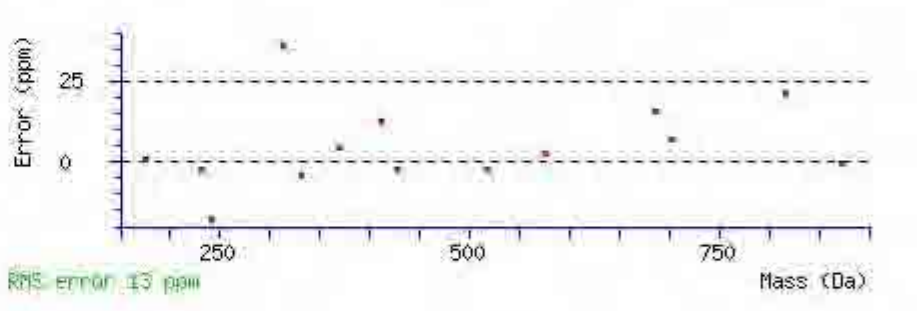
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Ions Score: 65 **Expect:** 5.3e-005
Matches : 14/58 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	*873.494114*	437.250695	856.467565	428.737421	8
3	**242.149918**	121.578597			L	*816.472650*	408.739963	799.446101	400.226689	7
4	**370.208496**	185.607886	353.181947	177.094612	Q	*703.388586*	352.197931	686.362037	343.684657	6
5	**517.276910**	259.142093	500.250361	250.628819	F	*575.330008*	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	*428.261594*	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	*331.208830*	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	*232.140416*	116.573846	215.113867	108.060571	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	943.523956	0.003692	AGLQFPVGR
27.1	943.535172	-0.007524	QPKPFRR
25.0	943.519928	0.007720	QLDRTVGR
16.6	943.533829	-0.006181	KIGEVSSPK
16.1	943.523956	0.003692	AGSLVWGVR
15.6	943.533813	-0.006165	QIKEAIDK
15.6	943.533813	-0.006165	QLKEVAEK
15.6	943.535172	-0.007524	AGLPFQRR
14.3	943.519897	0.007751	QLKAQNSR
14.1	943.519897	0.007751	QITEAARR

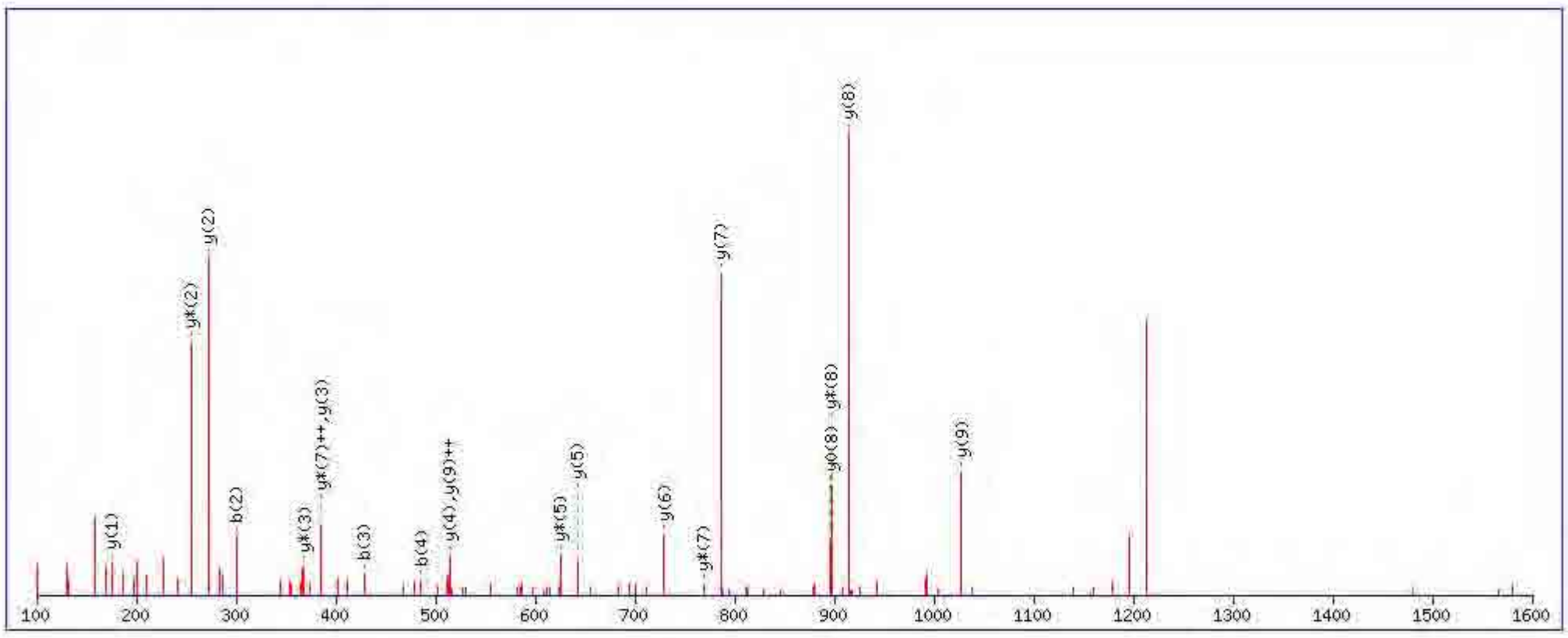
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

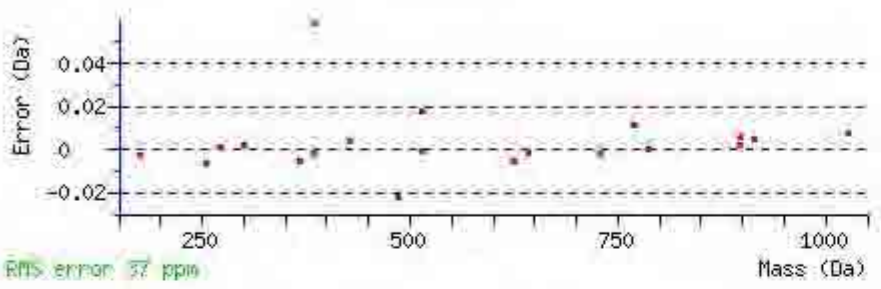
Match to Query 9890: 1212.630608 from(607.322580,2+) rtinseconds(1368) index(7510)
Title: Locus:1.1.1.1882.18
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

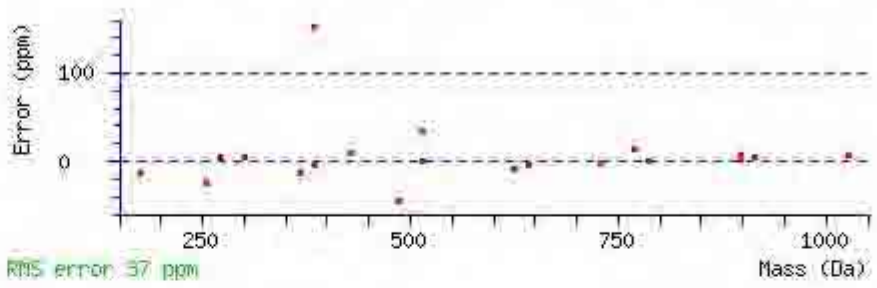
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1212.625107
Ions Score: 70 **Expect:** 1e-005
Matches : 20/90 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.086589	94.046932					W							10
2	300.170653	150.588965					L	*1027.553085*	514.280181	1010.526536	505.766906	1009.542520	505.274898	9
3	428.229231	214.618254	411.202682	206.104979			Q	*914.469021*	457.738148	897.442472	449.224874	896.458456	448.732866	8
4	485.250695	243.128986	468.224146	234.615711			G	*786.410443*	393.708860	769.383894	385.195585	768.399878	384.703577	7
5	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	S	*729.388979*	365.198128	712.362430	356.684853	711.378414	356.192845	6
6	700.341301	350.674289	683.314752	342.161014	682.330736	341.669006	Q	*642.356951*	321.682114	625.330402	313.168839	624.346386	312.676831	5
7	829.383894	415.195585	812.357345	406.682311	811.373329	406.190303	E	*514.298373*	257.652825	497.271824	249.139550	496.287808	248.647542	4
8	942.467958	471.737617	925.441409	463.224343	924.457393	462.732335	L	*385.255780*	193.131528	368.229231	184.618253			3
9	1039.520722	520.263999	1022.494173	511.750724	1021.510157	511.258716	P	*272.171716*	136.589496	255.145167	128.076221			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WLQGSQELPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.0	1212.625107	0.005501	WLQGSQELPR
16.0	1212.636353	-0.005745	GTIRYHTPPR
13.3	1212.625107	0.005501	QWGSPEKLPR
13.1	1212.636353	-0.005745	GTIRYHTPPR
12.3	1212.632507	-0.001899	VEAKVVCFYR
12.2	1212.636337	-0.005729	WTNVDPSRAR
12.1	1212.640366	-0.009758	LWPPPYRPR
12.1	1212.640366	-0.009758	LWPPPYRPR
12.1	1212.640366	-0.009758	LWPPPYRPR
11.5	1212.639038	-0.008430	SVPEFPLSPPK

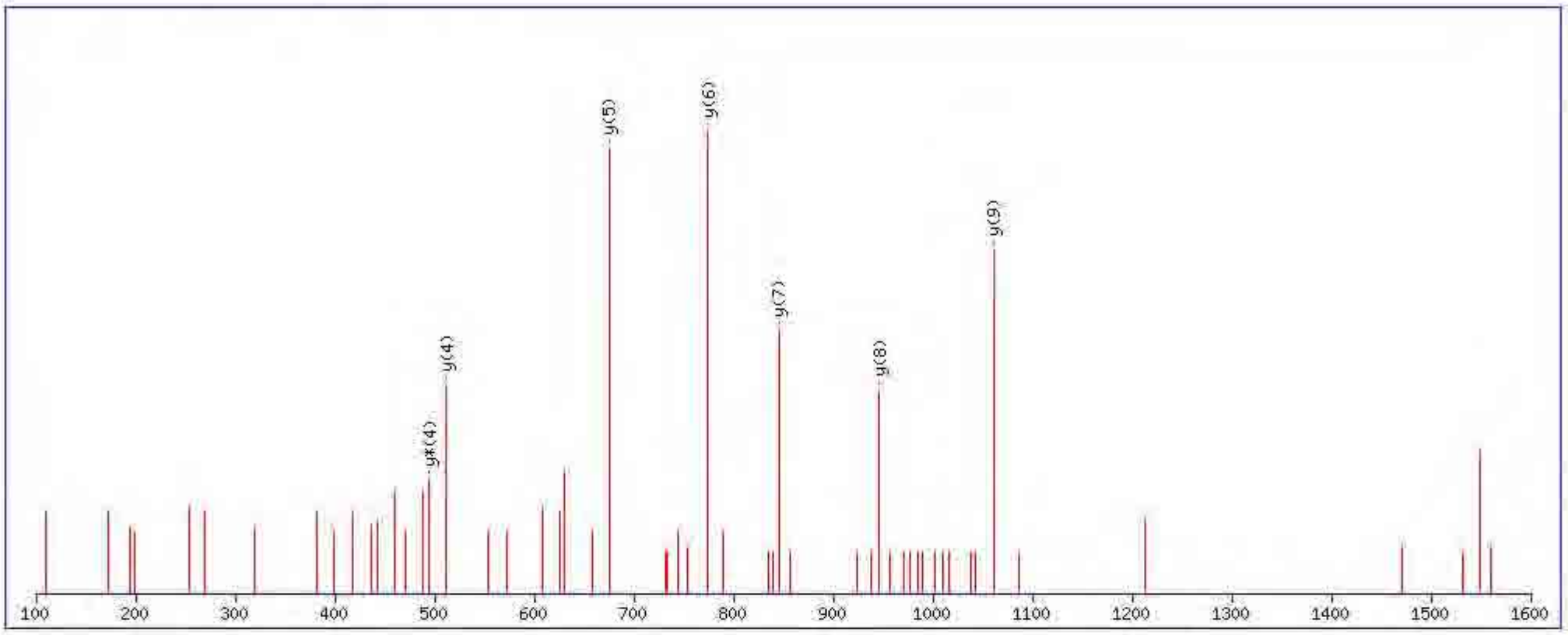
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEDTAVYYCAR**
Found in **HV302_HUMAN**, Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1

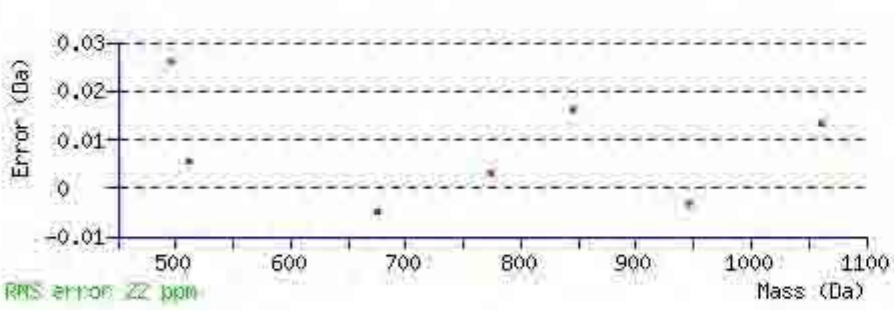
Match to Query 10936: 1260.551848 from(631.283200,2+) rtinseconds(1165) index(5257)
Title: Locus:1.1.1.1767.25
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

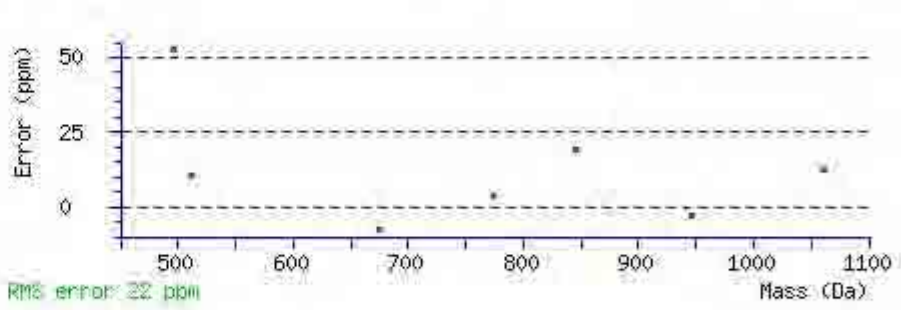
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1260.544464
Ions Score: 43 **Expect:** 0.00016
Matches : 7/84 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	201.086983	101.047130	183.076418	92.041847	E	1190.514652	595.760964	1173.488103	587.247690	1172.504087	586.755682	10
3	316.113926	158.560601	298.103361	149.555319	D	*1061.472059*	531.239668	1044.445510	522.726393	1043.461494	522.234385	9
4	417.161605	209.084441	399.151040	200.079158	T	*946.445116*	473.726196	929.418567	465.212922	928.434551	464.720914	8
5	488.198719	244.602998	470.188154	235.597715	A	*845.397437*	423.202357	828.370888	414.689082			7
6	587.267133	294.137205	569.256568	285.131922	V	*774.360323*	387.683800	757.333774	379.170525			6
7	750.330462	375.668869	732.319897	366.663587	Y	*675.291909*	338.149593	658.265360	329.636318			5
8	913.393791	457.200534	895.383226	448.195251	Y	*512.228580*	256.617928	495.202031	248.104654			4
9	1016.402976	508.705126	998.392411	499.699844	C	349.165251	175.086264	332.138702	166.572989			3
10	1087.440090	544.223683	1069.429525	535.218401	A	246.156066	123.581671	229.129517	115.068397			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AEDTAVYYCAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	1260.544464	0.007384	AEDTAVYYCAR
43.3	1260.544464	0.007384	AEBTAVYYCAR
43.3	1260.544464	0.007384	AZBTAVYYCAR
2.7	1260.547852	0.003996	CPSEAGAMTQPAV

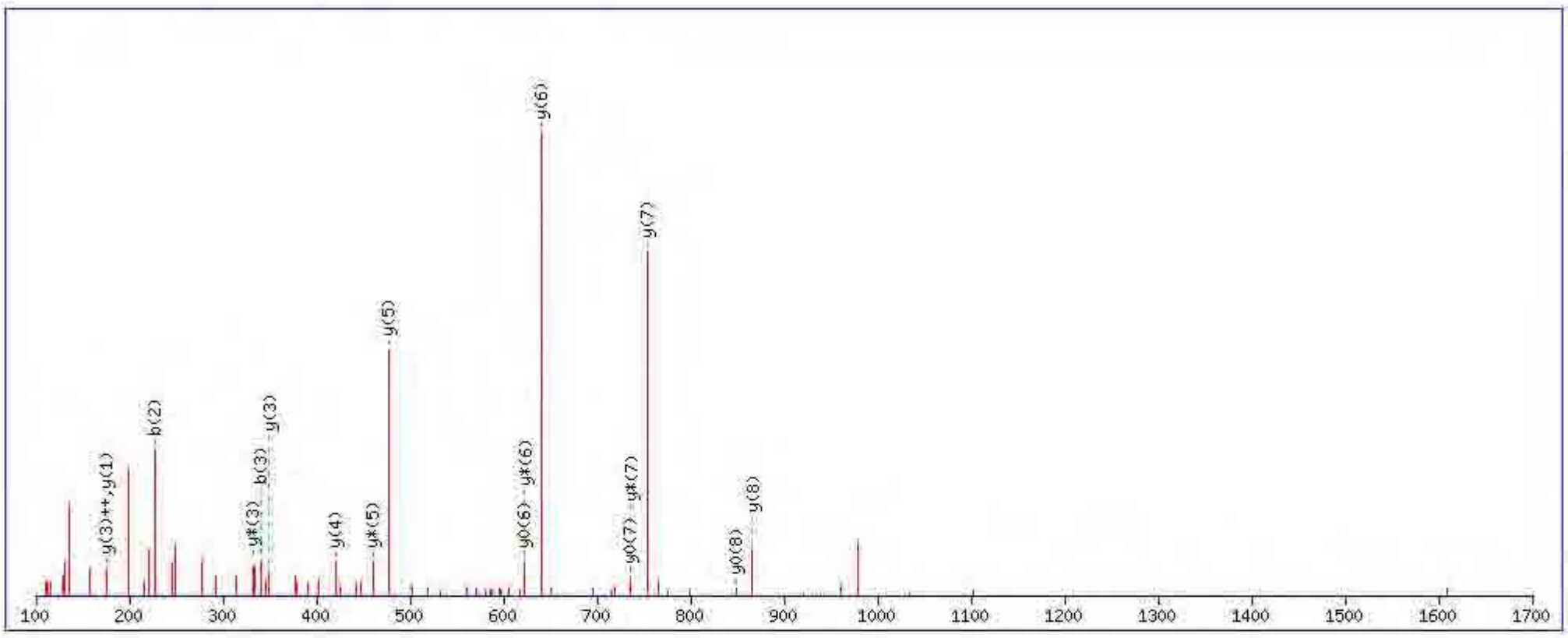
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASSR**
Found in **KV302_HUMAN**, Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1

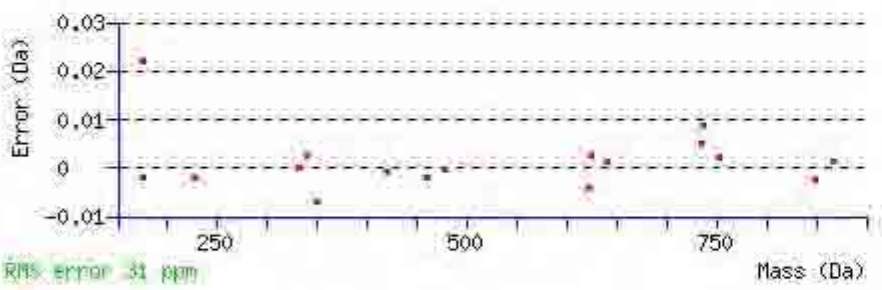
Match to Query 4181: 978.556728 from(490.285640,2+) rtinseconds(1274) index(6497)
Title: Locus:1.1.1.1829.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

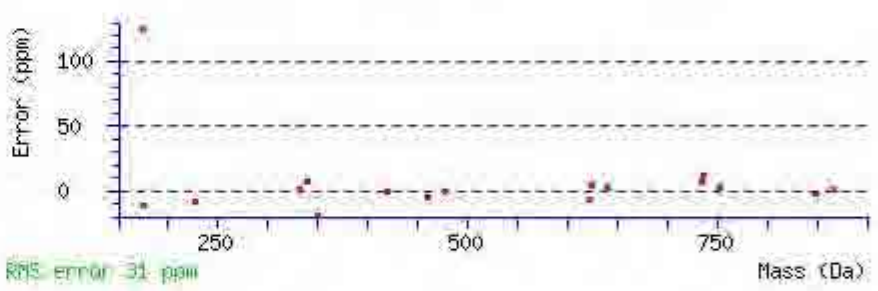
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 978.549805
Ions Score: 46 **Expect:** 0.0022
Matches : 17/66 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	866.473043	433.740160	849.446494	425.226885	848.462478	424.734877	8
3	340.259468	170.633372			I	753.388979	377.198128	736.362430	368.684853	735.378414	368.192845	7
4	503.322797	252.165036			Y	640.304915	320.656096	623.278366	312.142821	622.294350	311.650813	6
5	560.344261	280.675769			G	477.241586	239.124431	460.215037	230.611156	459.231021	230.119148	5
6	631.381375	316.194326			A	420.220122	210.613699	403.193573	202.100424	402.209557	201.608416	4
7	718.413403	359.710340	700.402838	350.705057	S	349.183008	175.095142	332.156459	166.581867	331.172443	166.089859	3
8	805.445431	403.226354	787.434866	394.221071	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIYGASSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	978.549805	0.006923	LLIYGASSR
37.5	978.549805	0.006923	LLLHENQL
26.2	978.561066	-0.004338	IPLHTVRQ
26.2	978.561050	-0.004322	IPPHRLSK
26.2	978.549820	0.006908	LLLHLQQD
26.2	978.561050	-0.004322	PIIHSPKR
18.7	978.561050	-0.004322	PILQHISR
18.2	978.549805	0.006923	LLHLEKPN
17.9	978.557205	-0.000477	ILLTFMNK
17.9	978.549820	0.006908	IPLPPASPR

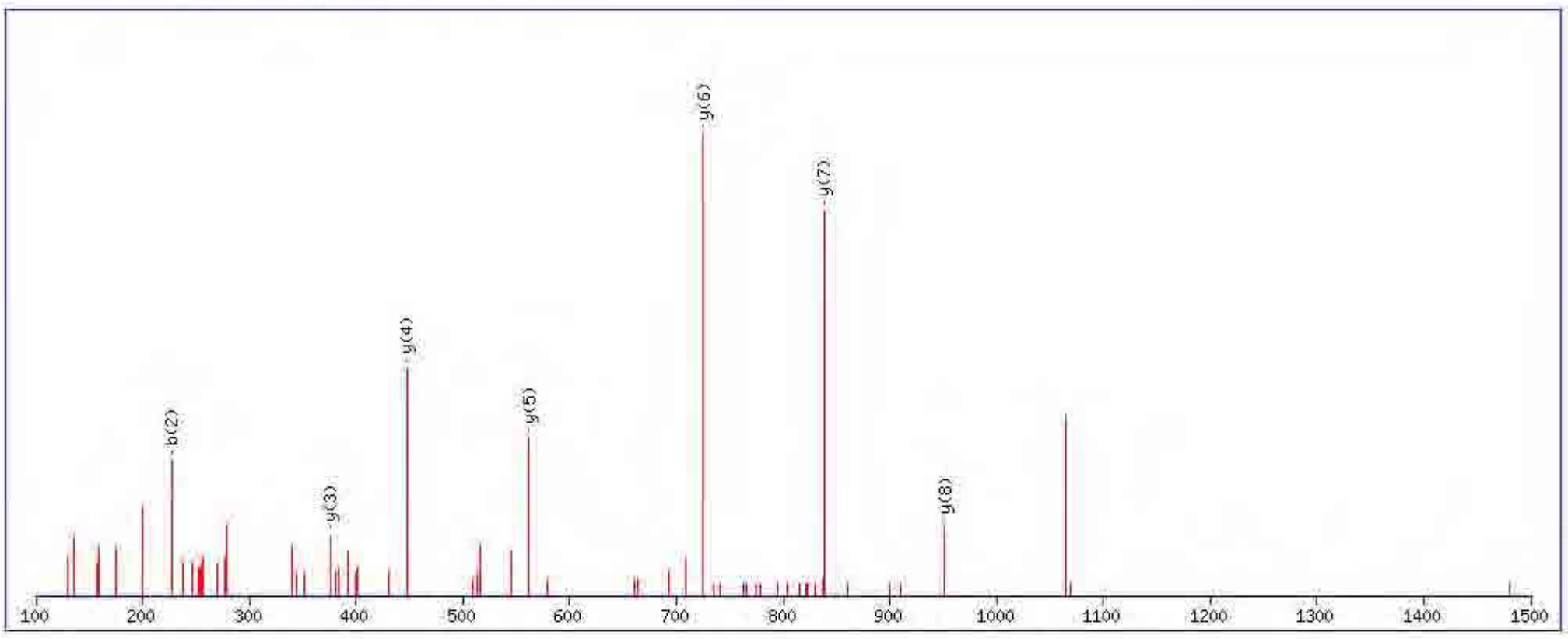
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

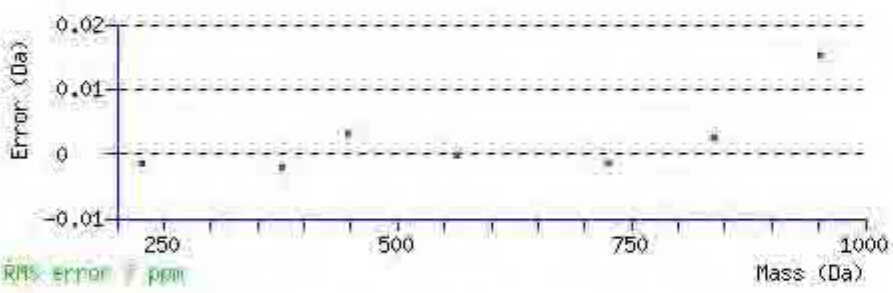
Match to Query 5952: 1063.568088 from(532.791320,2+) rtinseconds(1343) index(7194)
Title: Locus:1.1.1.1868.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

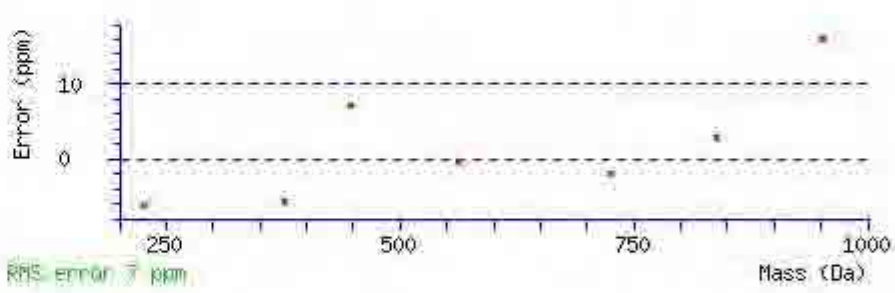
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 50 **Expect:** 0.0017
Matches : 7/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*951.489421*	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	*838.405357*	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	*725.321293*	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	*562.257964*	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	*447.231021*	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	*376.193907*	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1063.566177	0.001911	LLIYDASNR
24.4	1063.573593	-0.005505	LLPNFGKML
22.0	1063.577408	-0.009320	LLPAAEAHAR
20.8	1063.559006	0.009082	LLLPPGYFP
14.8	1063.566208	0.001880	LPLAQVSAHP
13.0	1063.577438	-0.009350	PLPRPAPPR
12.7	1063.566208	0.001880	ILPPDQRPP
12.7	1063.566208	0.001880	ILPPDQRPP
12.2	1063.570221	-0.002133	IIYIPPPDH
11.8	1063.573593	-0.005505	LIAQACVSIF

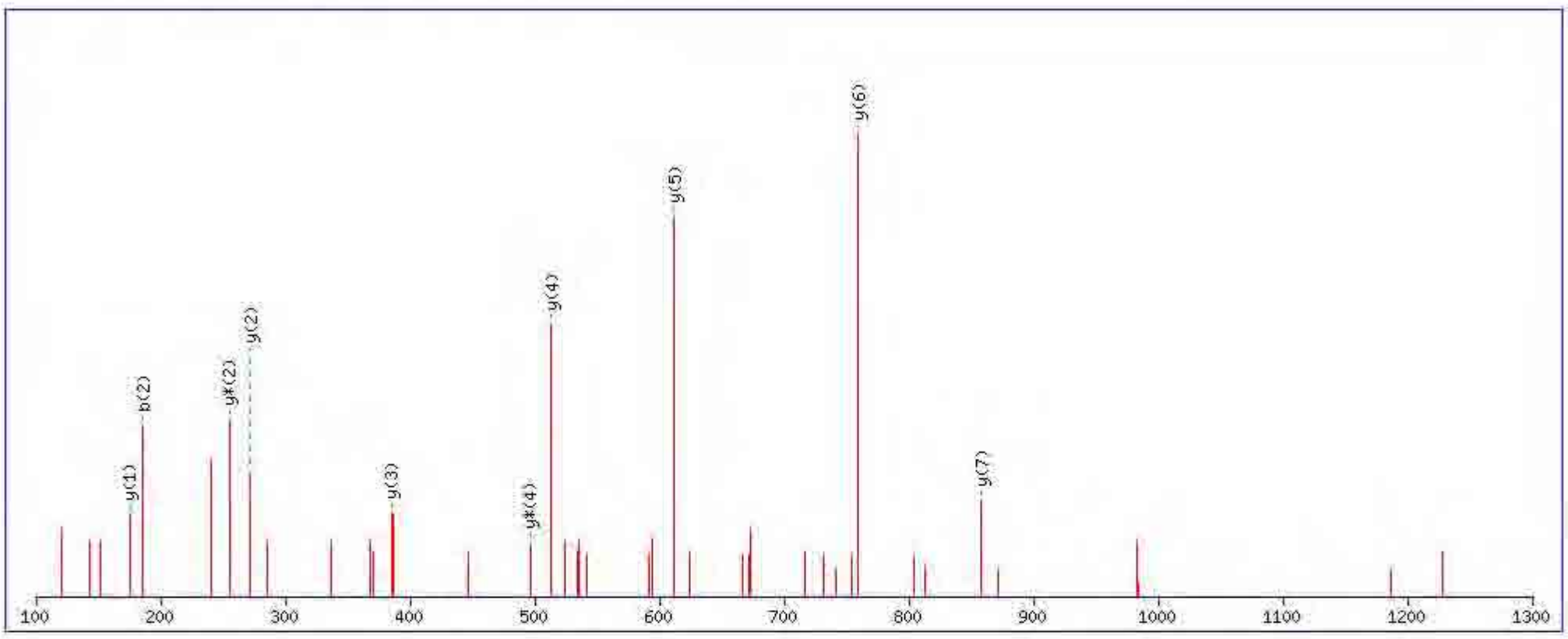
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANVFVQLPR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

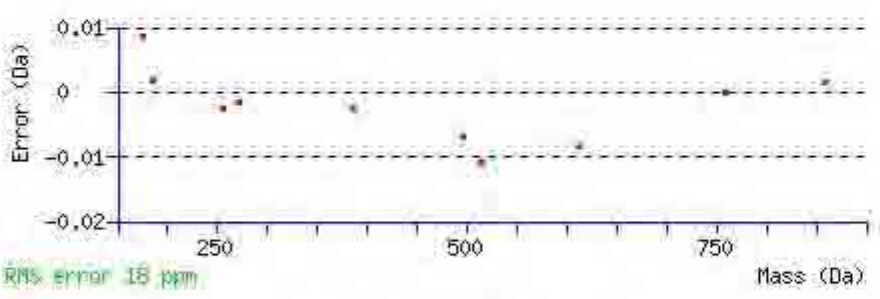
Match to Query 5466: 1042.596688 from(522.305620,2+) rtinseconds(1618) index(10691)
Title: Locus:1.1.1.2019.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

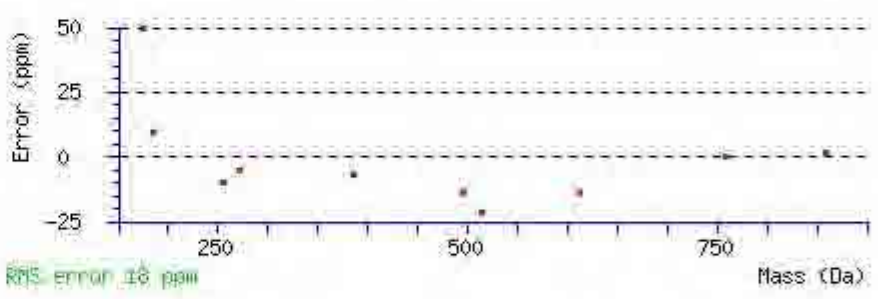
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1042.592361
Ions Score: 38 **Expect:** 0.0034
Matches : 10/62 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	186.087317	93.547296	169.060768	85.034022	N	972.562527	486.784902	955.535978	478.271627	8
3	285.155731	143.081504	268.129182	134.568229	V	*858.519600*	429.763438	841.493051	421.250164	7
4	432.224145	216.615710	415.197596	208.102436	F	*759.451186*	380.229231	742.424637	371.715957	6
5	531.292559	266.149918	514.266010	257.636643	V	*612.382772*	306.695024	595.356223	298.181750	5
6	659.351137	330.179207	642.324588	321.665932	Q	*513.314358*	257.160817	496.287809	248.647543	4
7	772.435201	386.721239	755.408652	378.207964	L	*385.255780*	193.131528	368.229231	184.618253	3
8	869.487965	435.247621	852.461416	426.734346	P	*272.171716*	136.589496	255.145167	128.076221	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ANVFVQLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	1042.592361	0.004327	ANVFVQLPR
11.1	1042.592377	0.004311	KGVFGPPLGR
11.1	1042.592377	0.004311	KGVFGPPLGR
9.9	1042.588318	0.008370	RGLSSSALPR
8.3	1042.602264	-0.005576	PSVTKVTPAK
7.0	1042.592361	0.004327	TPGAFKGLPR
6.1	1042.588318	0.008370	GARSLLSSPR
1.6	1042.602249	-0.005561	GKVGSLPLEK
0.8	1042.588318	0.008370	NGLDRIISR
0.7	1042.588333	0.008355	APSLARTVGR

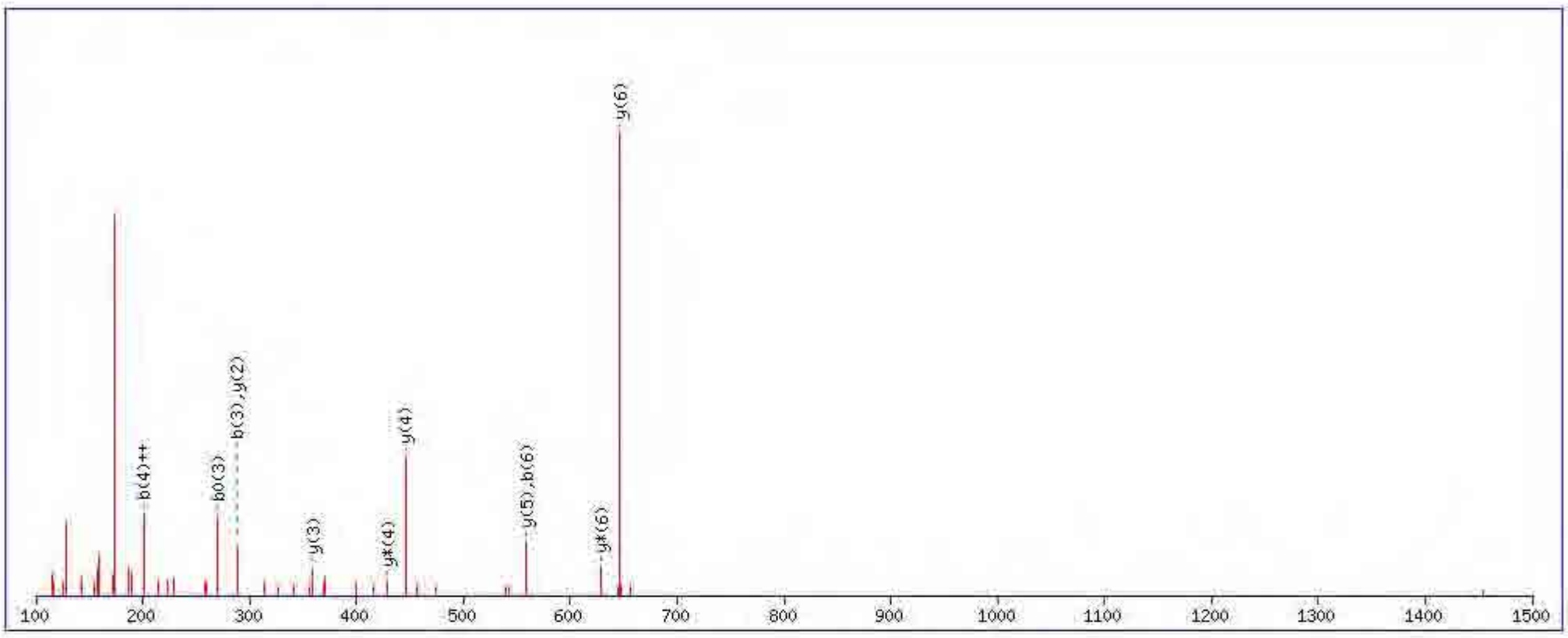
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSLSAIR**
Found in **LRC48_HUMAN**, Leucine-rich repeat-containing protein 48 OS=Homo sapiens GN=LRRC48 PE=2 SV=2

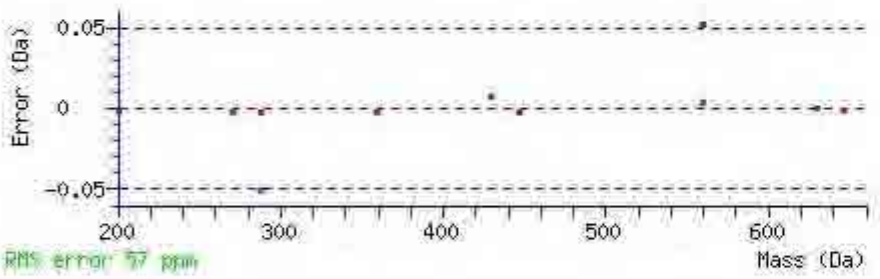
Match to Query 1575: 845.490508 from(423.752530,2+) rtinseconds(1172) index(5330)
Title: Locus:1.1.1.1772.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

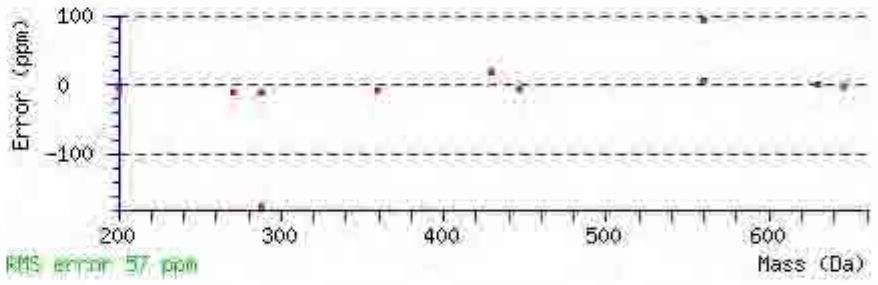
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 845.497040
Ions Score: 42 **Expect:** 0.0052
Matches : 12/62 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	**201.123368**	101.065322	183.112803	92.060039	S	733.420278	367.213777	716.393729	358.700502	715.409713	358.208494	7
3	**288.155396**	144.581336	270.144831	135.576053	S	***646.388250***	323.697763	629.361701	315.184488	628.377685	314.692480	6
4	401.239460	201.123368	383.228895	192.118085	L	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	5
5	488.271488	244.639382	470.260923	235.634099	S	***446.272158***	223.639717	429.245609	215.126442	428.261593	214.634434	4
6	**559.308602**	280.157939	541.298037	271.152656	A	***359.240130***	180.123703	342.213581	171.610428			3
7	672.392666	336.699971	654.382101	327.694688	I	***288.203016***	144.605146	271.176467	136.091871			2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSLSAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	845.497040	-0.006532	LSSLSAIR
30.5	845.485840	0.004668	TVSISVQI
30.3	845.485809	0.004699	SLSAALLTA
25.2	845.497055	-0.006547	TVSSLAIR
21.8	845.485825	0.004683	ISSALSVLG
19.0	845.485809	0.004699	SLSAEKVL
18.1	845.485825	0.004683	ISSIQSIV
18.1	845.485825	0.004683	ISSPVISK
18.1	845.485809	0.004699	LSSIGELK
18.1	845.485809	0.004699	LSSLAVEK

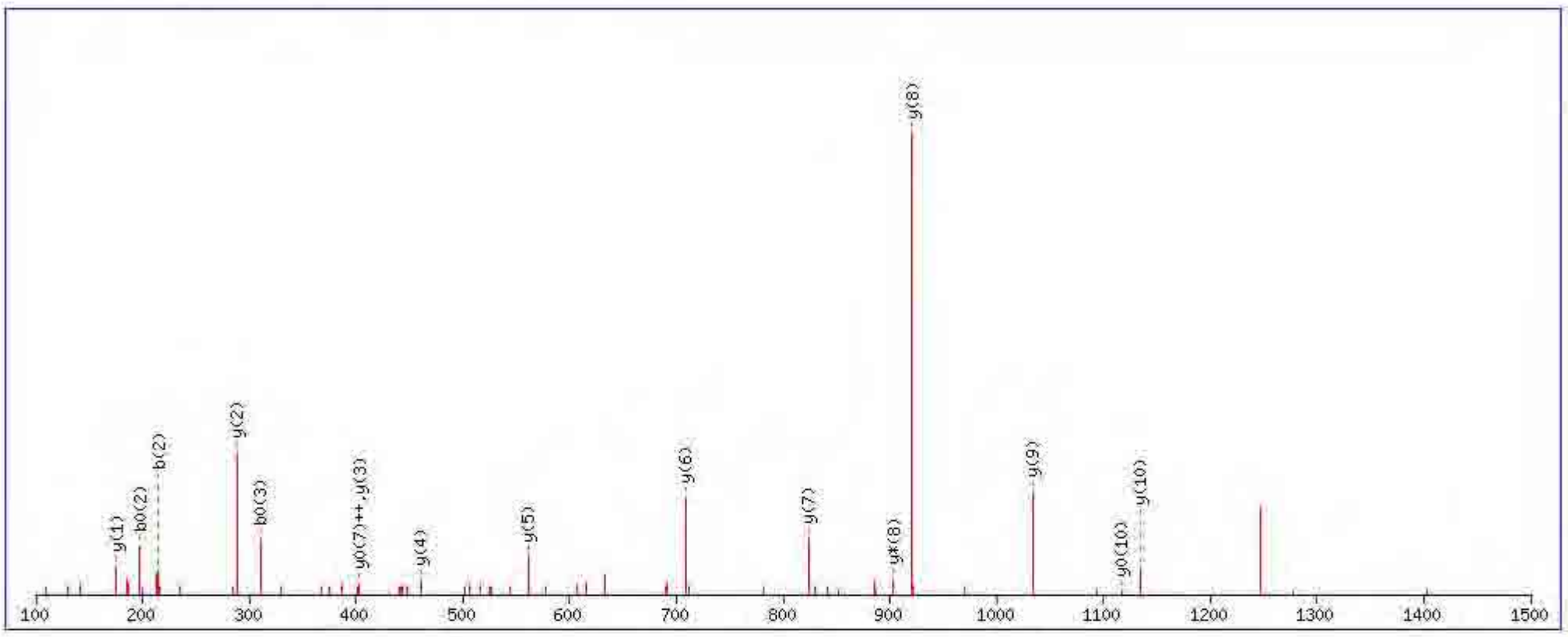
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLPDFTGDLR**
Found in **LBP_HUMAN**, Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3

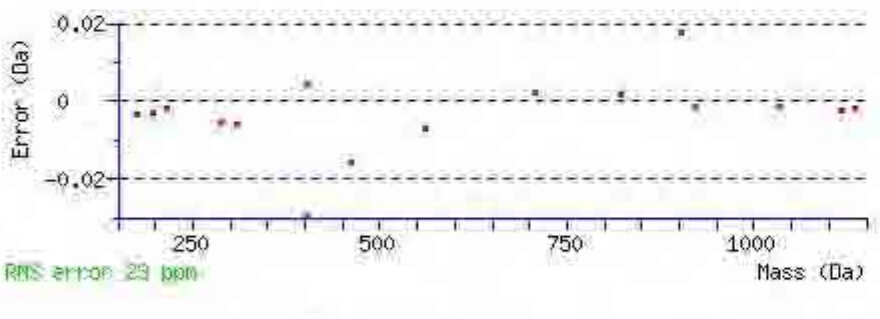
Match to Query 10662: 1246.660108 from(624.337330,2+) rtinseconds(2107) index(16742)
Title: Locus:1.1.1.2288.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

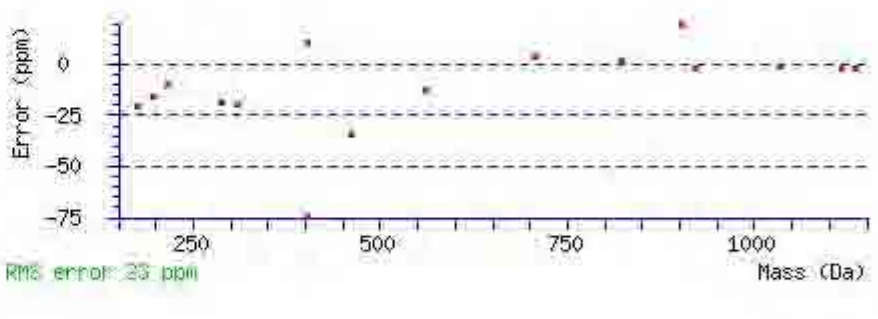
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1246.655762
Ions Score: 81 **Expect:** 1.5e-006
Matches : 16/94 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	*1134.578966*	567.793121	1117.552417	559.279847	1116.568401	558.787839	10
3	328.223083	164.615179	310.212518	155.609897	L	*1033.531287*	517.269282	1016.504738	508.756007	1015.520722	508.263999	9
4	425.275847	213.141561	407.265282	204.136279	P	*920.447223*	460.727249	903.420674	452.213975	902.436658	451.721967	8
5	540.302790	270.655033	522.292225	261.649750	D	*823.394459*	412.200868	806.367910	403.687593	805.383894	403.195585	7
6	687.371204	344.189240	669.360639	335.183957	F	*708.367516*	354.687396	691.340967	346.174122	690.356951	345.682114	6
7	788.418883	394.713079	770.408318	385.707797	T	*561.299102*	281.153189	544.272553	272.639915	543.288537	272.147907	5
8	845.440347	423.223812	827.429782	414.218529	G	*460.251423*	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	960.467290	480.737283	942.456725	471.732000	D	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1073.551354	537.279315	1055.540789	528.274032	L	*288.203016*	144.605146	271.176467	136.091871			2
11					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLPDFTGDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.0	1246.655762	0.004346	ITLPDFTGDLR
18.2	1246.649216	0.010892	LPVREFSMPR
17.8	1246.659103	0.001005	LTPEIMKEVR
16.8	1246.659119	0.000989	PTDIAMLTLLR
16.8	1246.655762	0.004346	PTPPGQPPISPK
15.9	1246.653076	0.007032	PTPGQRLHPGR
13.7	1246.659103	0.001005	LSLECSLVDIR
13.1	1246.655762	0.004346	PPSIPTFATLR
12.3	1246.655762	0.004346	PFPTGSLLDLR
11.9	1246.656616	0.003492	LTLFMAVPPCR

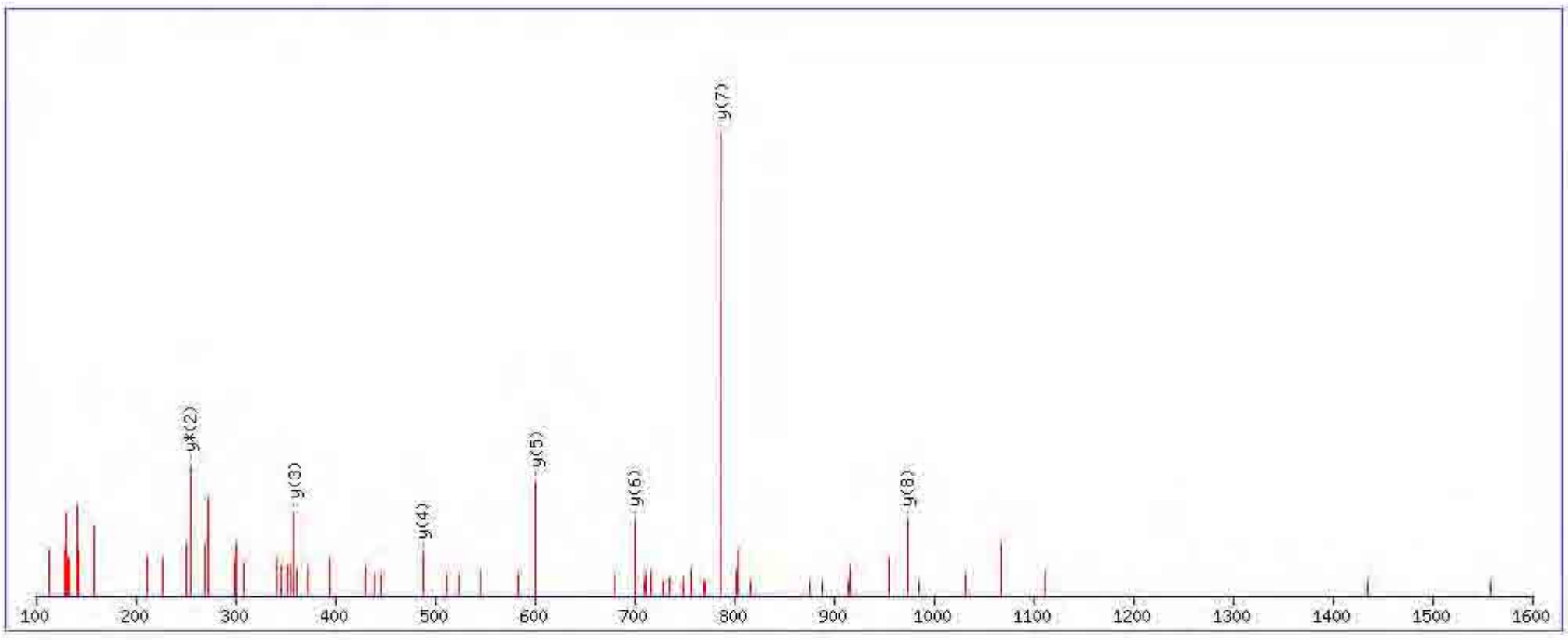
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IWSVLESPR**
Found in **MAMC2_HUMAN**, MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3

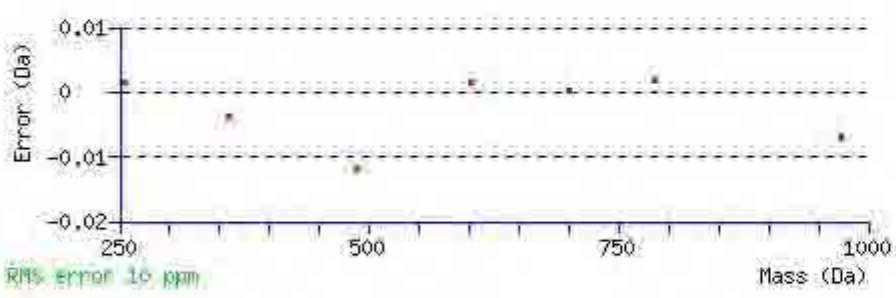
Match to Query 6452: 1085.593928 from(543.804240,2+) rtinseconds(1716) index(11949)
Title: Locus:1.1.1.2073.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

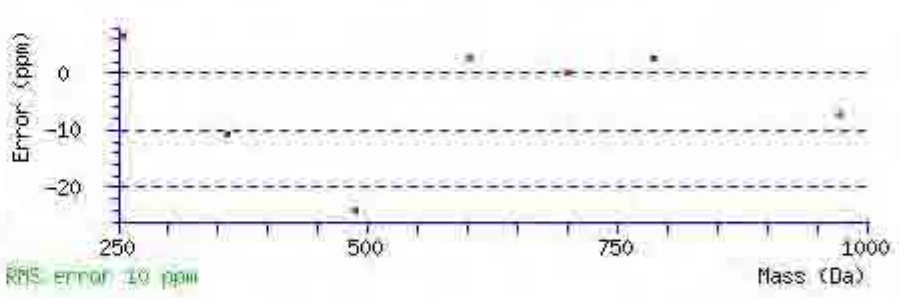
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1085.586929
Ions Score: 53 **Expect:** 0.00071
Matches : 7/72 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	300.170653	150.588965			W	*973.510156*	487.258716	956.483607	478.745442	955.499591	478.253434	8
3	387.202681	194.104979	369.192116	185.099696	S	*787.430843*	394.219060	770.404294	385.705785	769.420278	385.213777	7
4	486.271095	243.639186	468.260530	234.633903	V	*700.398815*	350.703046	683.372266	342.189771	682.388250	341.697763	6
5	599.355159	300.181218	581.344594	291.175935	L	*601.330401*	301.168839	584.303852	292.655564	583.319836	292.163556	5
6	728.397752	364.702514	710.387187	355.697232	E	*488.246337*	244.626807	471.219788	236.113532	470.235772	235.621524	4
7	815.429780	408.218528	797.419215	399.213246	S	*359.203744*	180.105510	342.177195	171.592236	341.193179	171.100228	3
8	912.482544	456.744910	894.471979	447.739628	P	272.171716	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IWSVLESPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.6	1085.586929	0.006999	IWSVLESPR
30.3	1085.596832	-0.002904	LGSEVLEQVL
20.1	1085.596817	-0.002889	IDADAIVEKI
20.1	1085.590958	0.002970	LWWLPVEK
17.0	1085.586929	0.006999	PAFGPLEALR
12.5	1085.598160	-0.004232	IADSLRHFK
11.8	1085.601532	-0.007604	LAPTCLQKGR
9.8	1085.586945	0.006983	WISVSPLPR
9.4	1085.586914	0.007014	EAVLWEALR
8.9	1085.596848	-0.002920	SVPSLVSIPAT

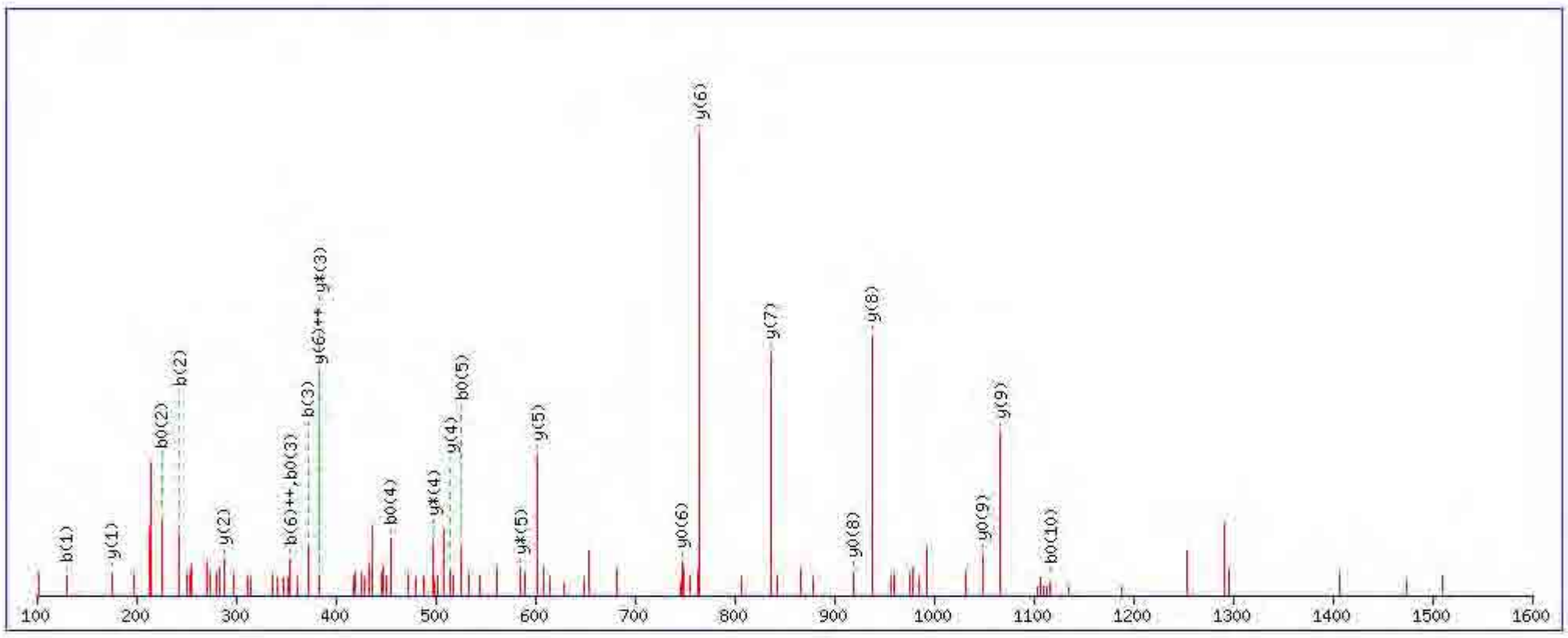
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELETAYSNLLR**
Found in **MYOC_HUMAN**, Myocilin OS=Homo sapiens GN=MYOC PE=1 SV=2

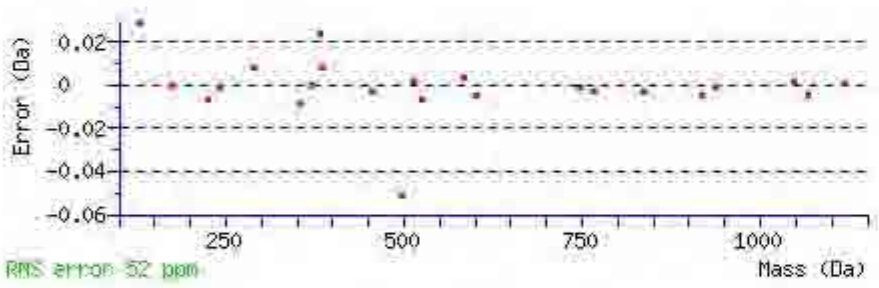
Match to Query 11968: 1307.675568 from(654.845060,2+) rtinseconds(1763) index(12584)
Title: Locus:1.1.1.2098.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

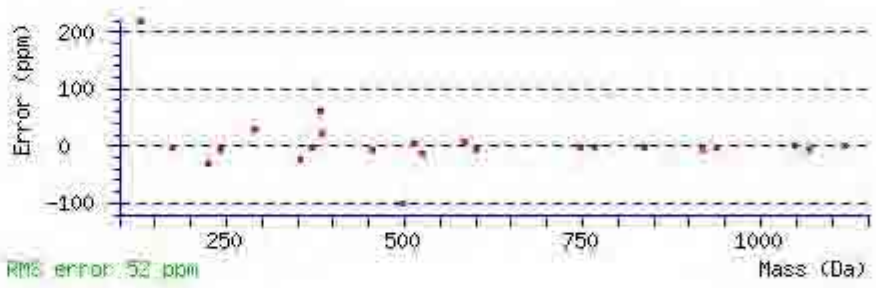
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1307.672089
Ions Score: 38 **Expect:** 0.0014
Matches : 24/98 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	L	1179.636814	590.322045	1162.610265	581.808770	1161.626249	581.316762	10
3	372.176526	186.591901			354.165961	177.586619	E	*1066.552750*	533.780013	1049.526201	525.266738	1048.542185	524.774730	9
4	473.224205	237.115741			455.213640	228.110458	T	*937.510157*	469.258716	920.483608	460.745442	919.499592	460.253434	8
5	544.261319	272.634298			526.250754	263.629015	A	*836.462478*	418.734877	819.435929	410.221602	818.451913	409.729594	7
6	707.324648	354.165962			689.314083	345.160680	Y	*765.425364*	383.216320	748.398815	374.703045	747.414799	374.211037	6
7	794.356676	397.681976			776.346111	388.676694	S	*602.362035*	301.684655	585.335486	293.171381	584.351470	292.679373	5
8	908.399603	454.703440	891.373054	446.190165	890.389038	445.698157	N	*515.330007*	258.168641	498.303458	249.655367			4
9	1021.483667	511.245472	1004.457118	502.732197	1003.473102	502.240189	L	401.287080	201.147178	384.260531	192.633903			3
10	1134.567731	567.787503	1117.541182	559.274229	1116.557166	558.782221	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ELETAYSNLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	1307.672089	0.003479	ELETAYSNLLR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
7.1	1307.672134	0.003434	EPSLTPPAVPPR
6.9	1307.672134	0.003434	DVLPDKPAPGAVN
6.1	1307.672165	0.003403	TPGPIGVPGPAGPK
5.2	1307.672165	0.003403	TPGPIGVPGPAGPK

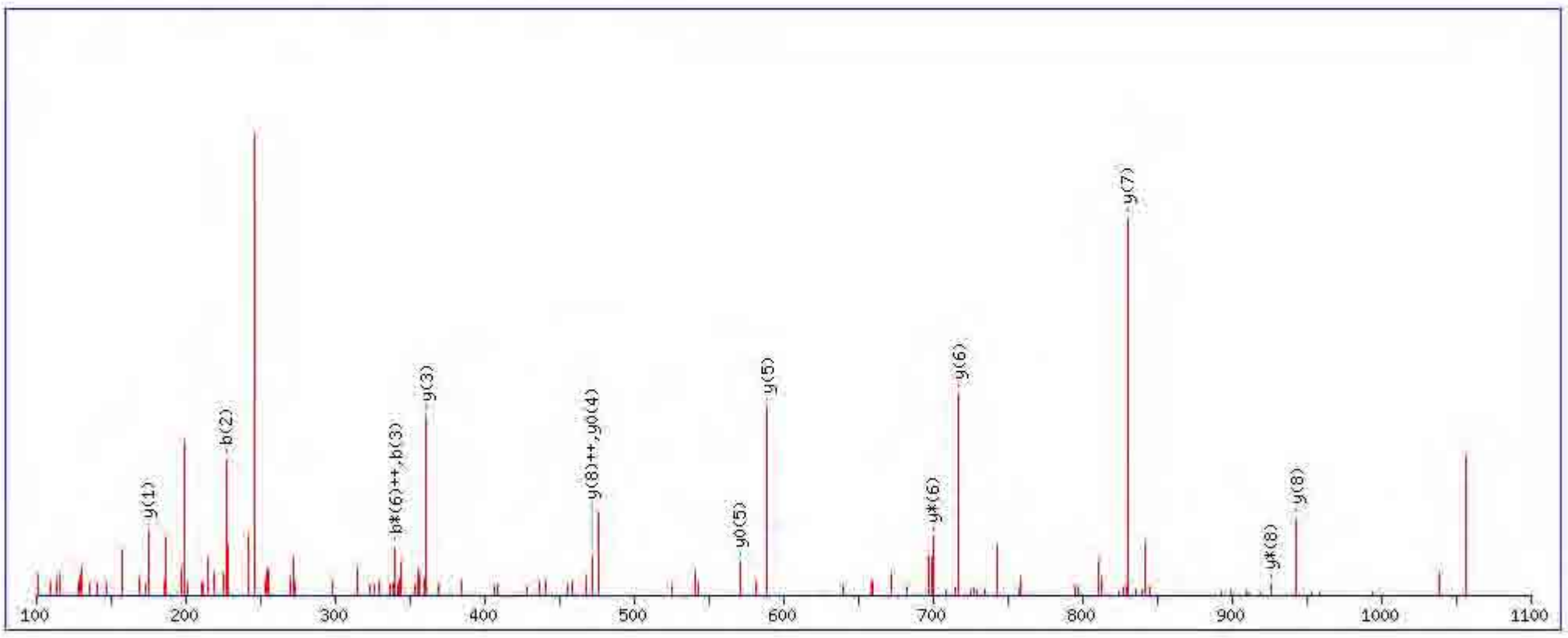
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLIKVEEGR**
Found in **NR4A3_HUMAN**, Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=2 SV=3

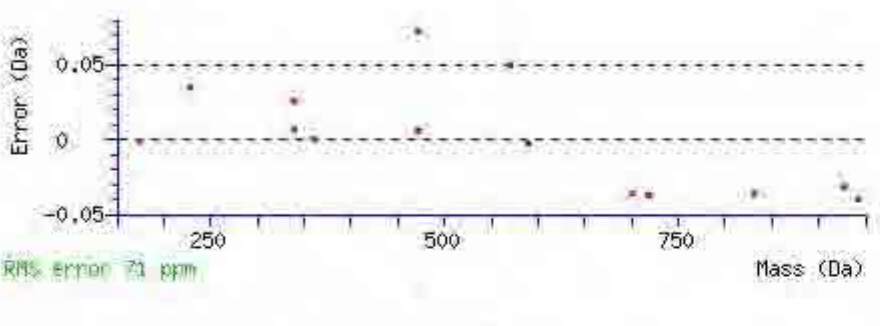
Match to Query 5757: 1055.603668 from(528.809110,2+) rtinseconds(1565) index(10016)
Title: Locus:1.1.1.1990.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

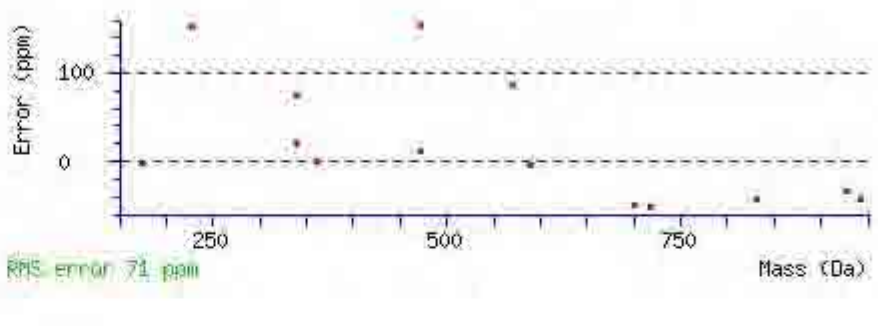
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597488
Variable modifications:
P1 : Oxidation (P)
Ions Score: 44 **Expect:** 0.0051
Matches : 14/76 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.054955	57.531116					P							9
2	227.139019	114.073147					L	*943.557107*	472.282192	926.530558	463.768917	925.546542	463.276909	8
3	340.223083	170.615179					I	*830.473043*	415.740160	813.446494	407.226885	812.462478	406.734877	7
4	468.318046	234.662661	451.291497	226.149386			K	*717.388979*	359.198128	700.362430	350.684853	699.378414	350.192845	6
5	567.386460	284.196868	550.359911	275.683594			V	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	E	490.225602	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	825.471646	413.239461	808.445097	404.726187	807.461081	404.234179	E	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	882.493110	441.750193	865.466561	433.236919	864.482545	432.744911	G	232.140416	116.573846	215.113867	108.060571			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PLIKVEEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1055.597488	0.006180	PLIKVEEGR
41.5	1055.597504	0.006164	LLPQLTSPR
32.9	1055.612762	-0.009094	LLIQPGPRF
28.8	1055.608704	-0.005036	LLLRAEGER
27.0	1055.608704	-0.005036	ILLREAEGR
27.0	1055.612747	-0.009079	LLLPAATWR
23.2	1055.597488	0.006180	LLKLDPADR
23.2	1055.601532	0.002136	ILLGLWVQD
23.1	1055.597488	0.006180	LGPLALETAR
22.4	1055.597488	0.006180	LPASLSLPAR

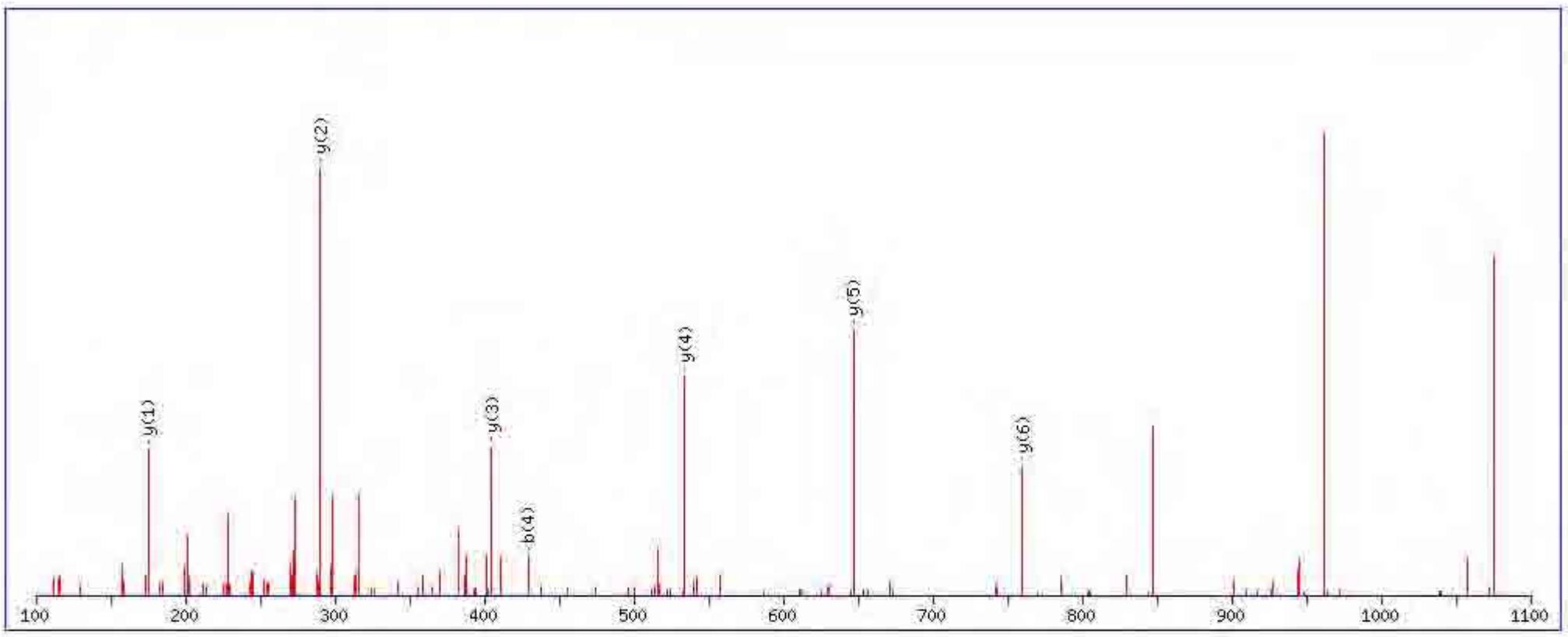
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTVIIEDDR**
Found in **PARD3_HUMAN**, Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2

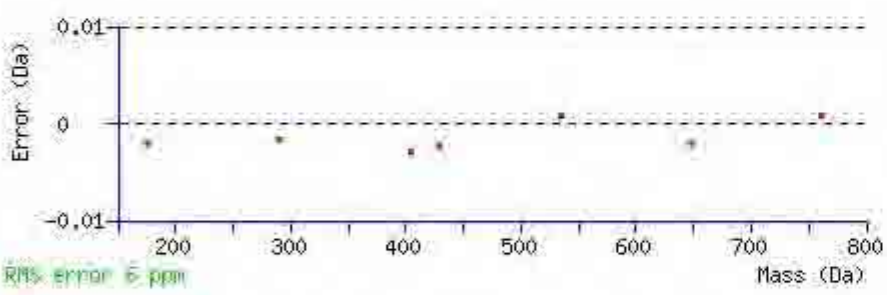
Match to Query 6204: 1074.522748 from(538.268650,2+) rtinseconds(1262) index(6367)
Title: Locus:1.1.1.1822.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

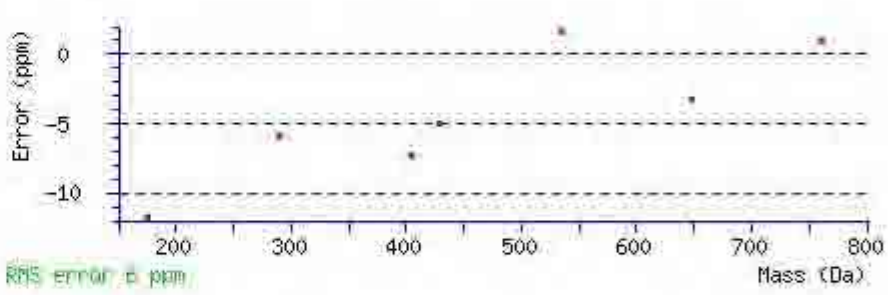
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1074.519318
Ions Score: 49 **Expect:** 0.0029
Matches : 7/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	217.081898	109.044587	199.071333	100.039304	T	960.499652	480.753464	943.473103	472.240190	942.489087	471.748182	8
3	316.150312	158.578794	298.139747	149.573512	V	859.451973	430.229625	842.425424	421.716350	841.441408	421.224342	7
4	429.234376	215.120826	411.223811	206.115544	I	*760.383559*	380.695418	743.357010	372.182143	742.372994	371.690135	6
5	542.318440	271.662858	524.307875	262.657576	I	*647.299495*	324.153386	630.272946	315.640111	629.288930	315.148103	5
6	671.361033	336.184155	653.350468	327.178872	E	*534.215431*	267.611354	517.188882	259.098079	516.204866	258.606071	4
7	786.387976	393.697626	768.377411	384.692343	D	*405.172838*	203.090057	388.146289	194.576782	387.162273	194.084774	3
8	901.414919	451.211097	883.404354	442.205815	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
9					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DTVIIEDDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	1074.519318	0.003430	DTVIIEDDR
33.9	1074.519287	0.003461	LEEGLEETR
28.5	1074.526688	-0.003940	LDSMAIEALP
25.4	1074.519333	0.003415	VTDPQGKSDI
22.3	1074.526688	-0.003940	LDSMAIEALP
22.0	1074.512772	0.009976	NSLNPEVMR
21.3	1074.523331	-0.000583	EKLYPPSPP
21.1	1074.520645	0.002103	LWTRNDDR
20.9	1074.513443	0.009305	PEWLDFPR
20.5	1074.530548	-0.007800	LTTPPSSNSR

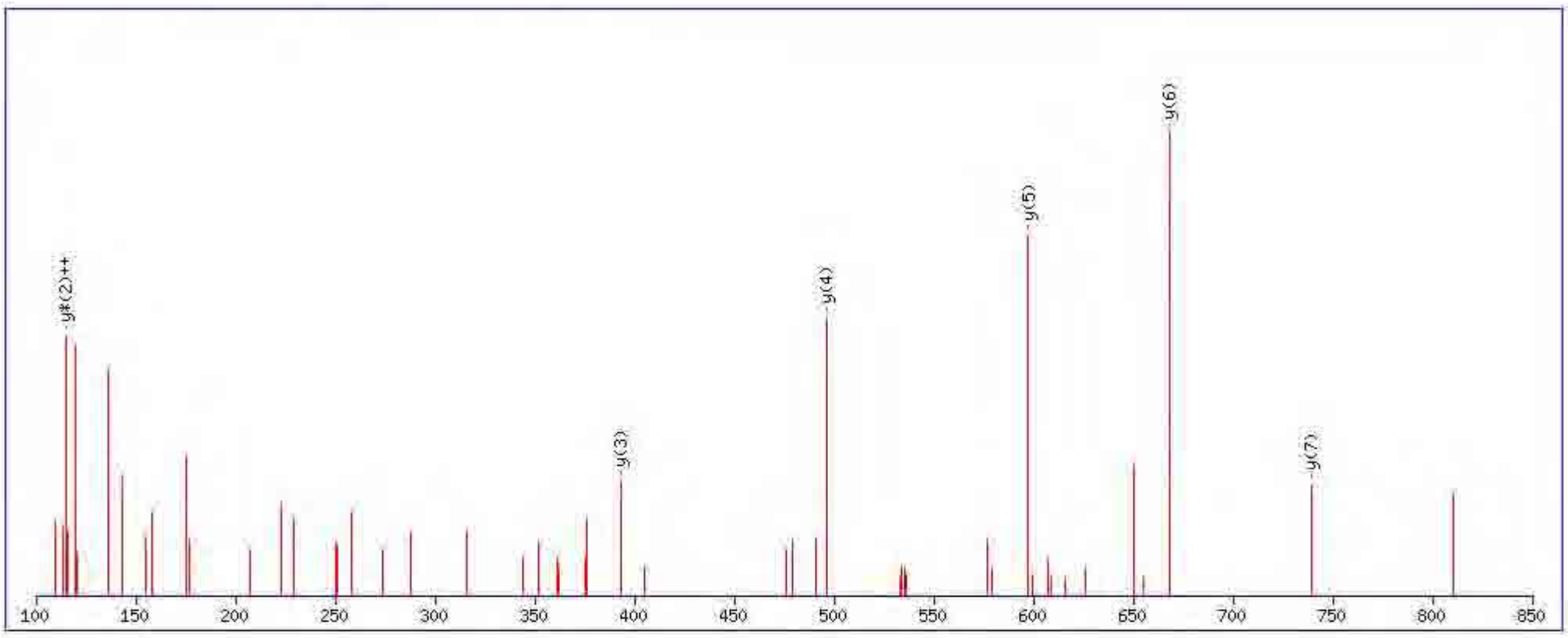
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAATCFAR**
Found in **PA2GA_HUMAN**, Phospholipase A2, membrane associated OS=Homo sapiens GN=PLA2G2A PE=1 SV=2

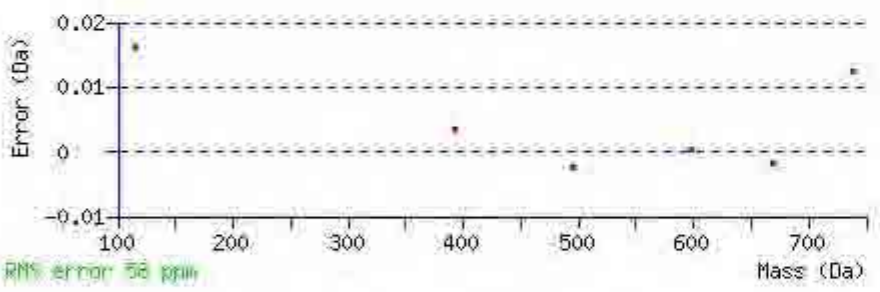
Match to Query 915: 809.389228 from(405.701890,2+) rtinseconds(744) index(1664)
Title: Locus:1.1.1.1528.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

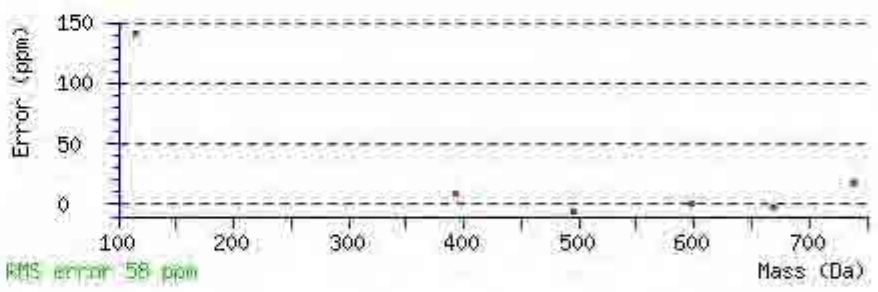
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 809.385391
Ions Score: 47 **Expect:** 0.0013
Matches : 6/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							8
2	143.081504	72.044390			A	*739.355572*	370.181424	722.329023	361.668150	721.345007	361.176142	7
3	214.118618	107.562947			A	*668.318458*	334.662867	651.291909	326.149593	650.307893	325.657585	6
4	315.166297	158.086786	297.155732	149.081504	T	*597.281344*	299.144310	580.254795	290.631036	579.270779	290.139028	5
5	418.175482	209.591379	400.164917	200.586097	C	*496.233665*	248.620471	479.207116	240.107196			4
6	565.243896	283.125586	547.233331	274.120304	F	*393.224480*	197.115878	376.197931	188.602604			3
7	636.281010	318.644143	618.270445	309.638861	A	246.156066	123.581671	229.129517	115.068397			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AAATCFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	809.385391	0.003837	AAATCFAR
15.3	809.388779	0.000449	GRTCMVK
3.2	809.391907	-0.002679	AENSYVK
3.0	809.391937	-0.002709	APQPTSPP
3.0	809.391937	-0.002709	APQPTSPP
2.7	809.382034	0.007194	NNFFPR
2.7	809.385391	0.003837	NNFMLR
2.5	809.385391	0.003837	CGKEFAR
1.5	809.385406	0.003822	NVFMSGR
1.0	809.391922	-0.002694	APYSTQK

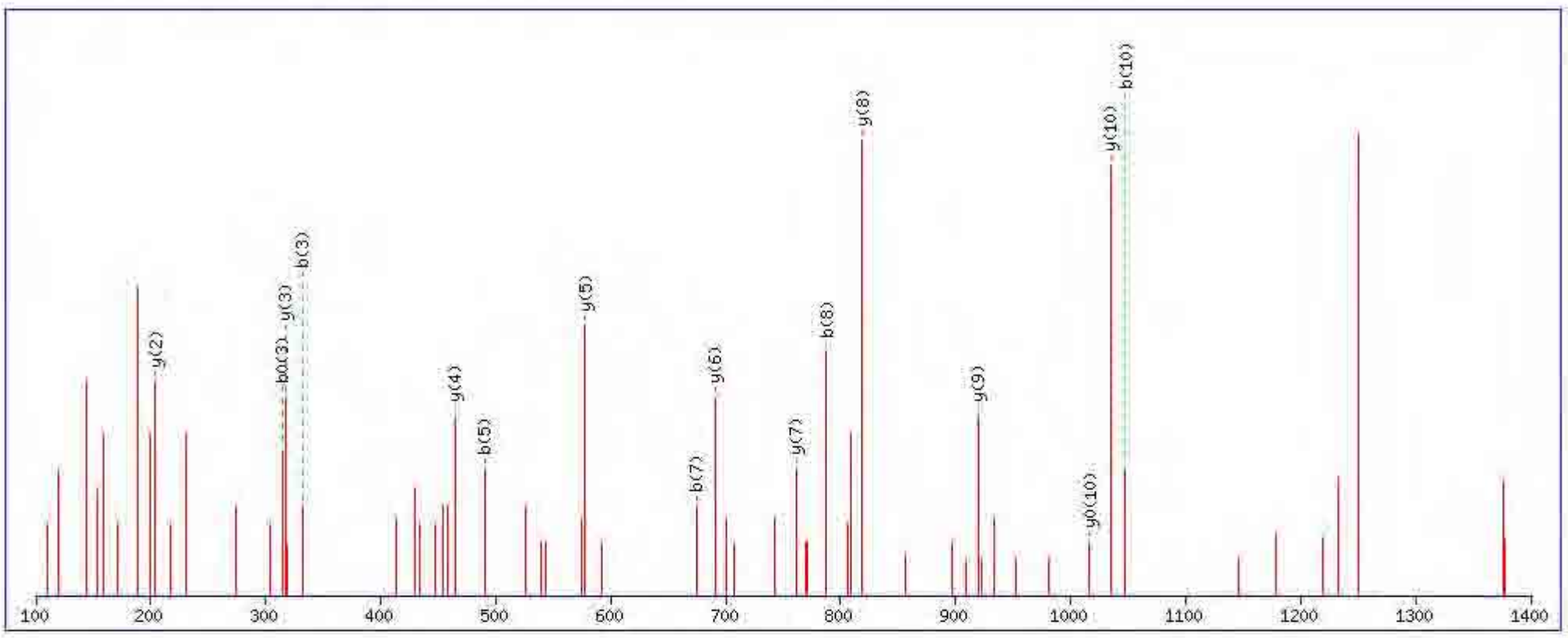
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTDTGALLFIGK**
Found in **PEDF_HUMAN**, Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4

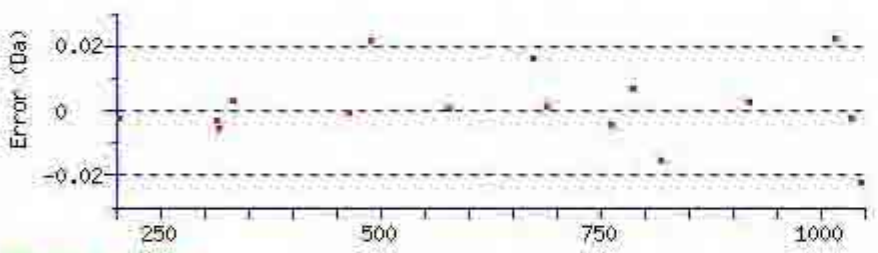
Match to Query 10740: 1249.662328 from(625.838440,2+) rtinseconds(2022) index(15595)
Title: Locus:1.1.1.2242.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

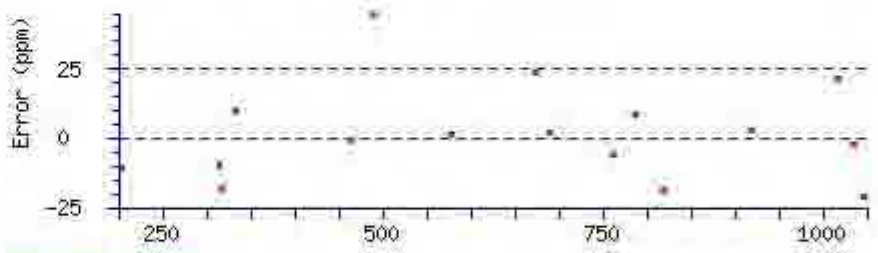
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1249.655426
Ions Score: 58 Expect: 6.2e-005
Matches : 16/94 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							12
2	217.081898	109.044587	199.071333	100.039304	T	1135.635753	568.321514	1118.609204	559.808240	1117.625188	559.316232	11
3	332.108841	166.558058	314.098276	157.552776	D	*1034.588074*	517.797675	1017.561525	509.284401	1016.577509	508.792393	10
4	433.156520	217.081898	415.145955	208.076616	T	*919.561131*	460.284203	902.534582	451.770929	901.550566	451.278921	9
5	490.177984	245.592630	472.167419	236.587347	G	*818.513452*	409.760364	801.486903	401.247089			8
6	561.215098	281.111187	543.204533	272.105905	A	*761.491988*	381.249632	744.465439	372.736357			7
7	674.299162	337.653219	656.288597	328.647937	L	*690.454874*	345.731075	673.428325	337.217800			6
8	787.383226	394.195251	769.372661	385.189969	L	*577.370810*	289.189043	560.344261	280.675768			5
9	934.451640	467.729458	916.441075	458.724176	F	*464.286746*	232.647011	447.260197	224.133736			4
10	1047.535704	524.271490	1029.525139	515.266207	I	*317.218332*	159.112804	300.191783	150.599529			3
11	1104.557168	552.782222	1086.546603	543.776939	G	*204.134268*	102.570772	187.107719	94.057497			2
12					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DTDTGALLFIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.1	1249.655426	0.006902	DTDTGALLFIGK
12.4	1249.656281	0.006047	LCCIFLLQQIG
8.3	1249.658783	0.003545	QLSTMITQLIS
7.8	1249.658768	0.003560	MPKSTIETALK
6.7	1249.666626	-0.004298	RYLQLTQSEL
5.8	1249.663483	-0.001155	MTVRGLLSAMR
5.8	1249.652725	0.009603	RPPGHILSSDR
5.8	1249.652725	0.009603	RPPGHILSSDR
5.3	1249.674057	-0.011729	PGPPPVILPGMK
5.3	1249.674057	-0.011729	PGPPPVILPGMK

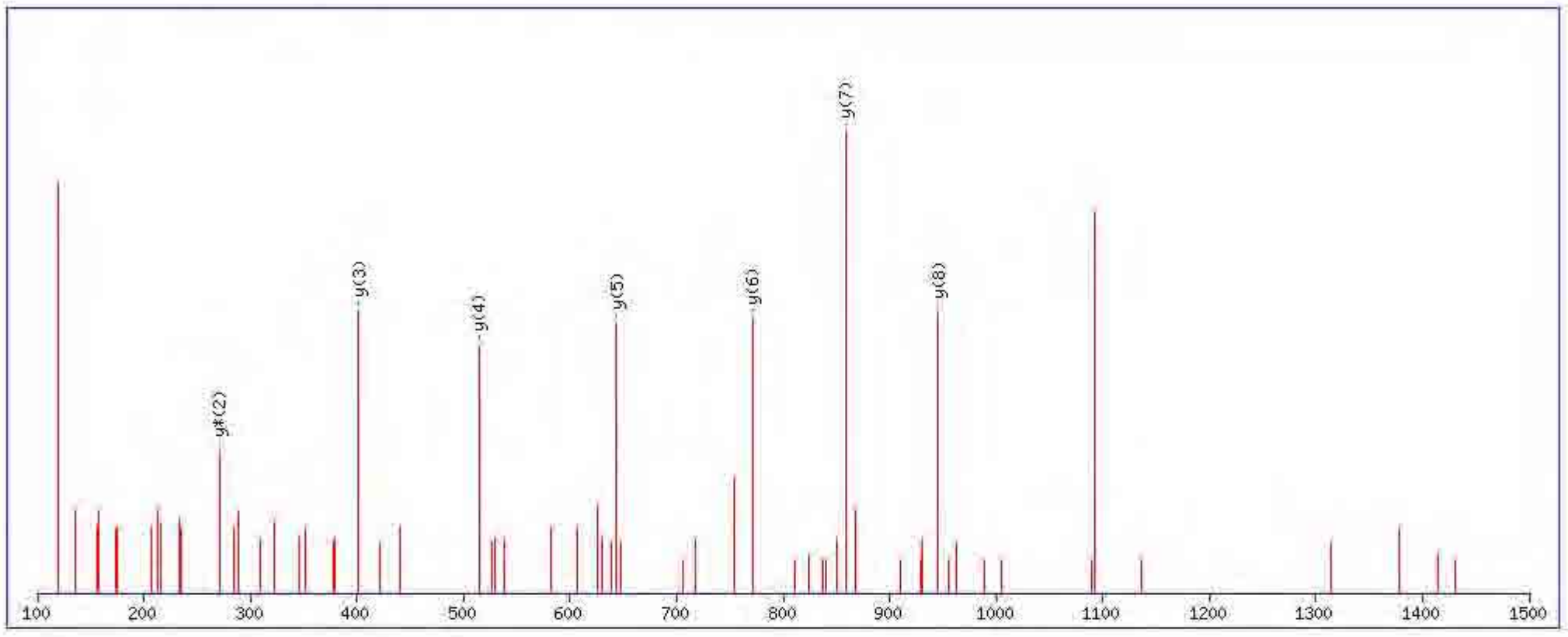
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSSQELILR**
Found in **TGM3_HUMAN**, Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4

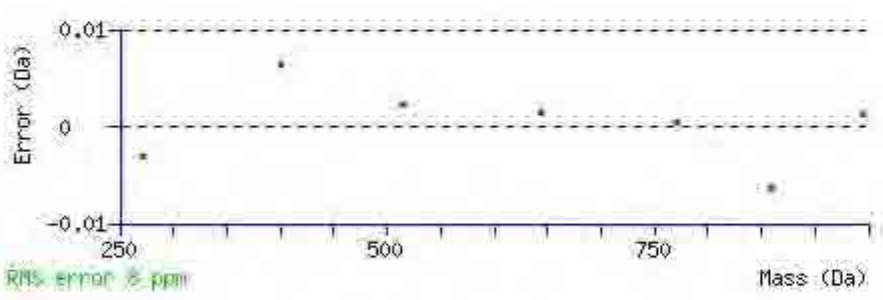
Match to Query 6579: 1091.602888 from(546.808720,2+) rtinseconds(1583) index(10220)
Title: Locus:1.1.1.2000.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

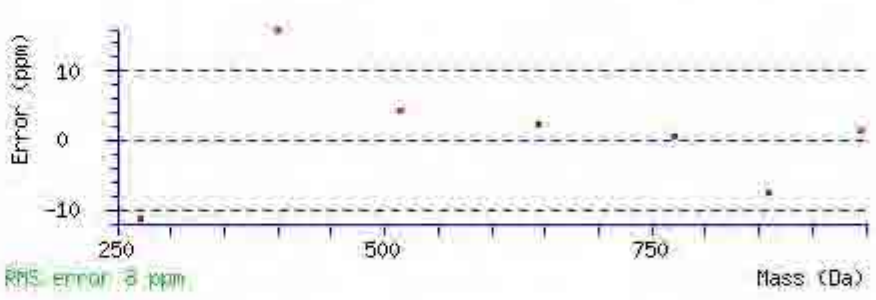
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1091.597488
Ions Score: 49 **Expect:** 0.0005
Matches : 7/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							9
2	235.107718	118.057497			217.097153	109.052214	S	*945.536371*	473.271824	928.509822	464.758549	927.525806	464.266541	8
3	322.139746	161.573511			304.129181	152.568229	S	*858.504343*	429.755810	841.477794	421.242535	840.493778	420.750527	7
4	450.198324	225.602800	433.171775	217.089526	432.187759	216.597518	Q	*771.472315*	386.239796	754.445766	377.726521	753.461750	377.234513	6
5	579.240917	290.124097	562.214368	281.610822	561.230352	281.118814	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	L	*514.371144*	257.689210	497.344595	249.175936			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	*401.287080*	201.147178	384.260531	192.633904			3
8	918.493109	459.750193	901.466560	451.236918	900.482544	450.744910	L	288.203016	144.605146	271.176467	136.091872			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FSSQELILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	1091.597488	0.005400	FSSQELILR
12.7	1091.597473	0.005415	YSAKPEILR
10.6	1091.608734	-0.005846	PQLQPQLPR
10.0	1091.612091	-0.009203	SMTSRILLR
9.7	1091.608734	-0.005846	FSQSVQKIR
9.5	1091.597488	0.005400	FSLASADLLR
9.5	1091.608719	-0.005831	FSQKSNLIR
7.9	1091.597473	0.005415	AYSQSPAIKK
7.4	1091.612762	-0.009874	FSPRPLKFT
6.8	1091.597504	0.005384	SFSQKGNLVL

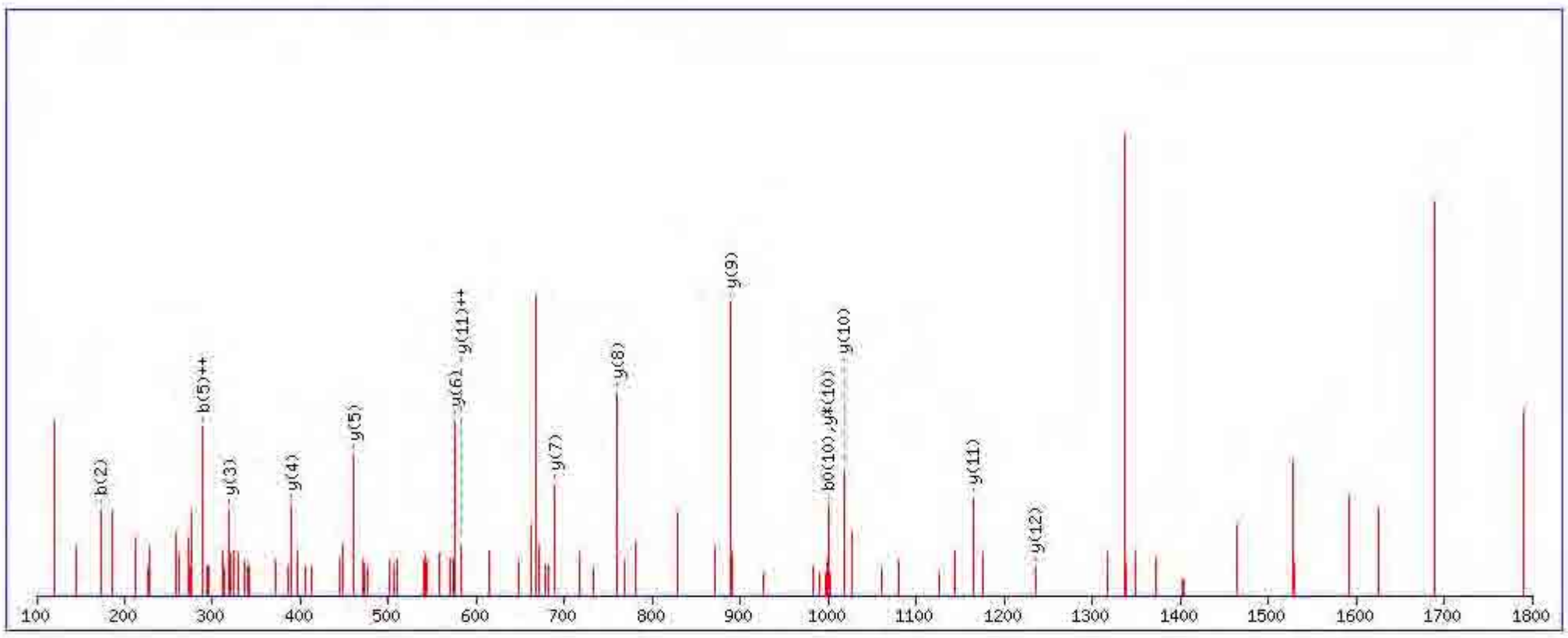
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

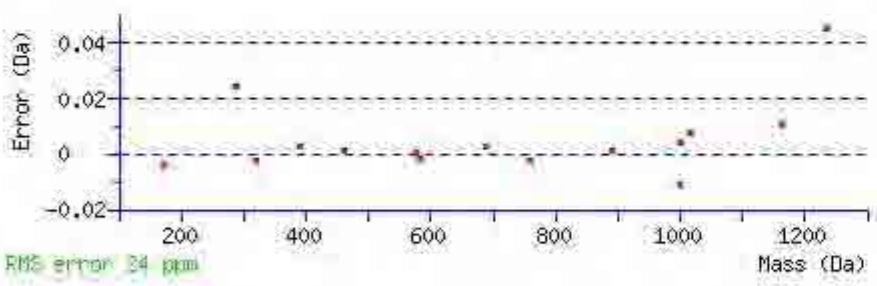
Match to Query 12566: 1335.643588 from(668.829070,2+) rtinseconds(1603) index(10500)
Title: Locus:1.1.1.2011.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

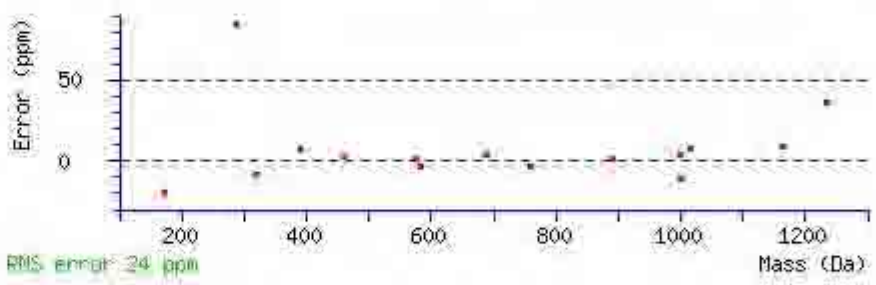
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 68 **Expect:** 2.5e-006
Matches : 15/136 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	*1235.590259*	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	*319.161211*	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	1335.630646	0.012942	TAFQEALDAAGDK
7.9	1335.651794	-0.008206	TSTSALSPGSKPST
4.8	1335.651794	-0.008206	TSTSALSPGSKPST
4.5	1335.649277	-0.005689	QGFQDIAVAMEK
2.8	1335.641876	0.001712	EQATKPSFESGR
1.2	1335.638031	0.005557	FIDISPAEMANL
1.0	1335.649277	-0.005689	LHSPPEVEGAMAV
1.0	1335.645233	-0.001645	STMQELNSRLAS

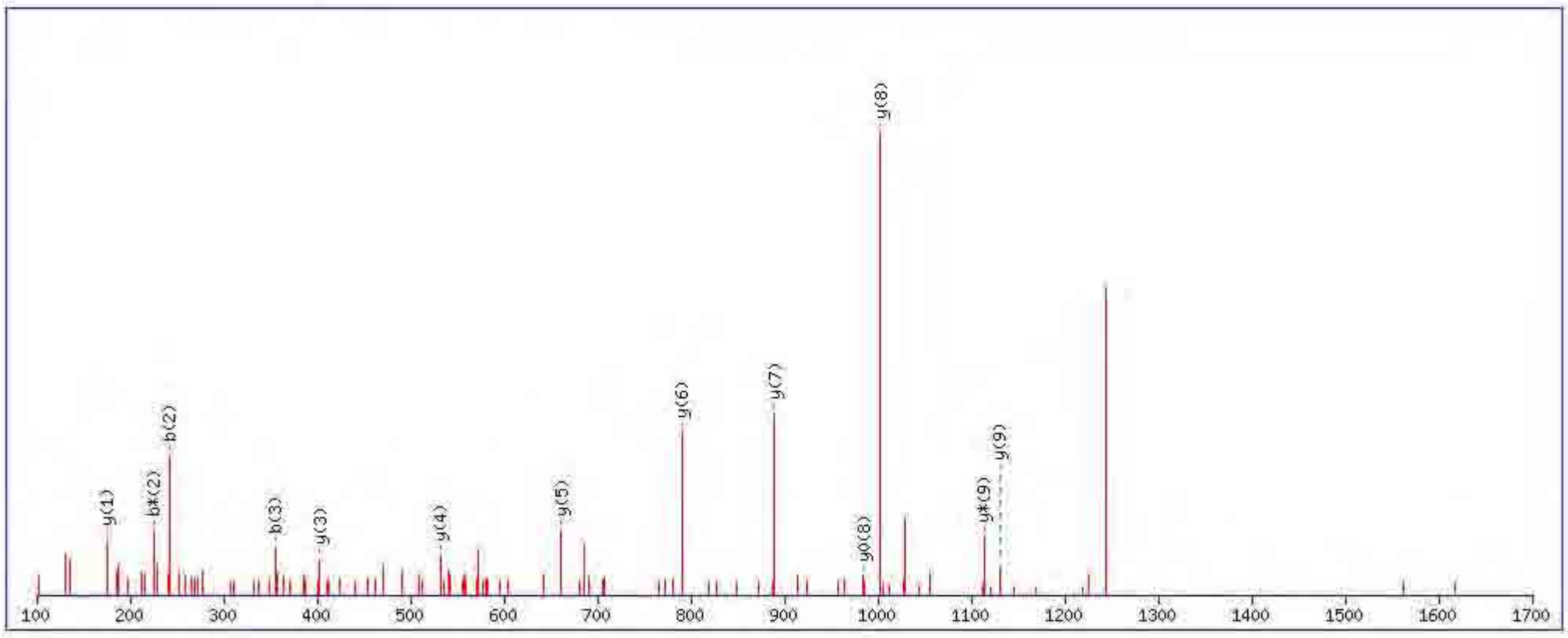
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQLVEEELDR**
Found in **TPM1_HUMAN**, Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2

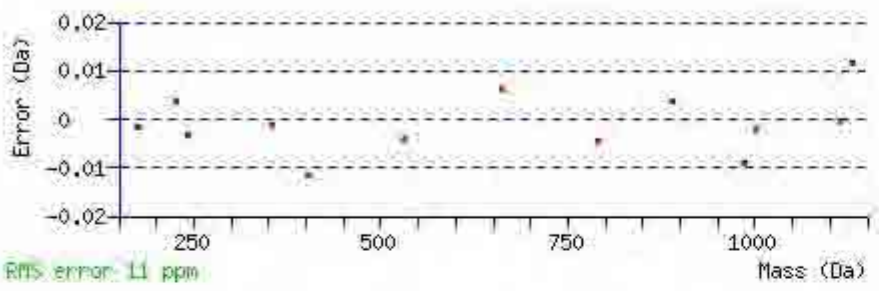
Match to Query 10588: 1242.651988 from(622.333270,2+) rtinseconds(1570) index(10056)
Title: Locus:1.1.1.1993.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_3.mgf

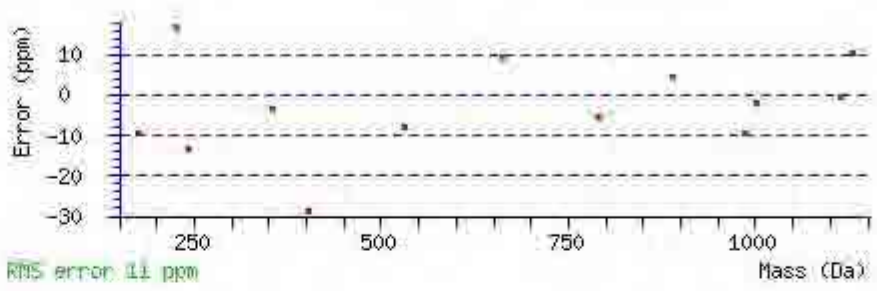
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1242.645554
Ions Score: 57 **Expect:** 0.00045
Matches : 13/96 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							10
2	**242.149918**	121.578597	225.123369	113.065323			Q	*1130.568794*	565.788035	1113.542245	557.274761	1112.558229	556.782753	9
3	**355.233982**	178.120629	338.207433	169.607355			L	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	8
4	454.302396	227.654836	437.275847	219.141562			V	*889.426152*	445.216714	872.399603	436.703440	871.415587	436.211432	7
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	E	*790.357738*	395.682507	773.331189	387.169233	772.347173	386.677225	6
6	712.387582	356.697429	695.361033	348.184155	694.377017	347.692147	E	*661.315145*	331.161211	644.288596	322.647936	643.304580	322.155928	5
7	841.430175	421.218726	824.403626	412.705451	823.419610	412.213443	E	*532.272552*	266.639914	515.246003	258.126640	514.261987	257.634632	4
8	954.514239	477.760758	937.487690	469.247483	936.503674	468.755475	L	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	1069.541182	535.274229	1052.514633	526.760955	1051.530617	526.268947	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQLVEEELDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	1242.645554	0.006434	IQLVEEELDR
23.1	1242.646912	0.005076	KPLDIPDHHR
15.4	1242.656799	-0.004811	LQPTSAAPISAR
15.2	1242.664200	-0.012212	LQPAQVCDILK
14.2	1242.656799	-0.004811	IQPALDPSRSK
13.1	1242.650284	0.001704	PQPSIQRMVR
13.1	1242.645554	0.006434	PKLLEDQQEK
12.7	1242.656799	-0.004811	IGALLQSSGPER
12.7	1242.656784	-0.004796	PGALSAAEVEKR
12.7	1242.650284	0.001704	IQLGLQCAGGAGR

Sibling 1 – technical replicate # 4

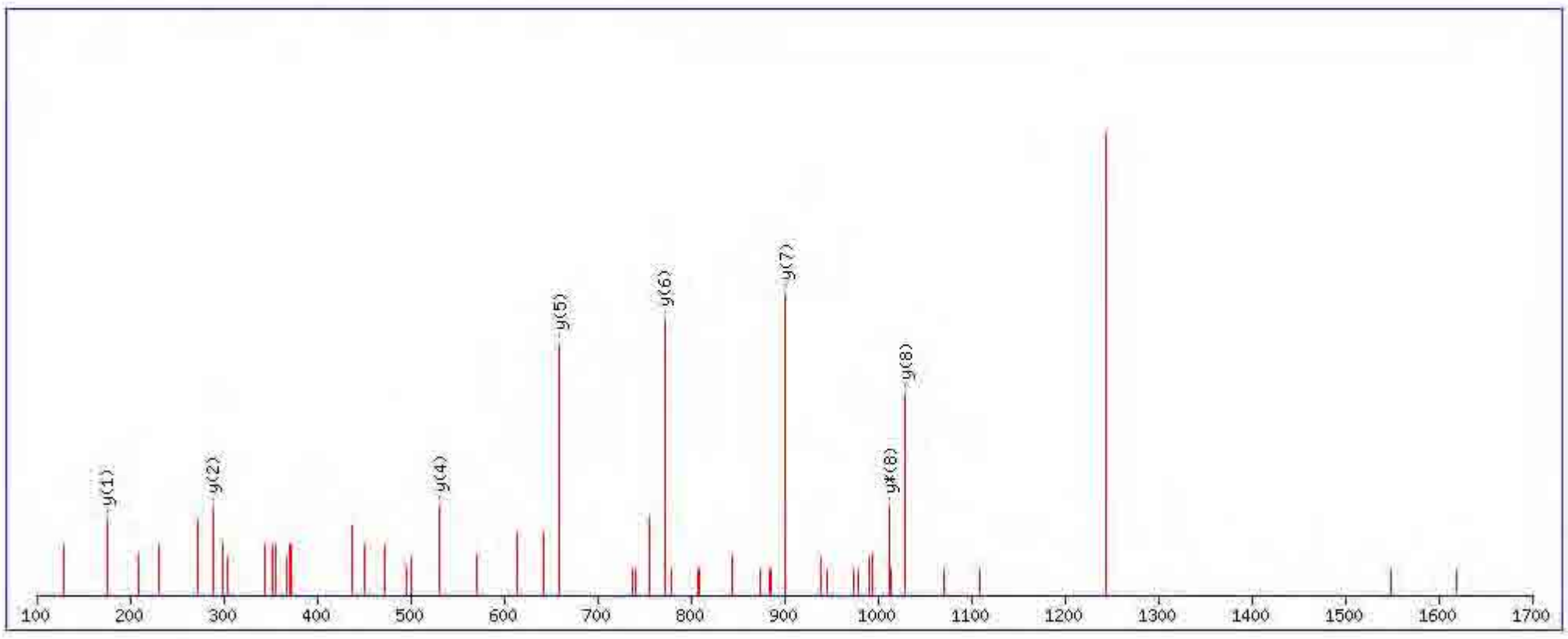
Mascot Search Results

Peptide View

MS/MS Fragmentation of TNQELQEINR
Found in ANXA2_HUMAN, Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

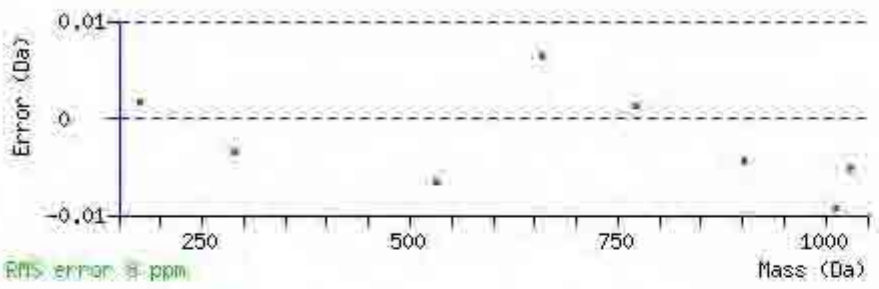
Match to Query 11070: 1243.620208 from(622.817380,2+) rtinseconds(900) index(3624)
Title: Locus:1.1.1.1485.24
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

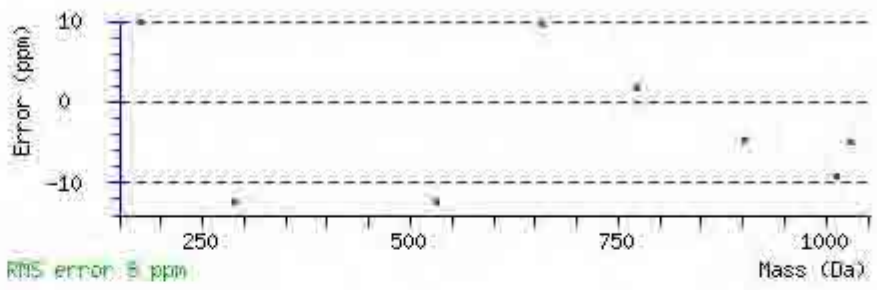
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1243.615646
Ions Score: 63 **Expect:** 4.5e-005
Matches : 8/100 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	N	1143.575276	572.291276	1126.548727	563.778002	1125.564711	563.285994	9
3	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	*1029.532349*	515.269813	1012.505800	506.756538	1011.521784	506.264530	8
4	473.199053	237.103164	456.172504	228.589890	455.188488	228.097882	E	*901.473771*	451.240524	884.447222	442.727249	883.463206	442.235241	7
5	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	L	*772.431178*	386.719227	755.404629	378.205953	754.420613	377.713945	6
6	714.341695	357.674486	697.315146	349.161211	696.331130	348.669203	Q	*659.347114*	330.177195	642.320565	321.663921	641.336549	321.171913	5
7	843.384288	422.195782	826.357739	413.682508	825.373723	413.190500	E	*531.288536*	266.147906	514.261987	257.634632	513.277971	257.142624	4
8	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	I	402.245943	201.626609	385.219394	193.113335			3
9	1070.511279	535.759278	1053.484730	527.246003	1052.500714	526.753995	N	*289.161879*	145.084577	272.135330	136.571303			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNQELQEINR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.5	1243.615646	0.004562	TNQELQEINR
15.4	1243.630905	-0.010697	KESQPAIWNR
14.0	1243.630905	-0.010697	HYSPTKELNR
12.8	1243.615662	0.004546	AKGSEGEQGPLR
10.7	1243.626892	-0.006684	QRSSSLPPSNR
8.6	1243.630920	-0.010712	YYTGTQSRIR
8.4	1243.615662	0.004546	SQQLQEKQQQ
8.0	1243.630966	-0.010758	GSAVTPGHFVTR
7.7	1243.615677	0.004531	SQRTATAGTASPP
7.5	1243.629578	-0.009370	GKDASISLEPDL

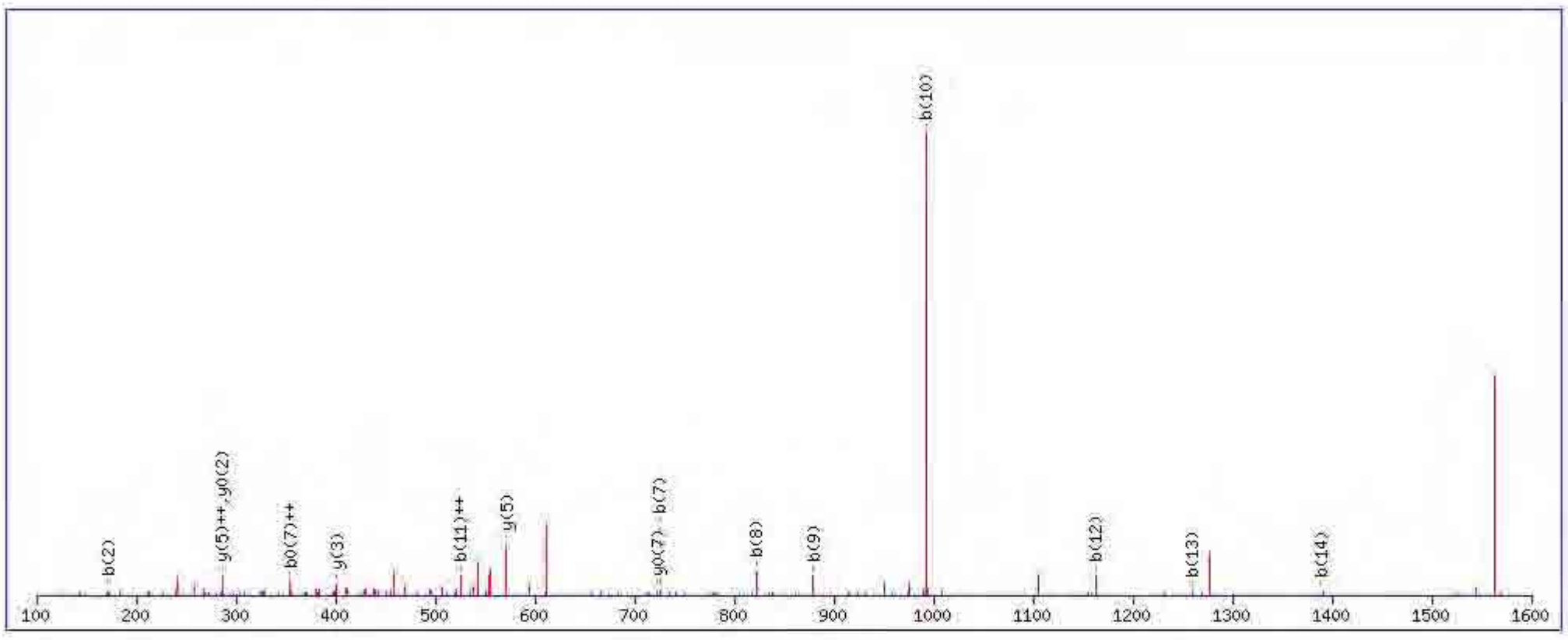
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAQPLEPGPGPPER**
Found in **KCTD2_HUMAN**, BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens GN=KCTD2 PE=1 SV=3

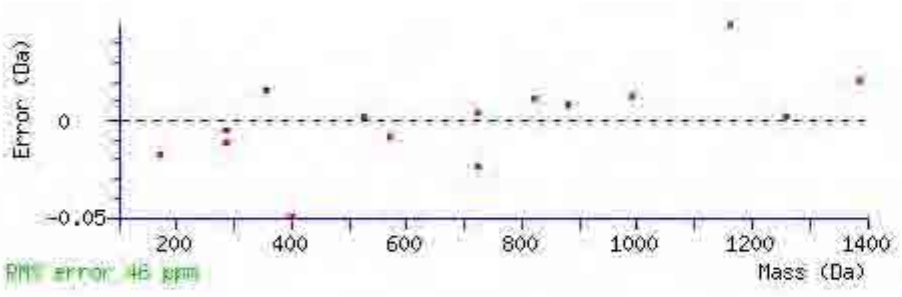
Match to Query 16575: 1561.785748 from(781.900150,2+) rtinseconds(1509) index(9970)
Title: Locus:1.1.1.1827.21
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

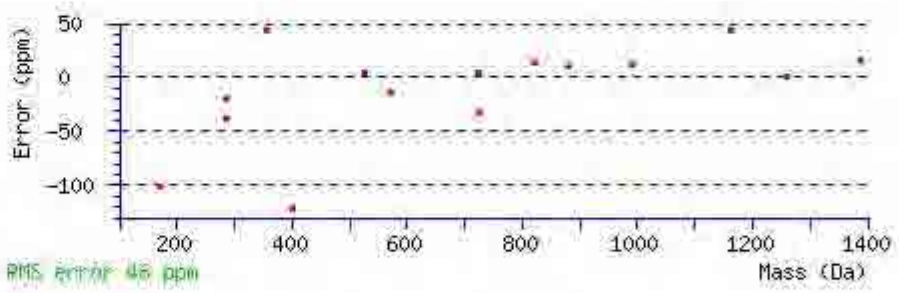
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1561.773636
Variable modifications:
P5 : Oxidation (P)
P10 : Oxidation (P)
P12 : Oxidation (P)
Ions Score: 49 **Expect:** 0.0028
Matches : 15/148 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	*171.112804*	86.060040					V	1491.743801	746.375539	1474.717252	737.862264	1473.733236	737.370256	14
3	242.149918	121.578597					A	1392.675387	696.841332	1375.648838	688.328057	1374.664822	687.836049	13
4	370.208496	185.607886	353.181947	177.094612			Q	1321.638273	661.322775	1304.611724	652.809500	1303.627708	652.317492	12
5	483.256175	242.131726	466.229626	233.618451			P	1193.579695	597.293486	1176.553146	588.780211	1175.569130	588.288203	11
6	596.340239	298.673758	579.313690	290.160483			L	1080.532016	540.769646	1063.505467	532.256372	1062.521451	531.764363	10
7	*725.382832*	363.195054	708.356283	354.681780	707.372267	354.189772	E	967.447952	484.227614	950.421403	475.714339	949.437387	475.222332	9
8	*822.435596*	411.721436	805.409047	403.208162	804.425031	402.716154	P	838.405359	419.706318	821.378810	411.193043	820.394794	410.701035	8
9	*879.457060*	440.232168	862.430511	431.718894	861.446495	431.226886	G	741.352595	371.179936	724.326046	362.666661	723.342030	362.174653	7
10	*992.504739*	496.756008	975.478190	488.242733	974.494174	487.750725	P	684.331131	342.669203	667.304582	334.155929	666.320566	333.663921	6
11	1049.526203	525.266740	1032.499654	516.753465	1031.515638	516.261457	G	571.283452	286.145364	554.256903	277.632089	553.272887	277.140081	5
12	*1162.573882*	581.790579	1145.547333	573.277305	1144.563317	572.785297	P	514.261988	257.634632	497.235439	249.121357	496.251423	248.629349	4
13	*1259.626646*	630.316961	1242.600097	621.803687	1241.616081	621.311679	P	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
14	*1388.669239*	694.838258	1371.642690	686.324983	1370.658674	685.832975	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVAQPLEPGPGPPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	1561.773636	0.012112	AVAQPLEPGPGPPER
36.1	1561.773636	0.012112	AVAQPLEPGPGPPER
32.2	1561.773636	0.012112	AVAQPLEPGPGPPER
31.7	1561.770966	0.014782	GGRARPGPGPGPGPER
31.5	1561.798782	-0.013034	ATLPDTAAPPGLPPAAA
30.1	1561.770966	0.014782	GGRARPGPGPGPGPER
30.1	1561.770966	0.014782	GGRARPGPGPGPGPER
28.3	1561.773636	0.012112	AVAQPLEPGPGPPER
26.6	1561.770981	0.014767	PTARGGQHGGGPGPLR
25.6	1561.770966	0.014782	GGRARPGPGPGPGPER

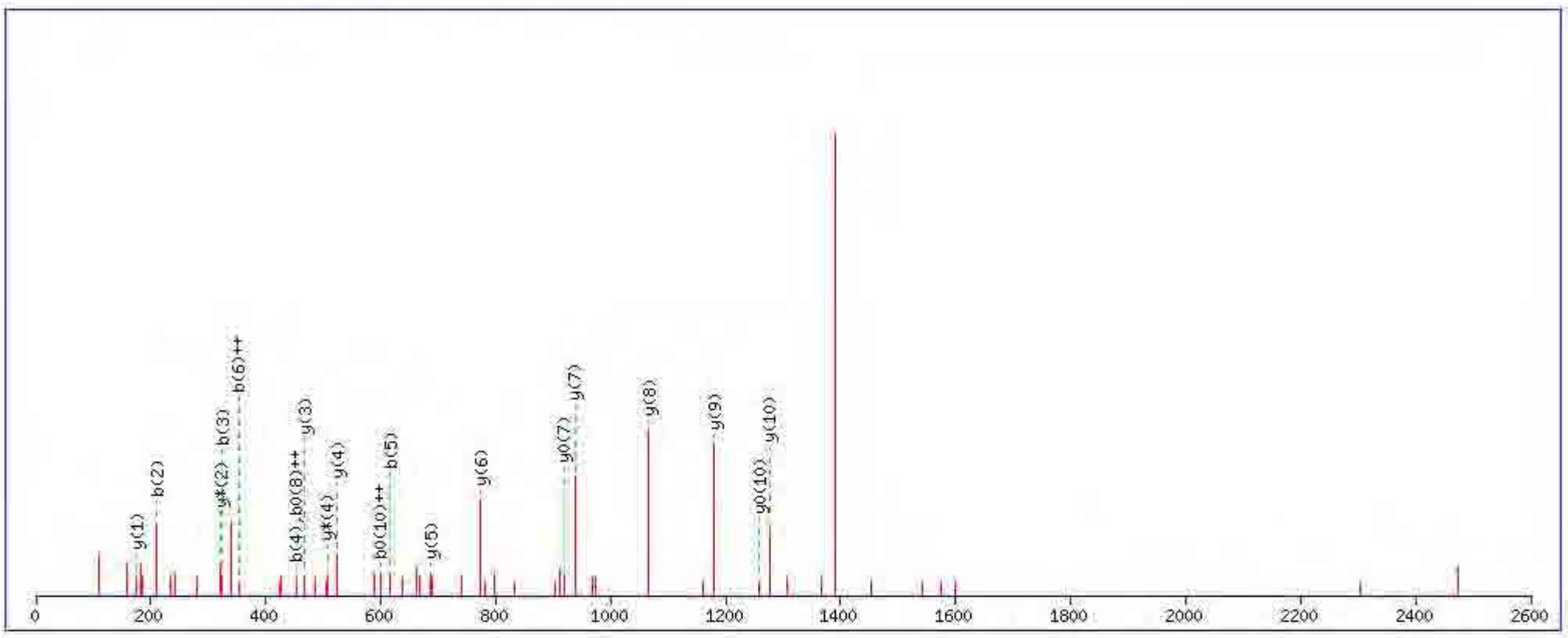
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

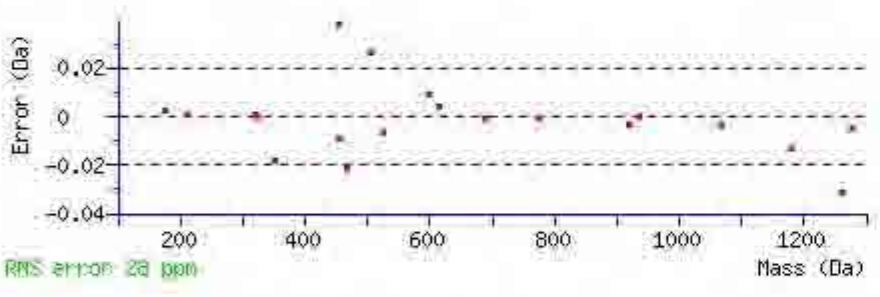
Match to Query 13935: 1388.669148 from(695.341850,2+) rtinseconds(1608) index(11196)
Title: Locus:1.1.1.1881.25
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

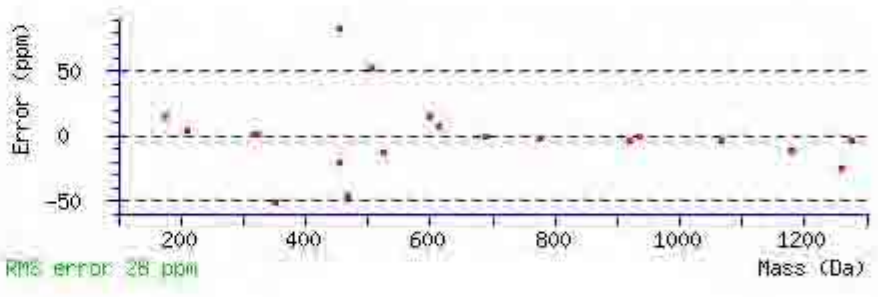
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 46 **Expect:** 0.0087
Matches : 20/90 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	1276.584445	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	1179.531681	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	1066.447617	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	937.405024	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	774.341695	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	687.309667	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	524.246338	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1388.661194	0.007954	LPLEYSYGEYR
22.3	1388.667114	0.002034	PPPELTDTATSTK
13.4	1388.657211	0.011937	LPEDQPPGPAALH
12.7	1388.667114	0.002034	PPPELTDTATSTK
12.6	1388.671082	-0.001934	IPELEEAELEAE
12.4	1388.667130	0.002018	IPTPVEGSDSVSSV
11.1	1388.667114	0.002034	PPPELTDTATSTK
10.1	1388.682358	-0.013210	IPLFNIDVDNLE
9.2	1388.667953	0.001195	IPELLASGMVDNM
8.7	1388.682373	-0.013225	PPEPQPPVTPDAL

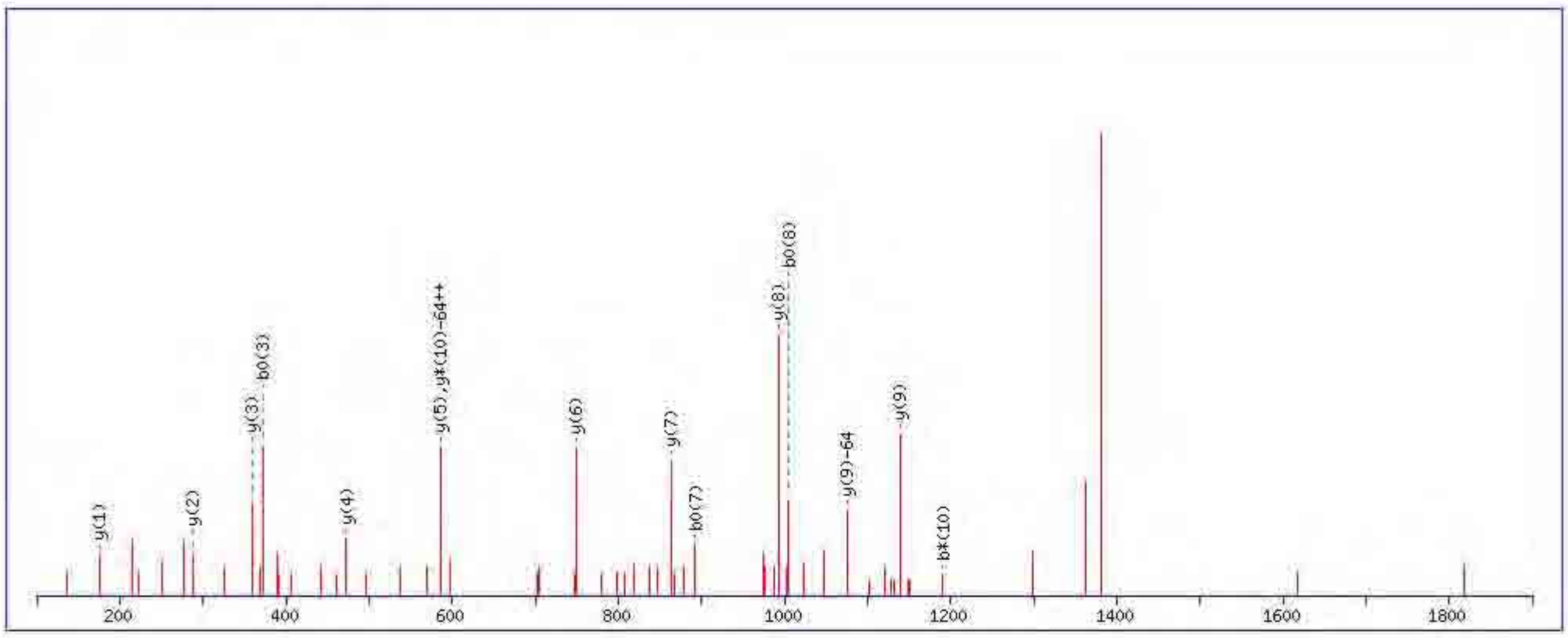
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

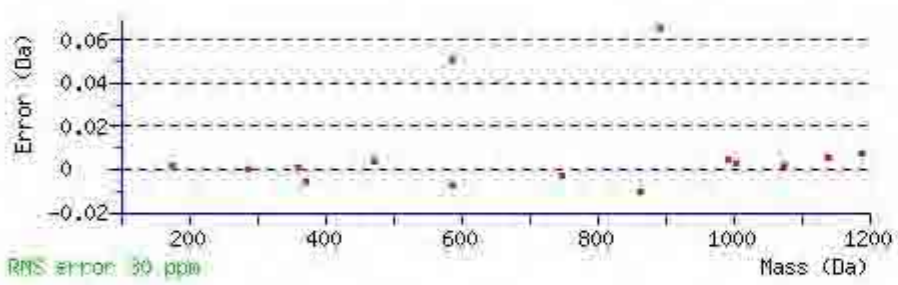
Match to Query 13769: 1380.671568 from(691.343060,2+) rtinseconds(1467) index(9468)
Title: Locus:1.1.1.1804.23
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

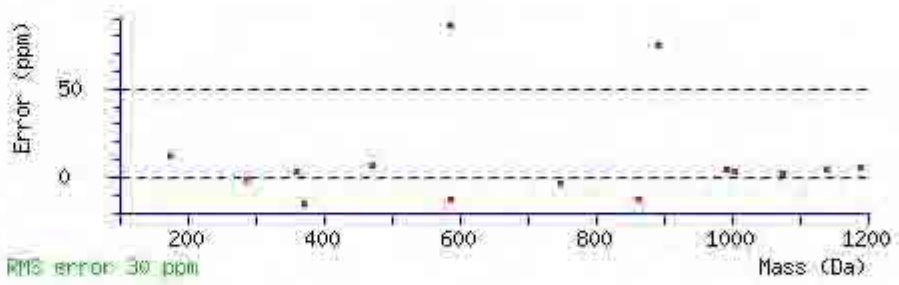
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 59 **Expect:** 0.0001
Matches : 15/154 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1252.635434	626.821355	1235.608885	618.308081	1234.624869	617.816073	10
3	390.169333	195.588304			372.158768	186.583022	M	*1139.551370*	570.279323	1122.524821	561.766049	1121.540805	561.274040	9
4	519.211926	260.109601			501.201361	251.104319	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	633.254853	317.131065	616.228304	308.617790	615.244288	308.125782	N	*863.473377*	432.240326	846.446828	423.727052			7
6	796.318182	398.662729	779.291633	390.149454	778.307617	389.657446	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	910.361109	455.684192	893.334560	447.170918	892.350544	446.678910	N	*586.367121*	293.687199	569.340572	285.173924			5
8	1023.445173	512.226224	1006.418624	503.712950	1005.434608	503.220942	I	*472.324194*	236.665735	455.297645	228.152460			4
9	1094.482287	547.744782	1077.455738	539.231507	1076.471722	538.739499	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1207.566351	604.286813	1190.539802	595.773539	1189.555786	595.281531	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1380.670700	0.000868	EIMENYNIALR
15.3	1380.659500	0.012068	MELENYKQPVV
9.0	1380.659485	0.012083	YIPEDEALMLR
7.0	1380.674118	-0.002550	CTEVTVAMAATLR
6.4	1380.663361	0.008207	GPGPEGQSPAPALR
5.3	1380.663361	0.008207	QPAQDTAPTPAPR
5.0	1380.670746	0.000822	ELMQTPNFRIT
4.7	1380.677261	-0.005693	YLLSSDSQEQLV
4.5	1380.670731	0.000837	AMASLDNEFVLR
4.2	1380.674576	-0.003008	PEQAPRPAPQSR

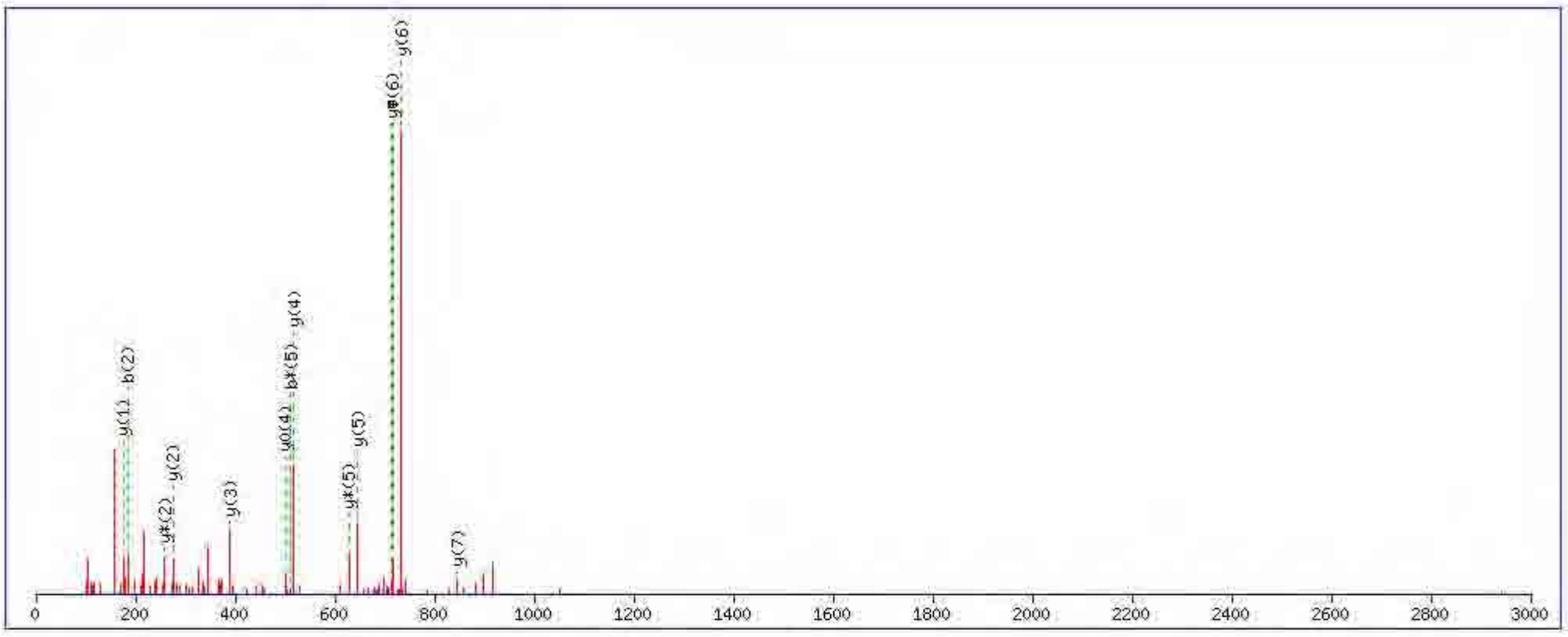
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALSQEITR**
Found in **CYTL1_HUMAN**, Cytokine-like protein 1 OS=Homo sapiens GN=CYTL1 PE=1 SV=1

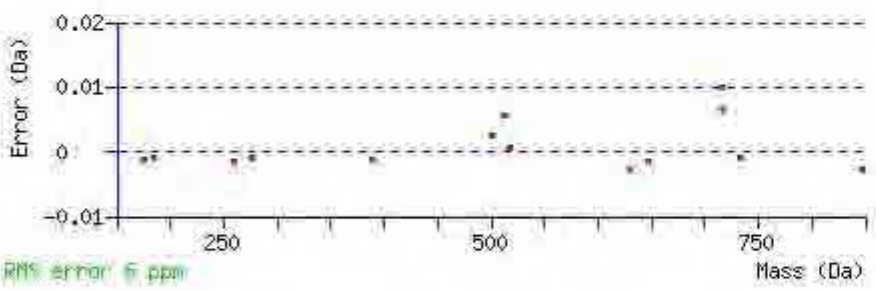
Match to Query 3271: 916.499428 from(459.256990,2+) rtinseconds(803) index(2822)
Title: Locus:1.1.1.1430.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

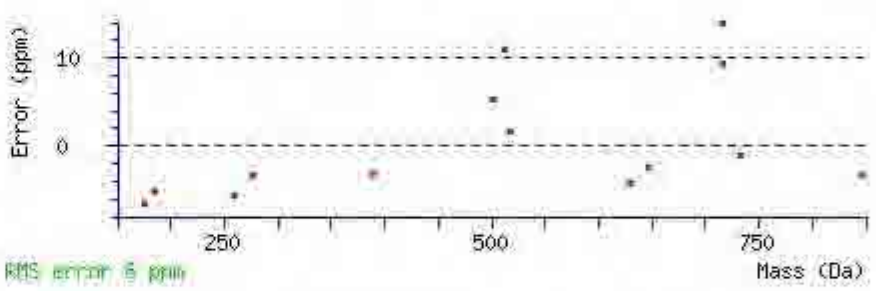
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 916.497772
Ions Score: 51 **Expect:** 0.0015
Matches : 14/72 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	185.128454	93.067865					L	*846.467958*	423.737617	829.441409	415.224343	828.457393	414.732335	7
3	272.160482	136.583879			254.149917	127.578596	S	*733.383894*	367.195585	716.357345	358.682311	715.373329	358.190303	6
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	Q	*646.351866*	323.679571	629.325317	315.166297	628.341301	314.674289	5
5	529.261653	265.134465	512.235104	256.621190	511.251088	256.129182	E	*518.293288*	259.650282	501.266739	251.137008	500.282723	250.645000	4
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	I	*389.250695*	195.128986	372.224146	186.615711	371.240130	186.123703	3
7	743.393396	372.200336	726.366847	363.687062	725.382831	363.195054	T	*276.166631*	138.586954	259.140082	130.073679	258.156066	129.581671	2
8							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ALSQEITR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.6	916.497772	0.001656	ALSQEITR
24.1	916.497772	0.001656	AINTLETR
23.9	916.497772	0.001656	ALSLQETR
20.7	916.497787	0.001641	ALSKGQNVT
19.9	916.497787	0.001641	ALSAGNGVTK
17.2	916.497757	0.001671	AEKAEITR
16.6	916.497772	0.001656	AITLENTR
14.4	916.501801	-0.002373	LASWASILG
14.4	916.497772	0.001656	APESLKTR
13.6	916.497772	0.001656	LSAKEDVR

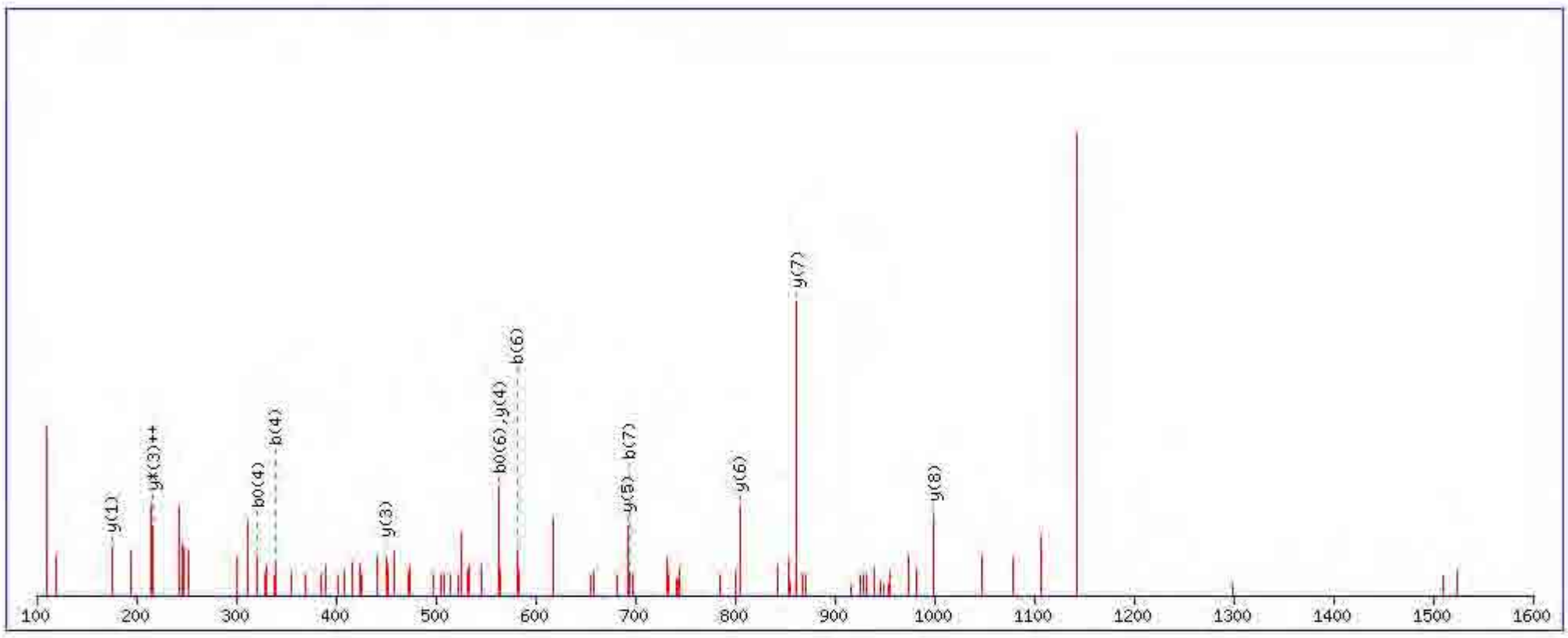
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSHGLEIFQR**
Found in **DKK1_HUMAN**, Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1

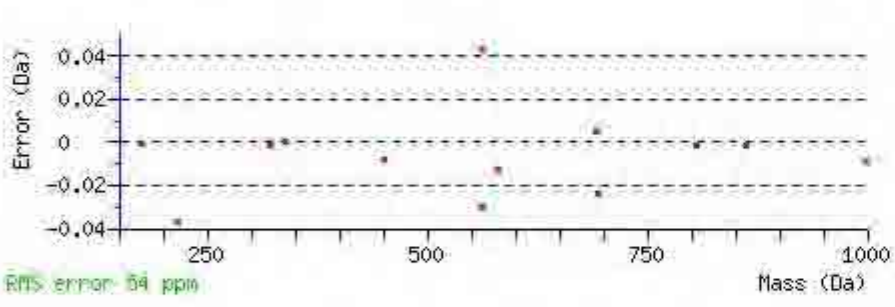
Match to Query 8180: 1142.592308 from(572.303430,2+) rtinseconds(1252) index(6957)
Title: Locus:1.1.1.1685.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

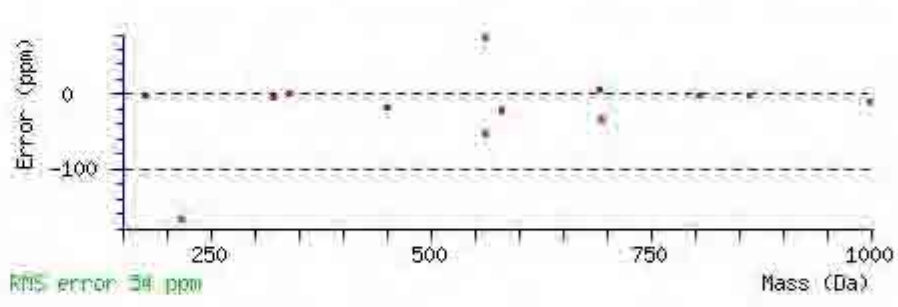
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1142.583252
Ions Score: 36 **Expect:** 0.0017
Matches : 13/82 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							10
2	145.060768	73.034022			127.050203	64.028740	S	1086.569069	543.788173	1069.542520	535.274898	1068.558504	534.782890	9
3	282.119680	141.563478			264.109115	132.558195	H	*999.537041*	500.272159	982.510492	491.758884	981.526476	491.266876	8
4	339.141144	170.074210			321.130579	161.068927	G	*862.478129*	431.742703	845.451580	423.229428	844.467564	422.737420	7
5	452.225208	226.616242			434.214643	217.610959	L	*805.456665*	403.231971	788.430116	394.718696	787.446100	394.226688	6
6	581.267801	291.137539			563.257236	282.132256	E	*692.372601*	346.689939	675.346052	338.176664	674.362036	337.684656	5
7	694.351865	347.679571			676.341300	338.674288	I	*563.330008*	282.168642	546.303459	273.655368			4
8	841.420279	421.213777			823.409714	412.208495	F	*450.245944*	225.626610	433.219395	217.113336			3
9	969.478857	485.243067	952.452308	476.729792	951.468292	476.237784	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GSHGLEIFQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1142.583252	0.009056	GSHGLEIFQR
6.0	1142.597855	-0.005547	SGLMGRTLHR
4.7	1142.581924	0.010384	LTPGPVPSESK
2.6	1142.581940	0.010368	TLPEPVGTQVS
1.8	1142.597839	-0.005531	SSRLHIMAGR
1.5	1142.581909	0.010399	LPGPIAPESSK
1.2	1142.586609	0.005699	EVSQHIKMR
0.8	1142.581940	0.010368	TSGLGITPSPIP
0.5	1142.581909	0.010399	PGPSEISTEVK

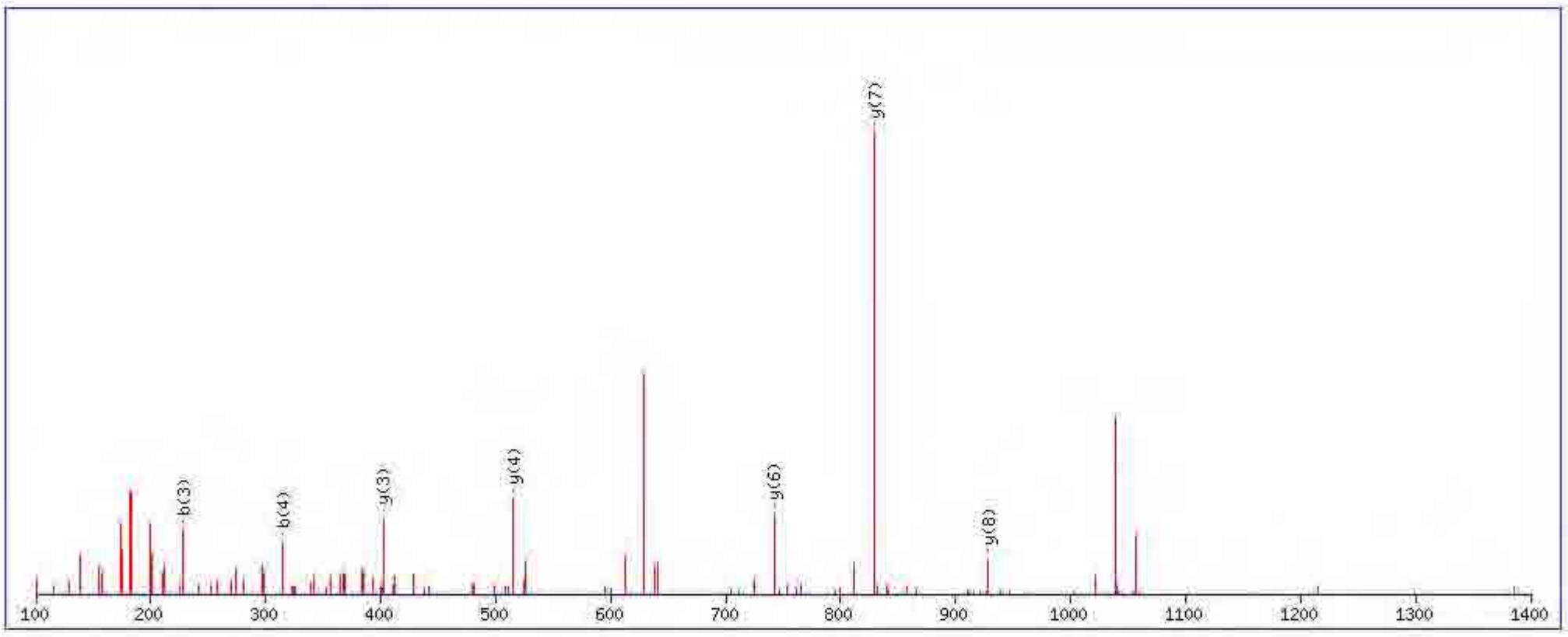
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVSQVLNRL**
Found in **RPB2_HUMAN**, DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1

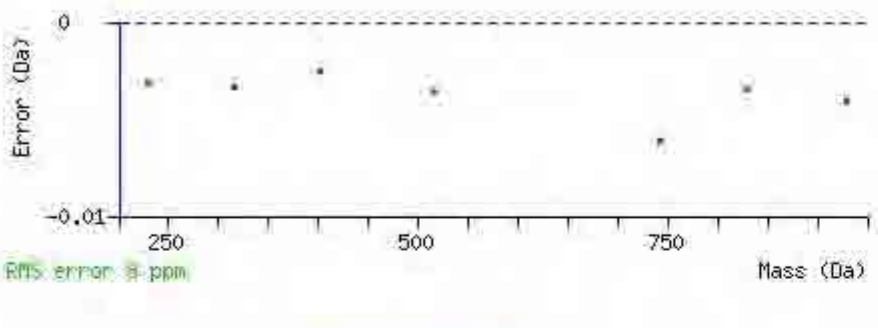
Match to Query 6115: 1055.609468 from(528.812010,2+) rtinseconds(1404) index(8673)
Title: Locus:1.1.1.1770.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

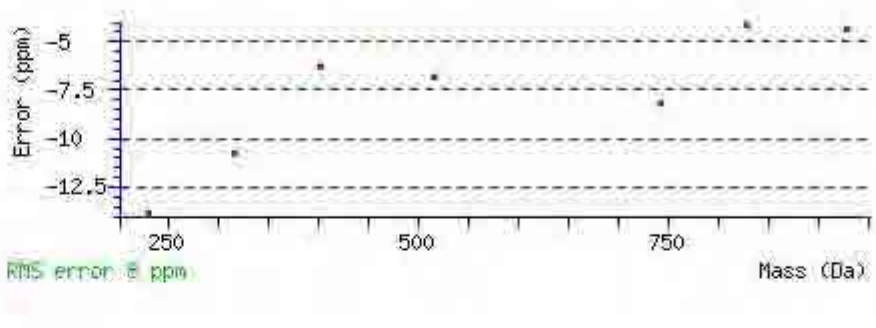
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.608734
Ions Score: 41 **Expect:** 0.0065
Matches : 7/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							10
2	129.065854	65.036565					G	985.578905	493.293091	968.552356	484.779816	967.568340	484.287808	9
3	228.134268	114.570772					V	928.557441	464.782359	911.530892	456.269084	910.546876	455.777076	8
4	315.166296	158.086786			297.155731	149.081504	S	829.489027	415.248152	812.462478	406.734877	811.478462	406.242869	7
5	443.224874	222.116075	426.198325	213.602801	425.214309	213.110793	Q	742.456999	371.732138	725.430450	363.218863			6
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	V	614.398421	307.702849	597.371872	299.189574			5
7	655.377352	328.192314	638.350803	319.679040	637.366787	319.187032	L	515.330007	258.168642	498.303458	249.655367			4
8	769.420279	385.213778	752.393730	376.700503	751.409714	376.208495	N	402.245943	201.626609	385.219394	193.113335			3
9	925.521390	463.264333	908.494841	454.751059	907.510825	454.259051	R	288.203016	144.605146	271.176467	136.091871			2
10							L	132.101905	66.554590					1





NCBI **BLAST** search of AGVSQVLNRL
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1055.608734	0.000734	AGVSQVLNRL
26.4	1055.608734	0.000734	QVSGIIGNLR
24.9	1055.608704	0.000764	KADLINNLR
15.8	1055.616104	-0.006636	INCAIPKGLK
15.4	1055.608719	0.000749	RASLGPLQSK
15.3	1055.608734	0.000734	SPNVGALKVR
14.7	1055.612747	-0.003279	KWLPNGTLK
14.5	1055.619980	-0.010512	TGRLQVAGVR
14.1	1055.608704	0.000764	LNLSNNLIR
11.7	1055.604874	0.004594	MPLALSLPAK

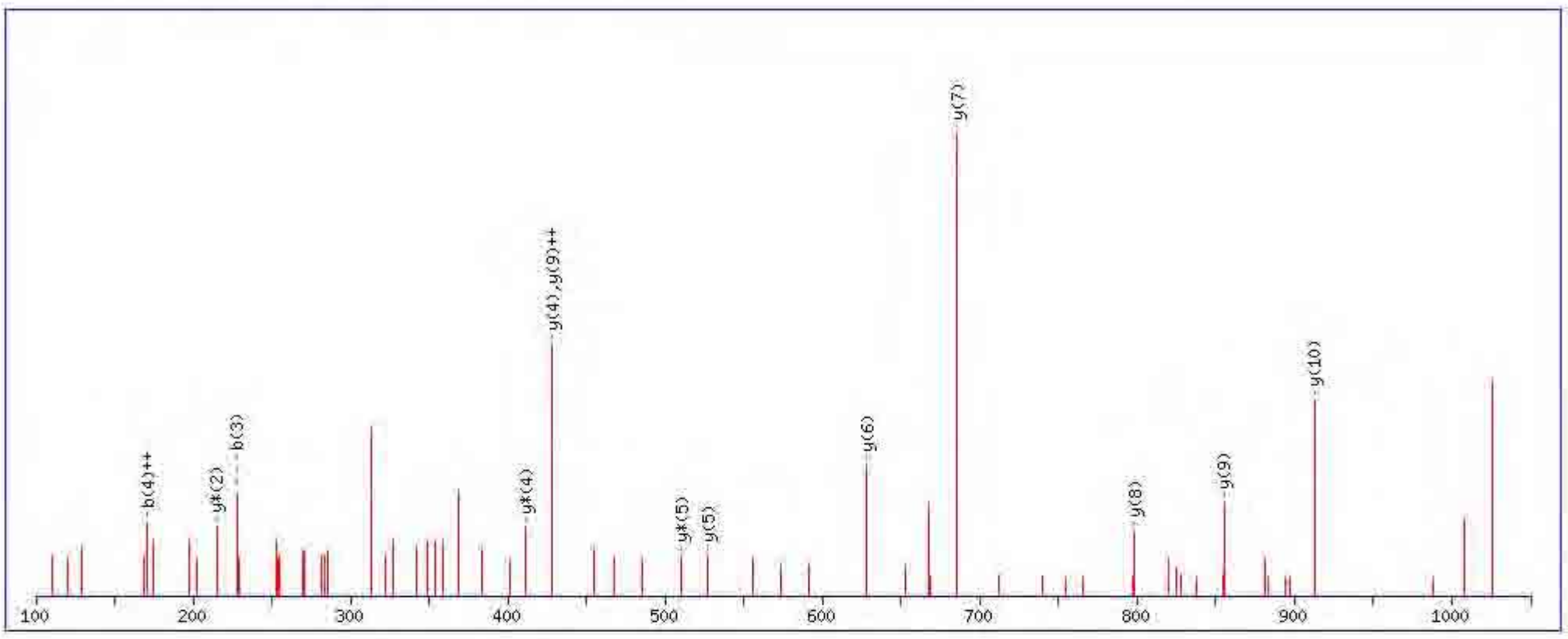
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

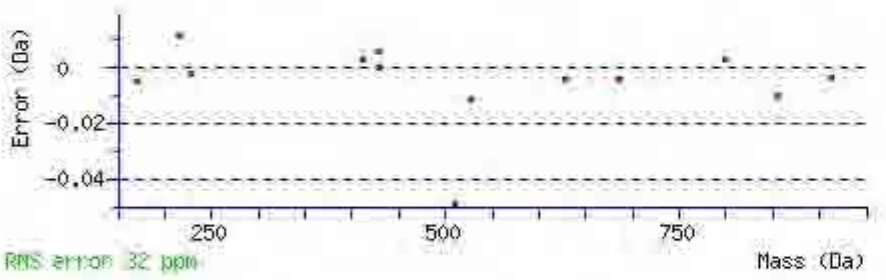
Match to Query 5413: 1024.602148 from(513.308350,2+) rtinseconds(1283) index(7234)
Title: Locus:1.1.1.1703.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

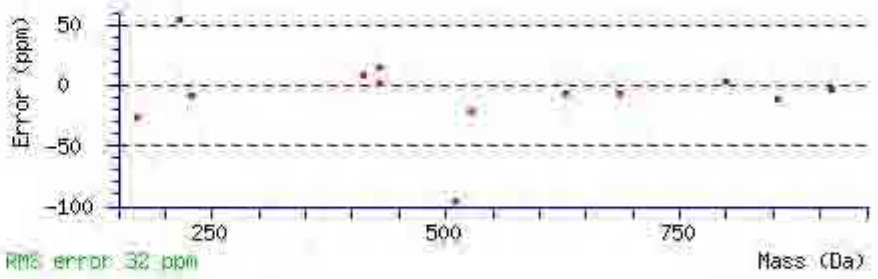
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 56 **Expect:** 0.00018
Matches : 14/80 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	*912.526143*	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	228.134268	114.570772			G	*855.504679*	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	341.218332	171.112804			I	*798.483215*	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	*685.399151*	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	*628.377687*	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	*527.330008*	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	*428.261594*	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	232.140416	116.573846	215.113867	108.060572			2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1024.602951	-0.000803	IGGIGTVPVGR
17.4	1024.602905	-0.000757	PGAVAAAAILR
14.7	1024.602905	-0.000757	INLKRPPTA
14.7	1024.602905	-0.000757	INLKRPPTA
10.5	1024.602951	-0.000803	IGVQGTPVVR
8.8	1024.602905	-0.000757	LNLKPRSTP
8.8	1024.602905	-0.000757	LNLPEGKVR
7.4	1024.602936	-0.000788	LGKTVSHGVK
7.1	1024.602890	-0.000742	INQNKAPLK
7.0	1024.602936	-0.000788	LGAGISGPVRV

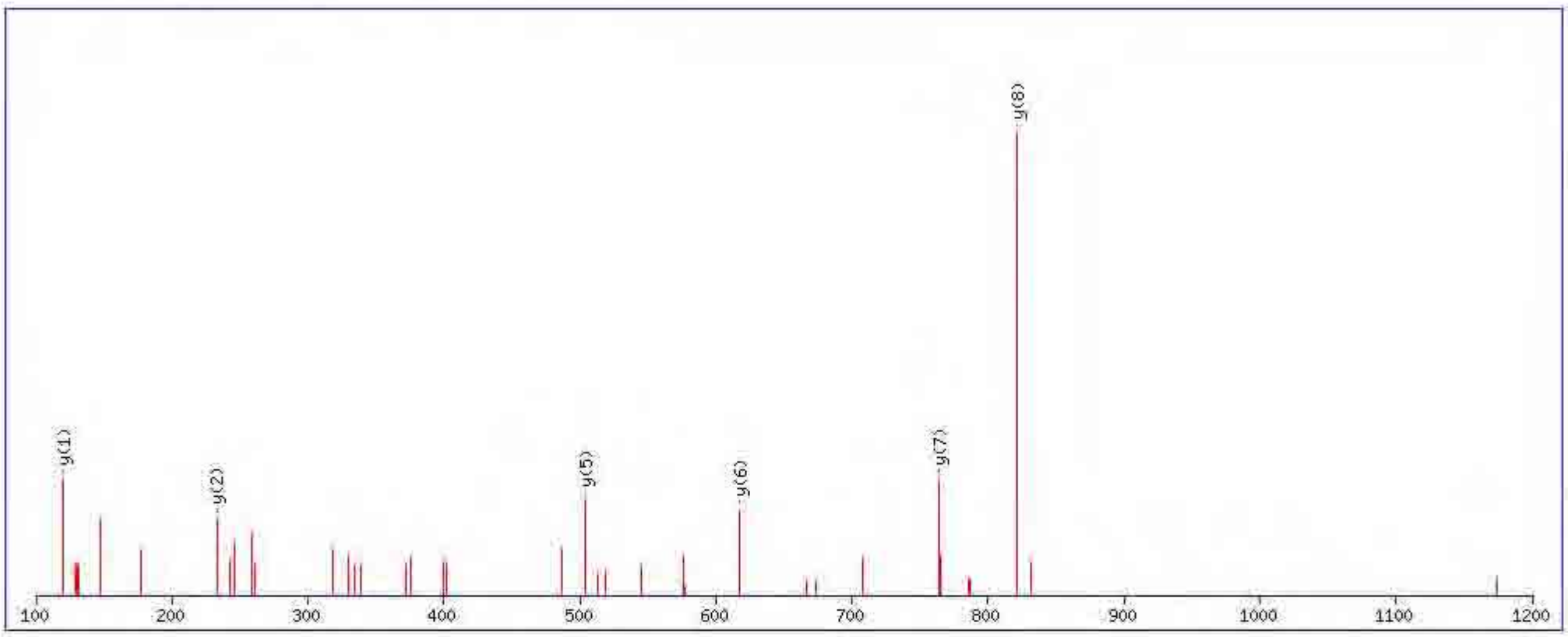
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFLAEALT**
Found in **EPHAA_HUMAN**, Ephrin type-A receptor 10 OS=Homo sapiens GN=EPHA10 PE=2 SV=1

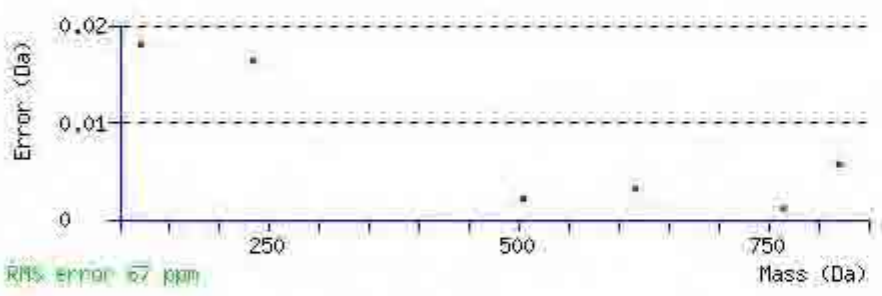
Match to Query 3601: 933.520188 from(467.767370,2+) rtinseconds(1513) index(10015)
Title: Locus:1.1.1.1830.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

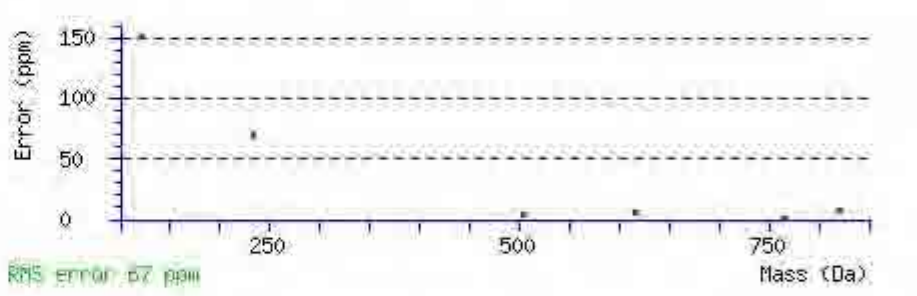
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 933.517120
Ions Score: 55 **Expect:** 0.0004
Matches : 6/54 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L					9
2	171.112804	86.060040			G	*821.440347*	411.223812	803.429782	402.218529	8
3	318.181218	159.594247			F	*764.418883*	382.713080	746.408318	373.707797	7
4	431.265282	216.136279			L	*617.350469*	309.178873	599.339904	300.173590	6
5	502.302396	251.654836			A	*504.266405*	252.636840	486.255840	243.631558	5
6	631.344989	316.176133	613.334424	307.170850	E	433.229291	217.118283	415.218726	208.113001	4
7	702.382103	351.694690	684.371538	342.689407	A	304.186698	152.596987	286.176133	143.591704	3
8	815.466167	408.236722	797.455602	399.231439	L	*233.149584*	117.078430	215.139019	108.073148	2
9					T	*120.065520*	60.536398	102.054955	51.531116	1





NCBI **BLAST** search of LGFLAEALT
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.6	933.517120	0.003068	LGFLAEALT
40.0	933.517120	0.003068	IGFIEEVK
25.1	933.528351	-0.008163	IGFIDKNK
24.9	933.517120	0.003068	IGFELVEK
23.4	933.517151	0.003037	LGFTPSVTI
23.1	933.520493	-0.000305	LLCALTSLT
23.0	933.517151	0.003037	LPGFTGLTI
17.2	933.528351	-0.008163	LLYVQGNK
16.7	933.528336	-0.008148	ILYLGNNK
14.7	933.528351	-0.008163	PLYKNGVK

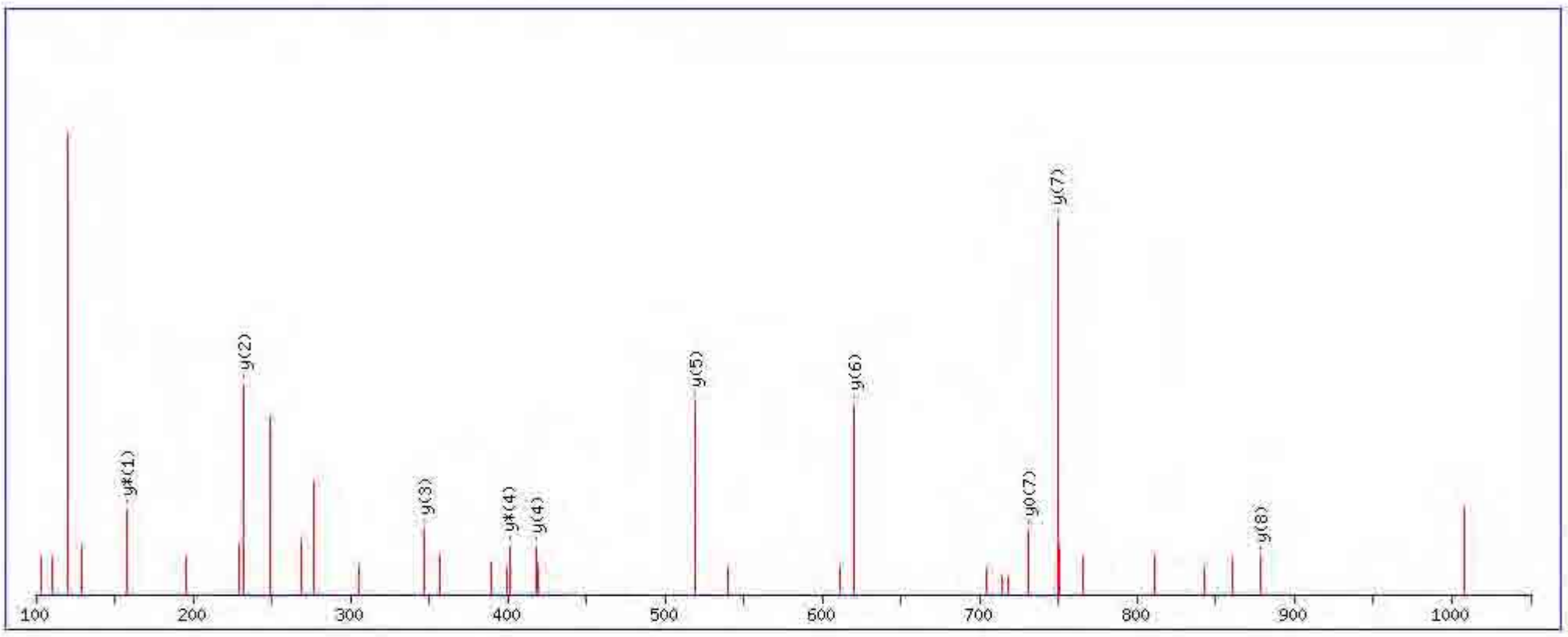
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEETTADGR**
Found in **FABP5_HUMAN**, Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3

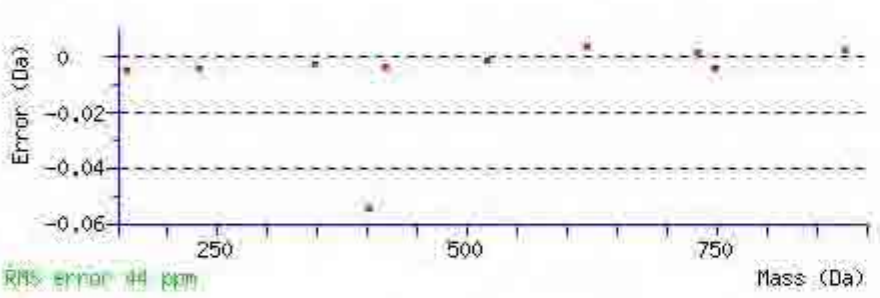
Match to Query 5397: 1024.454928 from(513.234740,2+) rtinseconds(560) index(832)
Title: Locus:1.1.1.1296.12
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

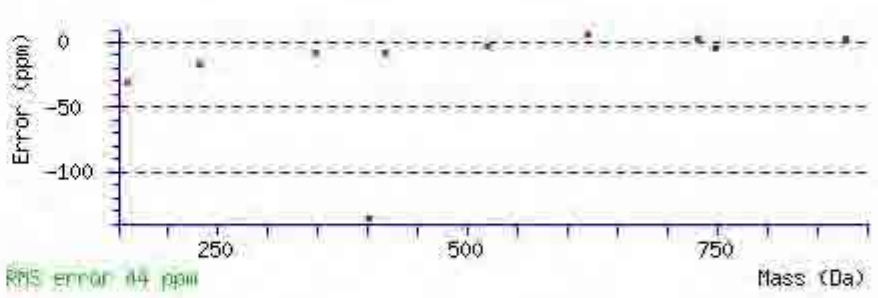
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.446152
Ions Score: 56 **Expect:** 0.00036
Matches : 10/74 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							9
2	277.118283	139.062779	259.107718	130.057497	E	*878.385017*	439.696147	861.358468	431.182872	860.374452	430.690864	8
3	406.160876	203.584076	388.150311	194.578793	E	*749.342424*	375.174850	732.315875	366.661576	731.331859	366.169568	7
4	507.208555	254.107915	489.197990	245.102633	T	*620.299831*	310.653554	603.273282	302.140279	602.289266	301.648271	6
5	608.256234	304.631755	590.245669	295.626473	T	*519.252152*	260.129714	502.225603	251.616440	501.241587	251.124432	5
6	679.293348	340.150312	661.282783	331.145030	A	*418.204473*	209.605875	401.177924	201.092600	400.193908	200.600592	4
7	794.320291	397.663784	776.309726	388.658501	D	*347.167359*	174.087318	330.140810	165.574043	329.156794	165.082035	3
8	851.341755	426.174516	833.331190	417.169233	G	*232.140416*	116.573846	215.113867	108.060572			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FEETTADGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1024.446152	0.008776	FEETTADGR
36.7	1024.446152	0.008776	YPETTEGGR
15.0	1024.453537	0.001391	MEQFPKET
13.9	1024.453537	0.001391	FEEDQKMV
11.5	1024.450134	0.004794	KAAYWEEE
10.9	1024.461411	-0.006483	EFAFSPDGR
8.0	1024.457367	-0.002439	QHPKNQEE
7.7	1024.457367	-0.002439	FEDSESRR
6.3	1024.464783	-0.009855	FPMSALDGR
6.1	1024.450180	0.004748	FEDDFGAPK

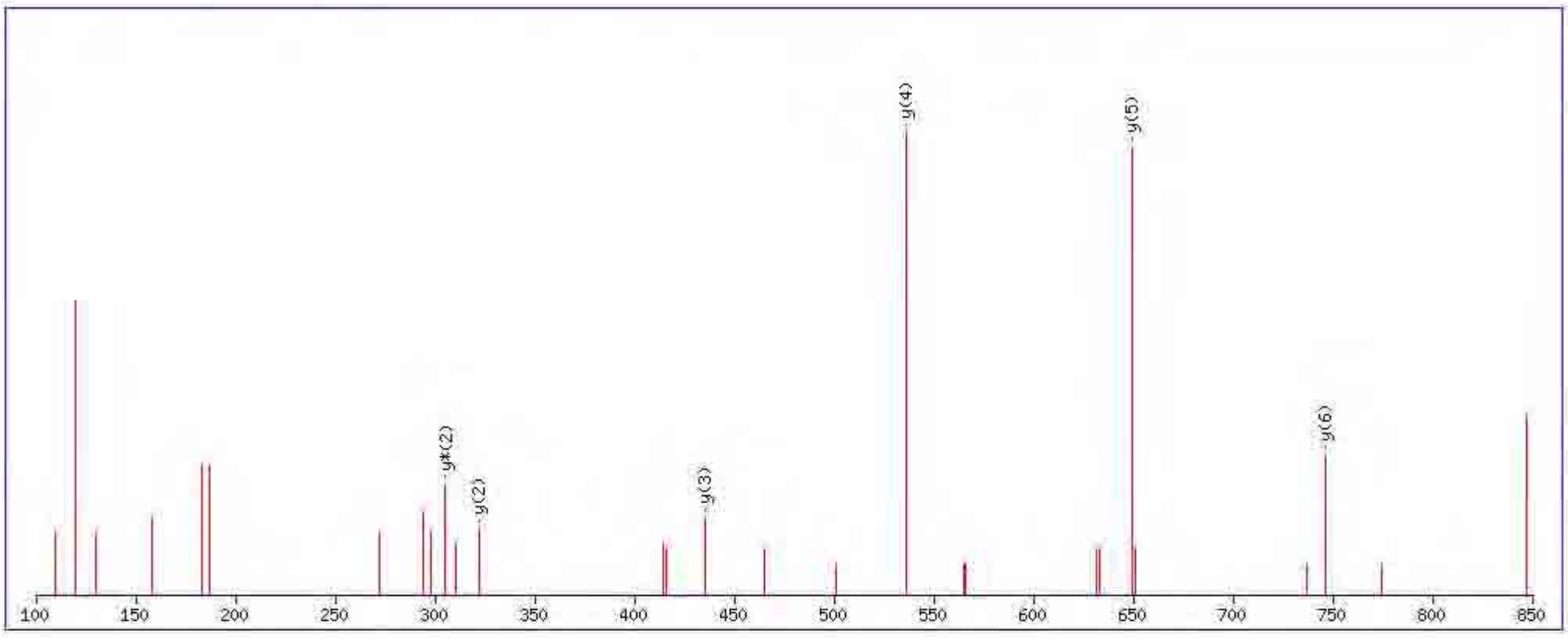
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPITLFR**
Found in **FBLN7_HUMAN**, Fibulin-7 OS=Homo sapiens GN=FBLN7 PE=2 SV=1

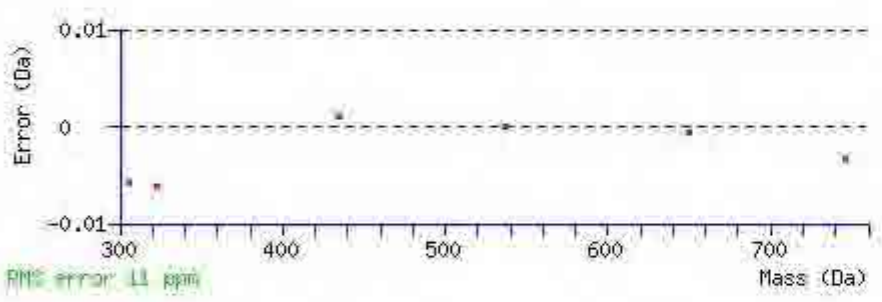
Match to Query 1828: 846.489188 from(424.251870,2+) rtinseconds(1568) index(10649)
Title: Locus:1.1.1.1860.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

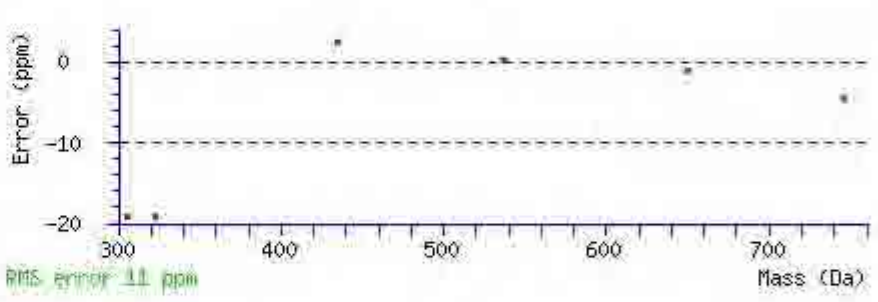
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 846.496338
Ions Score: 48 **Expect:** 0.0013
Matches : 6/54 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							7
2	199.107719	100.057497	181.097154	91.052215	P	*746.455937*	373.731607	729.429388	365.218332	728.445372	364.726324	6
3	312.191783	156.599529	294.181218	147.594247	I	*649.403173*	325.205224	632.376624	316.691950	631.392608	316.199942	5
4	413.239462	207.123369	395.228897	198.118087	T	*536.319109*	268.663193	519.292560	260.149918	518.308544	259.657910	4
5	526.323526	263.665401	508.312961	254.660119	L	*435.271430*	218.139353	418.244881	209.626078			3
6	673.391940	337.199608	655.381375	328.194325	F	*322.187366*	161.597321	305.160817	153.084046			2
7					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TPITLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	846.496338	-0.007150	TPITLFR
15.9	846.496338	-0.007150	TLPITFR
15.6	846.485092	0.004096	TPLLPYK
14.5	846.496338	-0.007150	TPIFTLR
14.5	846.496338	-0.007150	TPLFLTR
14.5	846.496338	-0.007150	TPLFTLR
13.8	846.485123	0.004065	TPFLLVGT
12.9	846.496353	-0.007165	TVIVPFR
3.6	846.496338	-0.007150	TLPFTLR
3.2	846.482407	0.006781	AHLIRHT

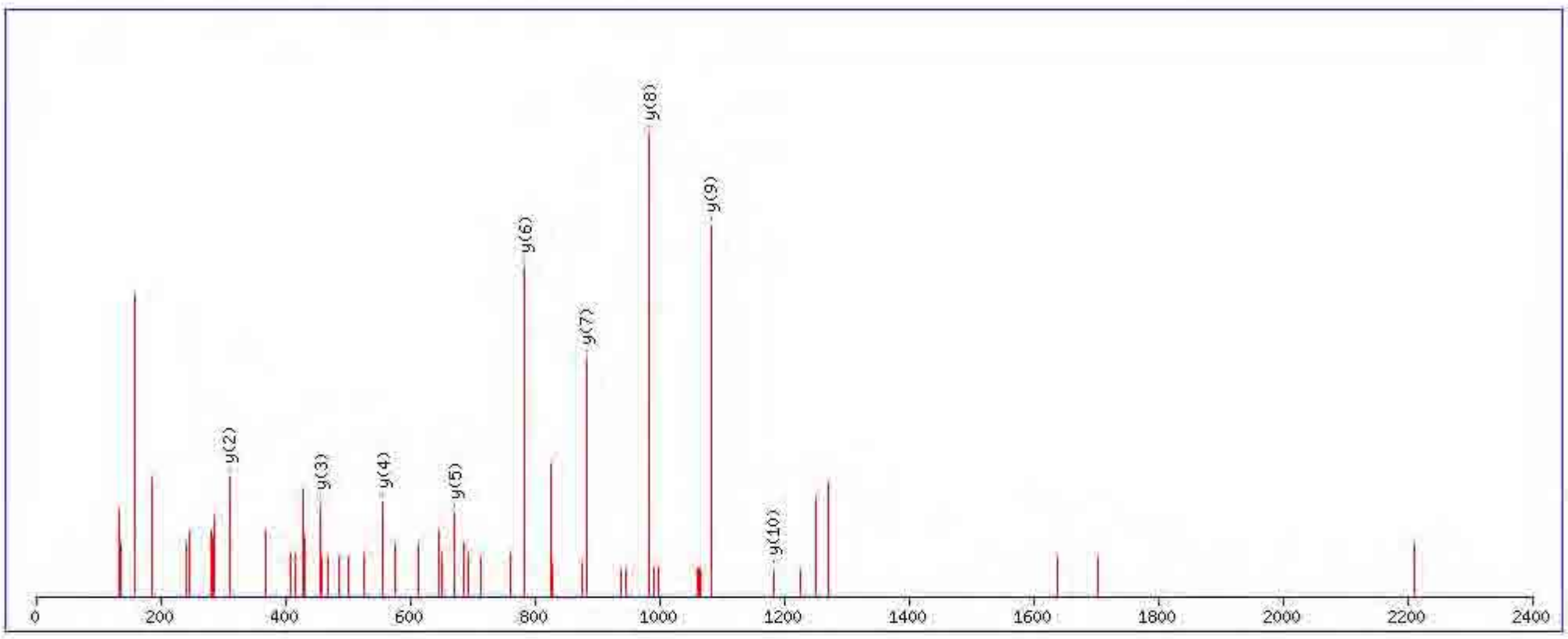
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVVTVIDVFYK**
Found in **FILA2_HUMAN**, Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1

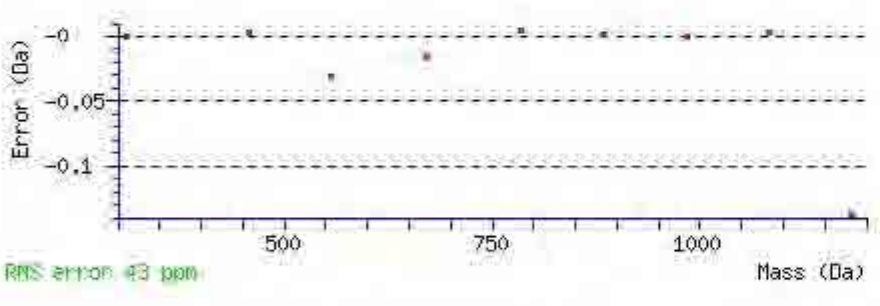
Match to Query 11602: 1268.700548 from(635.357550,2+) rtinseconds(2253) index(18838)
Title: Locus:1.1.1.2235.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

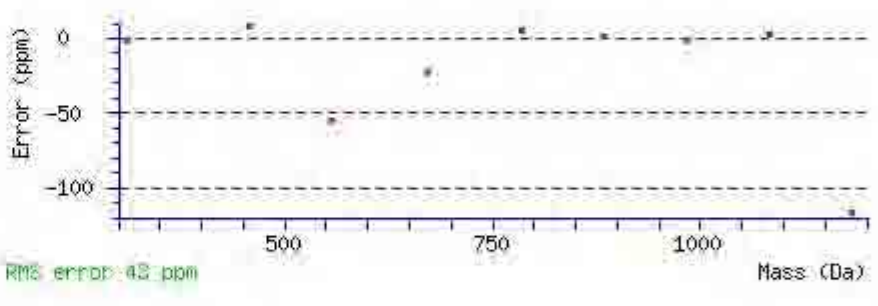
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1268.701660
Ions Score: 90 **Expect:** 2.3e-008
Matches : 9/92 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	187.107718	94.057497	169.097153	85.052214	V	*1182.676889*	591.842082	1165.650340	583.328808	1164.666324	582.836800	10
3	286.176132	143.591704	268.165567	134.586422	V	*1083.608475*	542.307876	1066.581926	533.794601	1065.597910	533.302593	9
4	387.223811	194.115544	369.213246	185.110261	T	*984.540061*	492.773668	967.513512	484.260394	966.529496	483.768386	8
5	486.292225	243.649751	468.281660	234.644468	V	*883.492382*	442.249829	866.465833	433.736554	865.481817	433.244546	7
6	599.376289	300.191783	581.365724	291.186500	I	*784.423968*	392.715622	767.397419	384.202347	766.413403	383.710339	6
7	714.403232	357.705254	696.392667	348.699972	D	*671.339904*	336.173590	654.313355	327.660315	653.329339	327.168307	5
8	813.471646	407.239461	795.461081	398.234178	V	*556.312961*	278.660119	539.286412	270.146844			4
9	960.540060	480.773668	942.529495	471.768385	F	*457.244547*	229.125911	440.217998	220.612637			3
10	1123.603389	562.305332	1105.592824	553.300050	Y	*310.176133*	155.591704	293.149584	147.078430			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVVTVIDVFYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.7	1268.701660	-0.001112	SVVTVIDVFYK
7.8	1268.712875	-0.012327	VSLWPVPVAASK
7.7	1268.712875	-0.012327	SIPTQPIVIWK
6.8	1268.702316	-0.001768	SVCPTRIPVAAR
6.7	1268.712845	-0.012297	WVIEAKDLPAK
6.7	1268.708832	-0.008284	SVELQQKPVNK
6.1	1268.708832	-0.008284	VSGEPLLAKPAR
5.4	1268.694916	0.005632	SPSPSTRPIRR
5.3	1268.708862	-0.008314	ESPGVPVAKVVR
5.3	1268.708847	-0.008299	LTTAVPSPSKPR

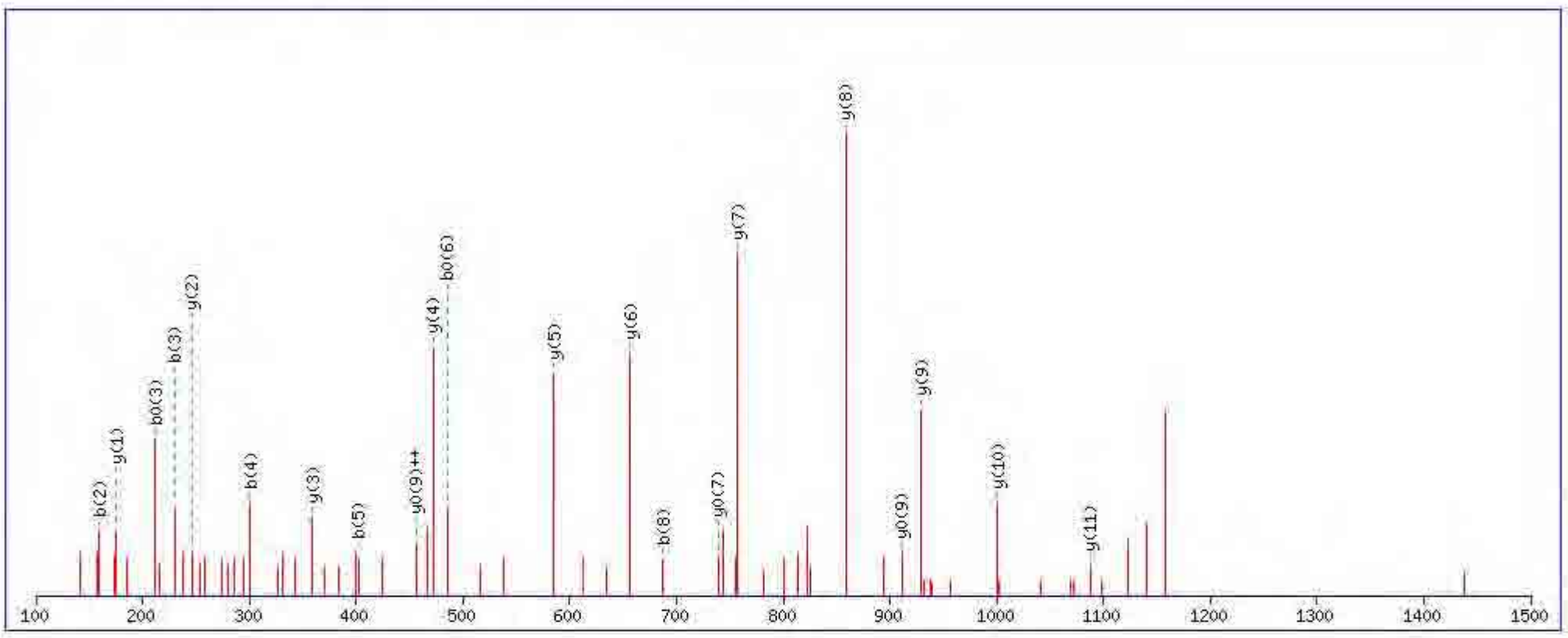
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAATTAILIAR**
Found in **GDN_HUMAN**, Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1

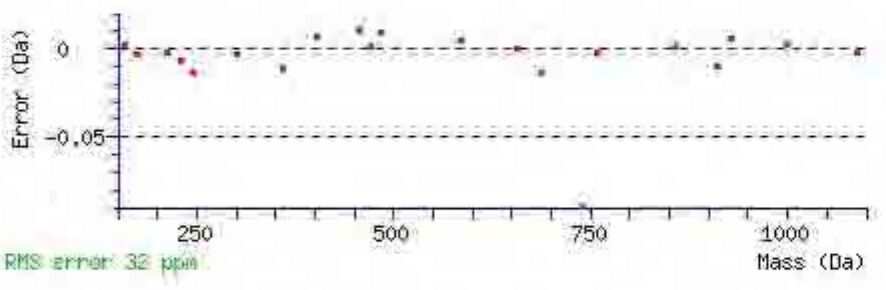
Match to Query 8680: 1157.670408 from(579.842480,2+) rtinseconds(1430) index(8971)
Title: Locus:1.1.1.1784.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

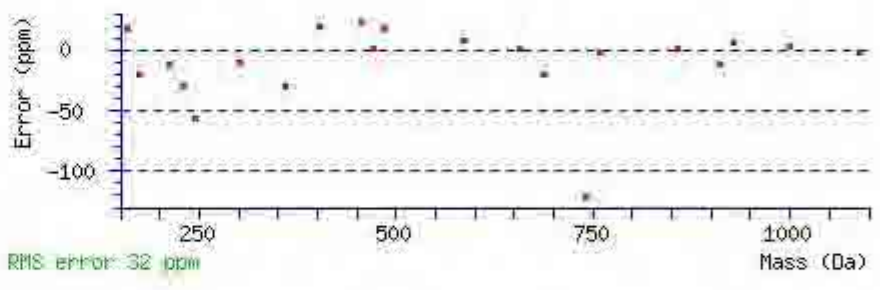
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1157.676788
Ions Score: 93 **Expect:** 5.2e-008
Matches : 21/96 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	159.076418	80.041847	141.065853	71.036564	S	*1087.646986*	544.327131	1070.620437	535.813857	1069.636421	535.321849	11
3	230.113532	115.560404	212.102967	106.555121	A	*1000.614958*	500.811117	983.588409	492.297843	982.604393	491.805835	10
4	301.150646	151.078961	283.140081	142.073679	A	*929.577844*	465.292560	912.551295	456.779286	911.567279	456.287278	9
5	402.198325	201.602801	384.187760	192.597518	T	*858.540730*	429.774003	841.514181	421.260729	840.530165	420.768721	8
6	503.246004	252.126640	485.235439	243.121358	T	*757.493051*	379.250164	740.466502	370.736889	739.482486	370.244881	7
7	574.283118	287.645197	556.272553	278.639915	A	*656.445372*	328.726324	639.418823	320.213050			6
8	687.367182	344.187229	669.356617	335.181947	I	*585.408258*	293.207767	568.381709	284.694493			5
9	800.451246	400.729261	782.440681	391.723979	L	*472.324194*	236.665735	455.297645	228.152461			4
10	913.535310	457.271293	895.524745	448.266011	I	*359.240130*	180.123703	342.213581	171.610429			3
11	984.572424	492.789850	966.561859	483.784568	A	*246.156066*	123.581671	229.129517	115.068397			2
12					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ASAATTAILIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.7	1157.676788	-0.006380	ASAATTAILIAR
17.4	1157.676804	-0.006396	TSIGILAAAVSR
16.6	1157.680817	-0.010409	GTAALPYPLKK
10.6	1157.666916	0.003492	WNTTVRLLR
9.3	1157.669601	0.000807	APFIELLPVK
8.6	1157.676804	-0.006396	VTNSTLAAIIR
7.9	1157.680832	-0.010424	FPVKPADLKK
7.9	1157.676788	-0.006380	LKETLAQLSR
7.1	1157.665573	0.004835	EKTLALGSVQL
6.9	1157.669617	0.000791	EFPTVPLVKL

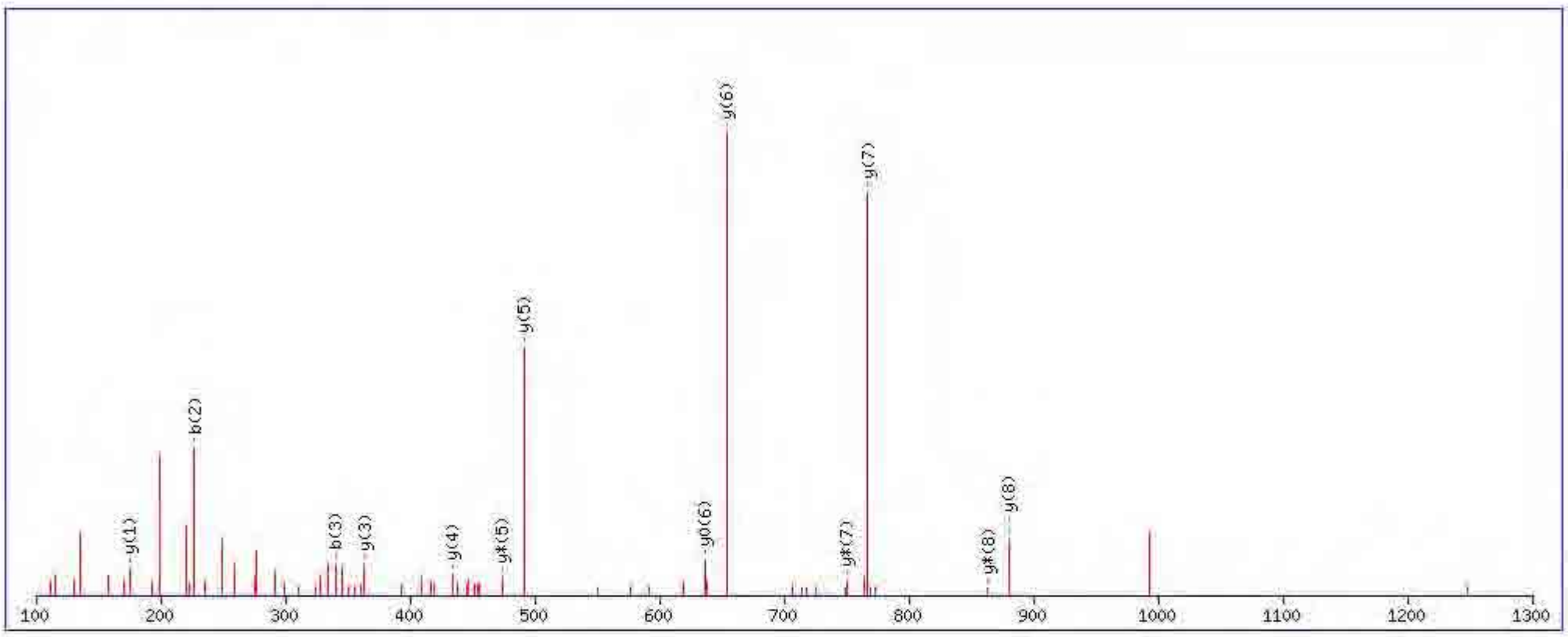
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

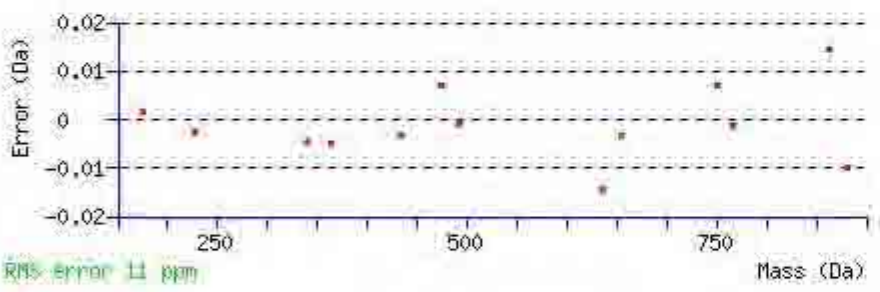
Match to Query 4785: 992.565968 from(497.290260,2+) rtinseconds(1303) index(7495)
Title: Locus:1.1.1.1714.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

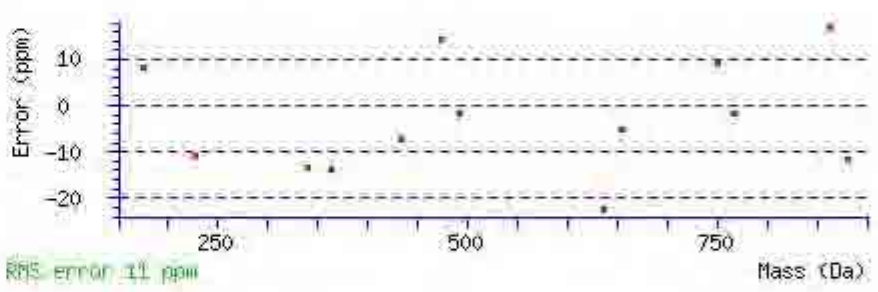
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 52 **Expect:** 0.00031
Matches : 13/66 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	880.488694	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	767.404630	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	654.320566	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	491.257237	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	434.235773	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	363.198659	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.3	992.565460	0.000508	LLIYGASTR
52.3	992.565460	0.000508	LLIYGATSR
19.0	992.565475	0.000493	LLPHVSSPK
17.8	992.565460	0.000508	LILGPHESK
17.6	992.565475	0.000493	PLLGPPDIR
16.7	992.565491	0.000477	PLPPPVAVR
16.7	992.565491	0.000477	PLPPPVAVR
15.3	992.565475	0.000493	ILPSVSHKP
14.4	992.566803	-0.000835	ILPHWRR
14.4	992.566803	-0.000835	PIIHRWR

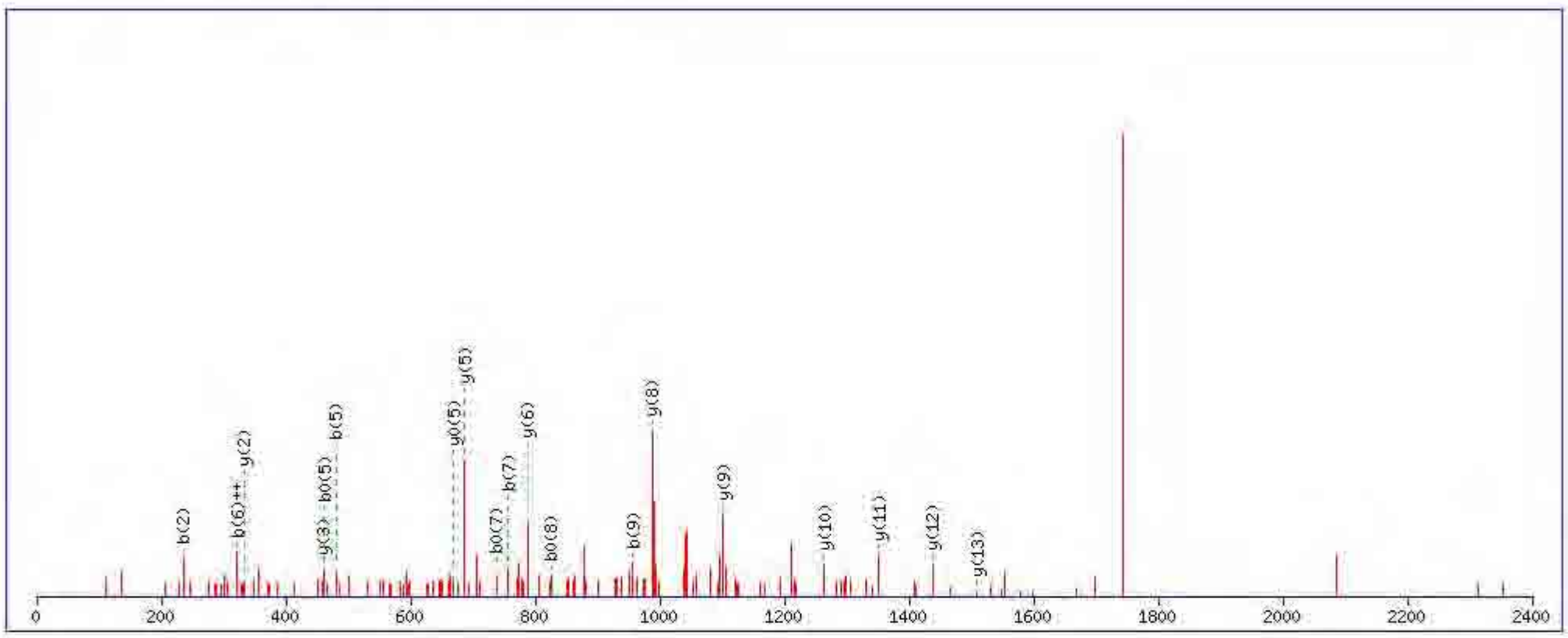
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAASSYLSLTPEQWK**
Found in **IGLL5_HUMAN**, Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2

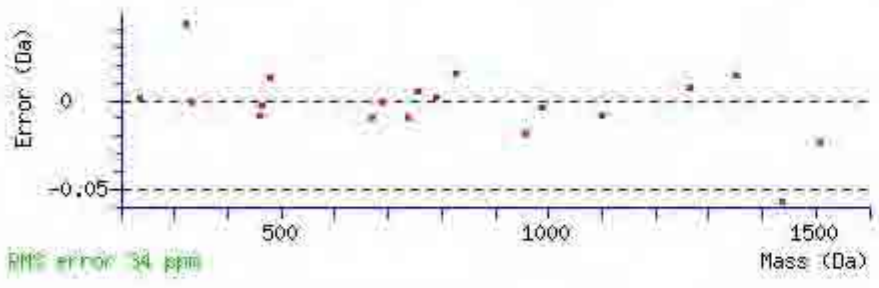
Match to Query 18826: 1742.867508 from(872.441030,2+) rtinseconds(2015) index(16056)
Title: Locus:1.1.1.2105.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

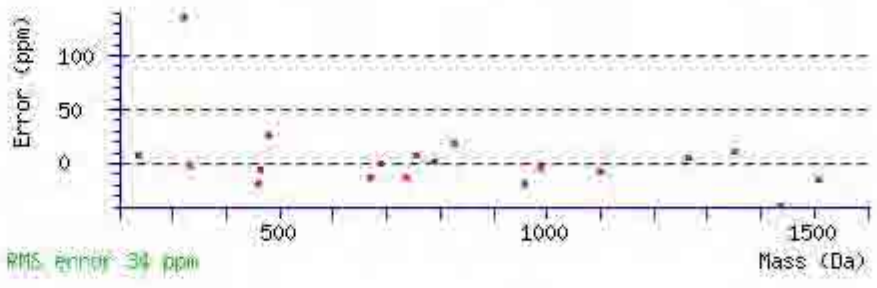
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1742.851517
Ions Score: 36 **Expect:** 0.00068
Matches : 19/132 fragment ions using 61 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.070605	82.538940					Y							15
2	235.107719	118.057498					A	1580.795500	790.901388	1563.768951	782.388114	1562.784935	781.896106	14
3	306.144833	153.576055					A	1509.758386	755.382831	1492.731837	746.869557	1491.747821	746.377549	13
4	393.176861	197.092068			375.166296	188.086786	S	1438.721272	719.864274	1421.694723	711.351000	1420.710707	710.858992	12
5	480.208889	240.608082			462.198324	231.602800	S	1351.689244	676.348260	1334.662695	667.834986	1333.678679	667.342978	11
6	643.272218	322.139747			625.261653	313.134465	Y	1264.657216	632.832246	1247.630667	624.318972	1246.646651	623.826964	10
7	756.356282	378.681779			738.345717	369.676497	L	1101.593887	551.300582	1084.567338	542.787307	1083.583322	542.295299	9
8	843.388310	422.197793			825.377745	413.192511	S	988.509823	494.758550	971.483274	486.245275	970.499258	485.753267	8
9	956.472374	478.739825			938.461809	469.734543	L	901.477795	451.242536	884.451246	442.729261	883.467230	442.237253	7
10	1057.520053	529.263665			1039.509488	520.258382	T	788.393731	394.700504	771.367182	386.187229	770.383166	385.695221	6
11	1154.572817	577.790047			1136.562252	568.784764	P	687.346052	344.176664	670.319503	335.663390	669.335487	335.171382	5
12	1283.615410	642.311343			1265.604845	633.306061	E	590.293288	295.650282	573.266739	287.137008	572.282723	286.645000	4
13	1411.673988	706.340632	1394.647439	697.827358	1393.663423	697.335350	Q	461.250695	231.128986	444.224146	222.615711			3
14	1597.753301	799.380289	1580.726752	790.867014	1579.742736	790.375006	W	333.192117	167.099696	316.165568	158.586422			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of YAASSYLSLTPEQWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1742.851517	0.015991	YAASSYLSLTPEQWK
2.1	1742.872665	-0.005157	NDHLYILLSTLEPTD
1.6	1742.868668	-0.001160	EGVSPRNSLEVVTPEV

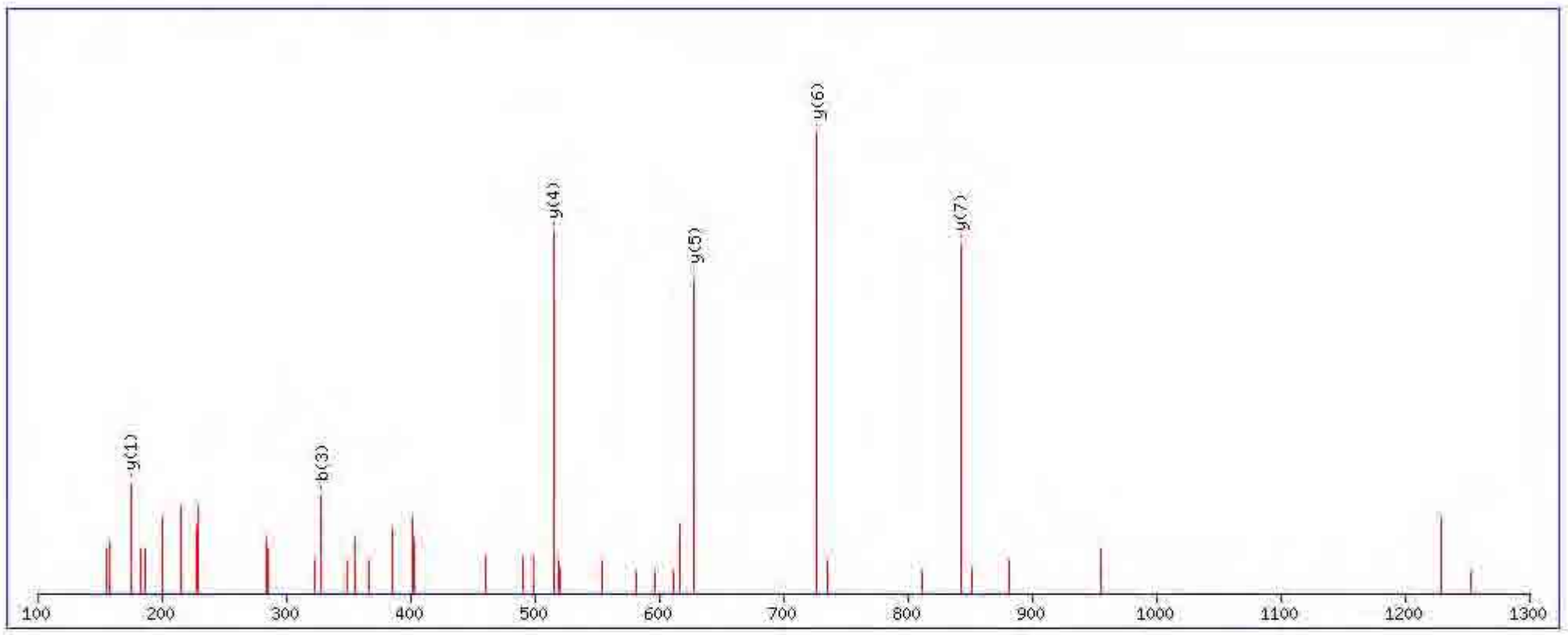
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDVLARLR**
Found in **INF2_HUMAN**, Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2

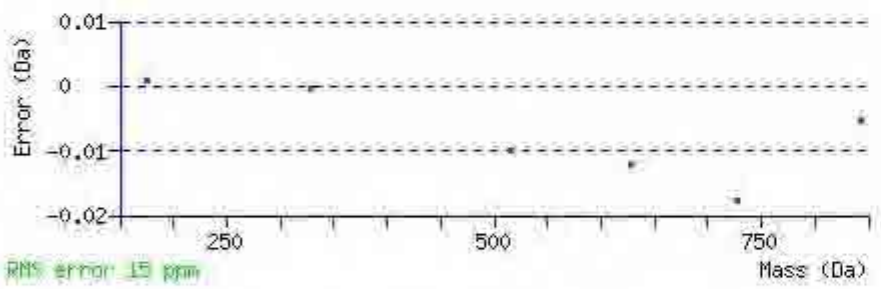
Match to Query 4027: 954.590568 from(478.302560,2+) rtinseconds(1650) index(11670)
Title: Locus:1.1.1.1905.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

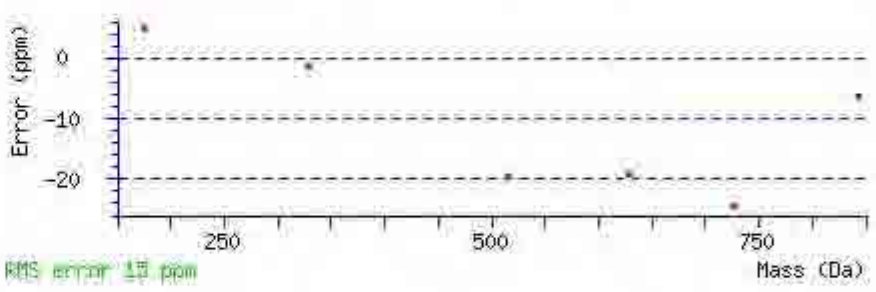
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 954.597427
Ions Score: 39 **Expect:** 0.0071
Matches : 6/60 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							8
2	229.118283	115.062779			211.107718	106.057497	D	*842.520662*	421.763969	825.494113	413.250695	824.510097	412.758687	7
3	328.186697	164.596986			310.176132	155.591704	V	*727.493719*	364.250498	710.467170	355.737223			6
4	441.270761	221.139018			423.260196	212.133736	L	*628.425305*	314.716291	611.398756	306.203016			5
5	512.307875	256.657576			494.297310	247.652293	A	*515.341241*	258.174259	498.314692	249.660984			4
6	668.408986	334.708131	651.382437	326.194857	650.398421	325.702849	R	444.304127	222.655702	427.277578	214.142427			3
7	781.493050	391.250163	764.466501	382.736889	763.482485	382.244881	L	288.203016	144.605146	271.176467	136.091872			2
8							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LDVLARLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	954.597427	-0.006859	LDVLARLR
38.0	954.586212	0.004356	IDPVLVKR
37.8	954.597427	-0.006859	IPTIIRAR
26.8	954.586212	0.004356	PLTLGLGLR
25.9	954.597427	-0.006859	LQKALGVAR
25.3	954.597427	-0.006859	PILTLARR
24.0	954.586197	0.004371	VEVLINRI
23.7	954.586197	0.004371	IITPNILR
23.7	954.586197	0.004371	ITLPNLLR
22.6	954.586212	0.004356	TLLPLQVR

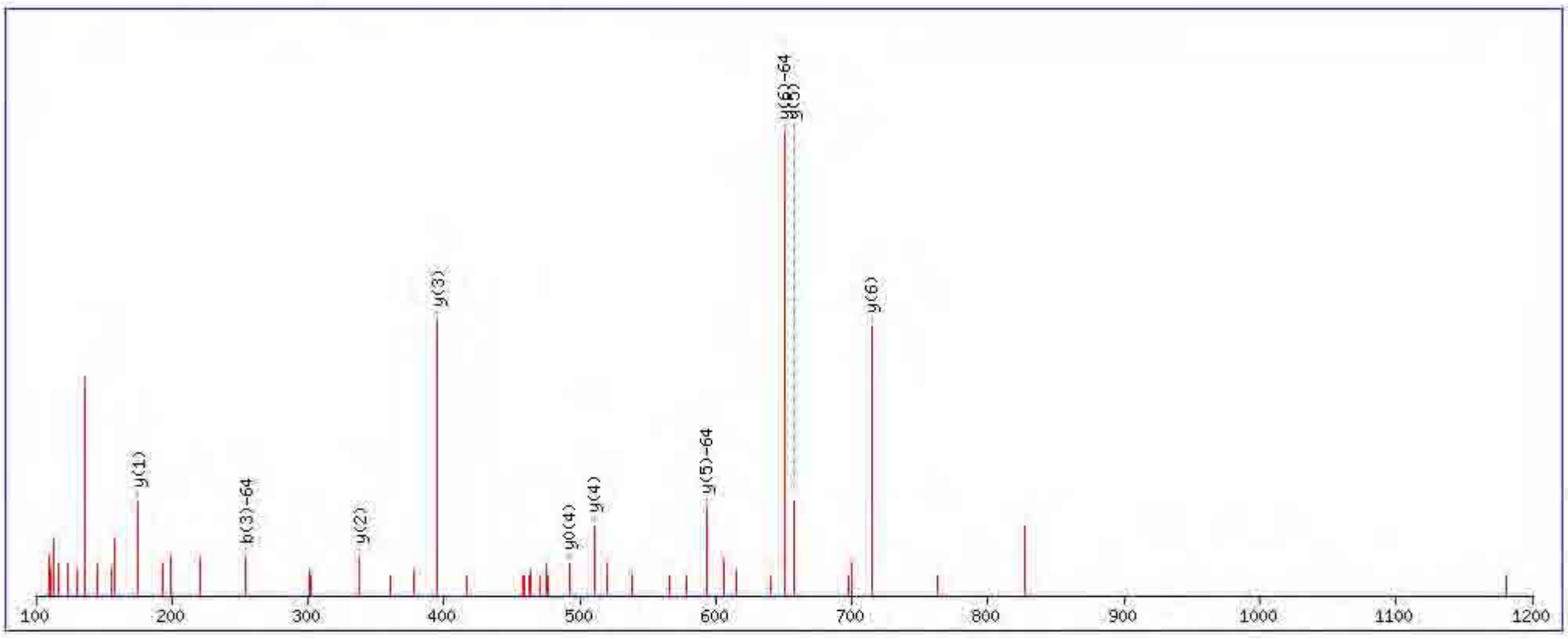
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGMDGYR**
Found in **LYSC_HUMAN**, Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1

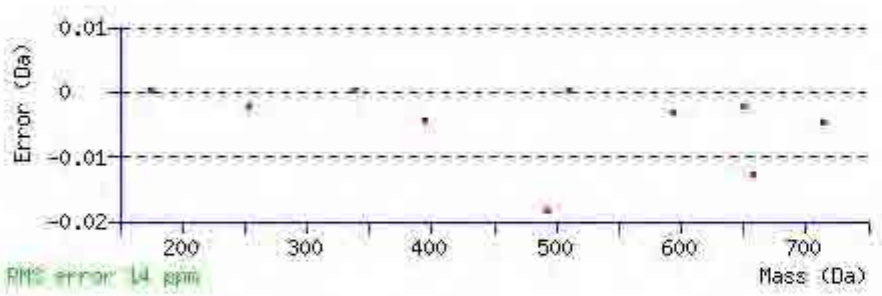
Match to Query 1343: 826.364628 from(414.189590,2+) rtinseconds(565) index(875)
Title: Locus:1.1.1.1299.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

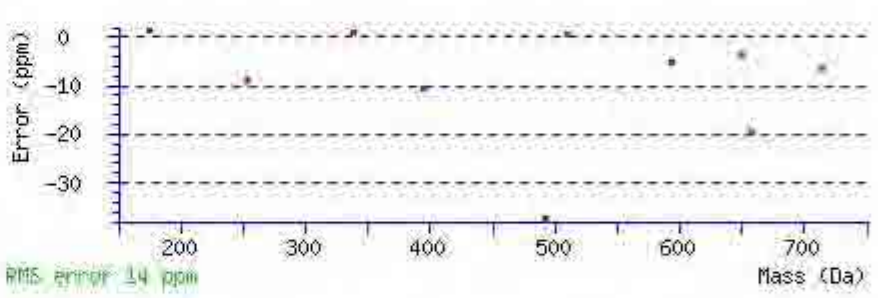
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 826.364334
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 53 **Expect:** 0.00049
Matches : 10/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	171.112804	86.060040			G	*714.287552*	357.647414	697.261003	349.134140	696.276987	348.642132	6
3	318.148204	159.577740			M	*657.266088*	329.136682	640.239539	320.623408	639.255523	320.131400	5
4	433.175147	217.091211	415.164582	208.085929	D	*510.230688*	255.618982	493.204139	247.105708	492.220123	246.613700	4
5	490.196611	245.601943	472.186046	236.596661	G	*395.203745*	198.105511	378.177196	189.592236			3
6	653.259940	327.133608	635.249375	318.128326	Y	*338.182281*	169.594779	321.155732	161.081504			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LGMDGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	826.364334	0.000294	LGMDGYR
24.0	826.364349	0.000279	PGMSTFR
11.7	826.364349	0.000279	PGMPHPK
9.7	826.364319	0.000309	IDNMYR
8.3	826.364334	0.000294	PASSMFR
7.6	826.364334	0.000294	AVMGYDR
7.1	826.356461	0.008167	LATMSAMS
4.5	826.367706	-0.003078	MSTVMSR
0.9	826.364334	0.000294	GLCTDYR
0.1	826.356476	0.008152	LMATQMT

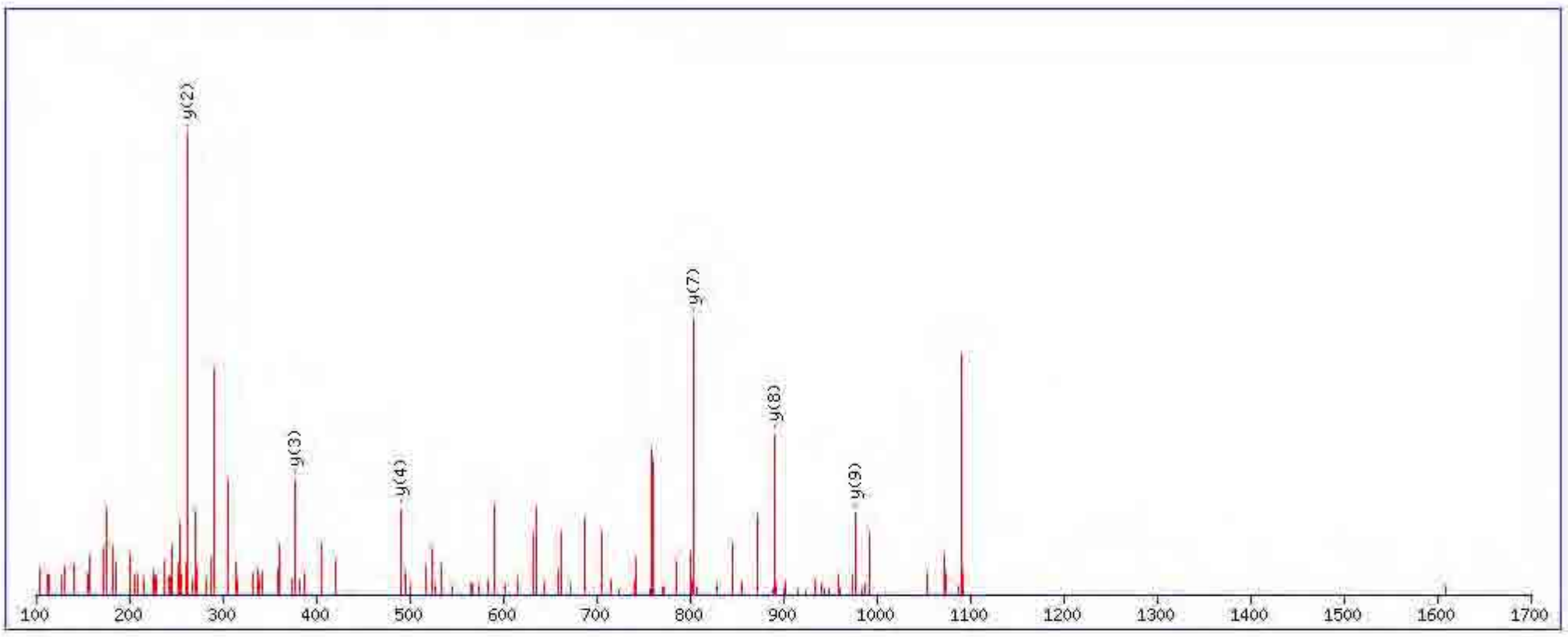
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSSLLSIDNE**
Found in **NKG2A_HUMAN**, NKG2-A/NKG2-B type II integral membrane protein OS=Homo sapiens GN=KLRC1 PE=1 SV=2

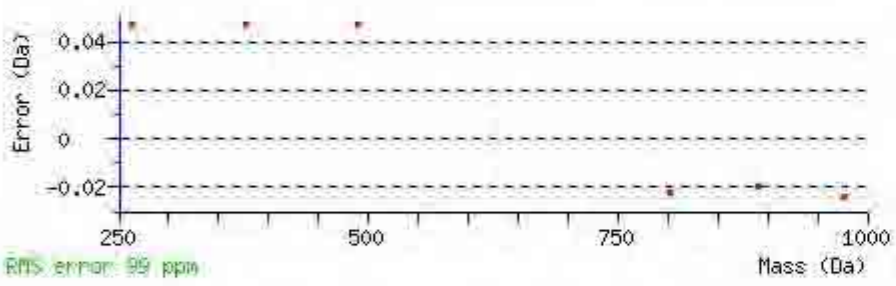
Match to Query 6932: 1090.522128 from(546.268340,2+) rtinseconds(912) index(3771)
Title: Locus:1.1.1.1492.13
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

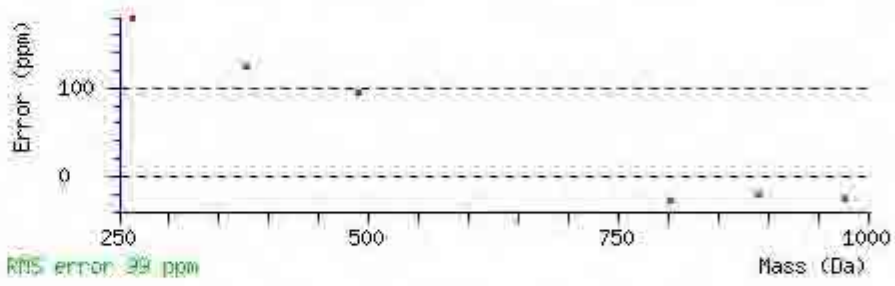
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1090.514206
Ions Score: 44 **Expect:** 0.0031
Matches : 6/104 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	*977.478580*	489.242928	960.452031	480.729654	959.468015	480.237646	9
3	289.114259	145.060768	272.087710	136.547493	271.103694	136.055485	S	*890.446552*	445.726914	873.420003	437.213640	872.435987	436.721632	8
4	402.198323	201.602800	385.171774	193.089525	384.187758	192.597517	L	*803.414524*	402.210900	786.387975	393.697626	785.403959	393.205618	7
5	515.282387	258.144832	498.255838	249.631557	497.271822	249.139549	L	690.330460	345.668868	673.303911	337.155594	672.319895	336.663586	6
6	602.314415	301.660846	585.287866	293.147571	584.303850	292.655563	S	577.246396	289.126836	560.219847	280.613562	559.235831	280.121554	5
7	715.398479	358.202878	698.371930	349.689603	697.387914	349.197595	I	*490.214368*	245.610822	473.187819	237.097548	472.203803	236.605540	4
8	830.425422	415.716349	813.398873	407.203075	812.414857	406.711067	D	*377.130304*	189.068790	360.103755	180.555516	359.119739	180.063508	3
9	944.468349	472.737813	927.441800	464.224538	926.457784	463.732530	N	*262.103361*	131.555319	245.076812	123.042044	244.092796	122.550036	2
10							E	148.060434	74.533855			130.049869	65.528573	1





NCBI **BLAST** search of NSSLLSIDNE
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	1090.514206	0.007922	NSSLLSIDNE
15.8	1090.514236	0.007892	NSVVTSEPDK
15.5	1090.525452	-0.003324	SSPADKLDSR
13.0	1090.525452	-0.003324	NSVSPSESLR
12.9	1090.519577	0.002551	NSTLWWER
12.7	1090.532852	-0.010724	NSSDAVLVACL
9.6	1090.525467	-0.003339	SLAPQTTDSR
8.0	1090.518921	0.003207	REALGGMDSR
7.0	1090.518936	0.003192	GGSPSKQQMR
6.9	1090.525467	-0.003339	DSLTGQLSDR

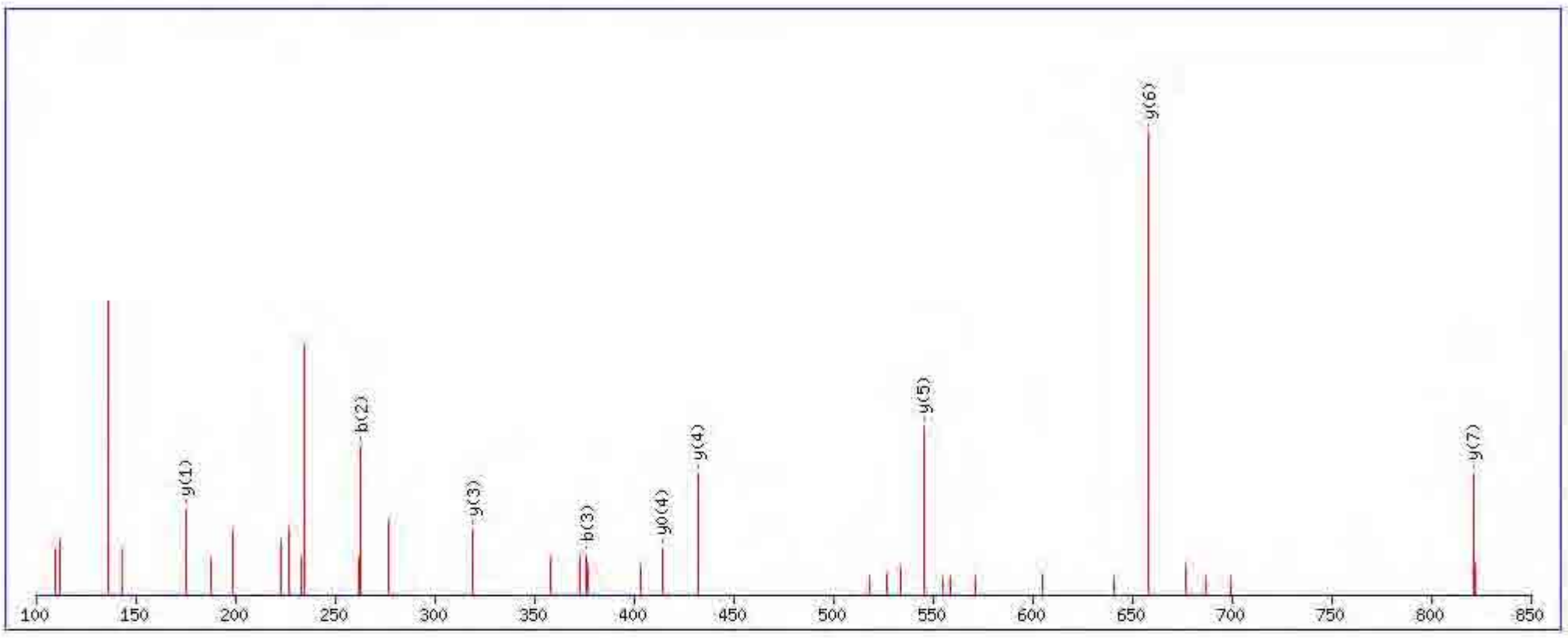
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYLLIGSR**
Found in **OLFL1_HUMAN**, Olfactomedin-like protein 1 OS=Homo sapiens GN=OLFML1 PE=1 SV=2

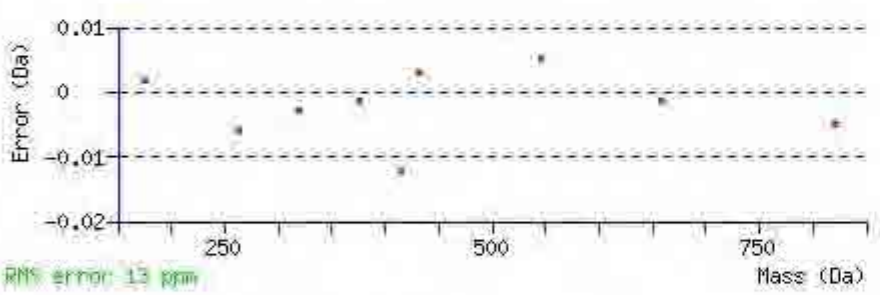
Match to Query 3321: 919.557968 from(460.786260,2+) rtinseconds(1613) index(11250)
Title: Locus:1.1.1.1884.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

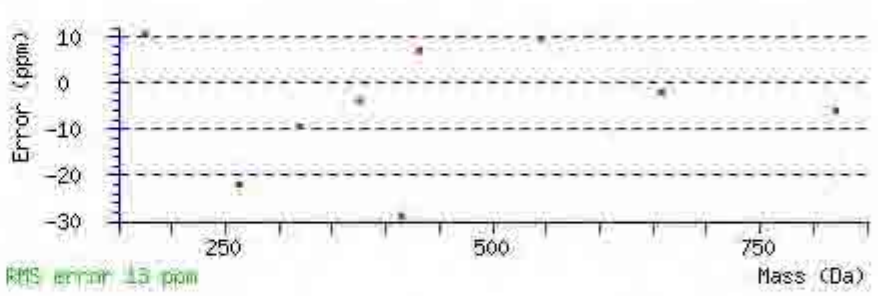
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 919.549088
Ions Score: 47 **Expect:** 0.00077
Matches : 9/56 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							8
2	263.139019	132.073148			Y	821.487965	411.247621	804.461416	402.734346	803.477400	402.242338	7
3	376.223083	188.615180			L	658.424636	329.715956	641.398087	321.202682	640.414071	320.710674	6
4	489.307147	245.157212			L	545.340572	273.173924	528.314023	264.660650	527.330007	264.168642	5
5	602.391211	301.699244			I	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
6	659.412675	330.209976			G	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	746.444703	373.725990	728.434138	364.720707	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VYLLIGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	919.549088	0.008880	VYLLIGSR
25.0	919.549088	0.008880	VYISAVLR
20.6	919.549072	0.008896	YVLLKER
12.5	919.549072	0.008896	VYLERLK
8.6	919.560318	-0.002350	VYTLRIR
4.8	919.560318	-0.002350	LVYLRTR
4.2	919.549103	0.008865	VLYGTVRI
2.6	919.549072	0.008896	VYEILKR
2.6	919.560318	-0.002350	VYRLITR
1.4	919.549072	0.008896	YVLERIK

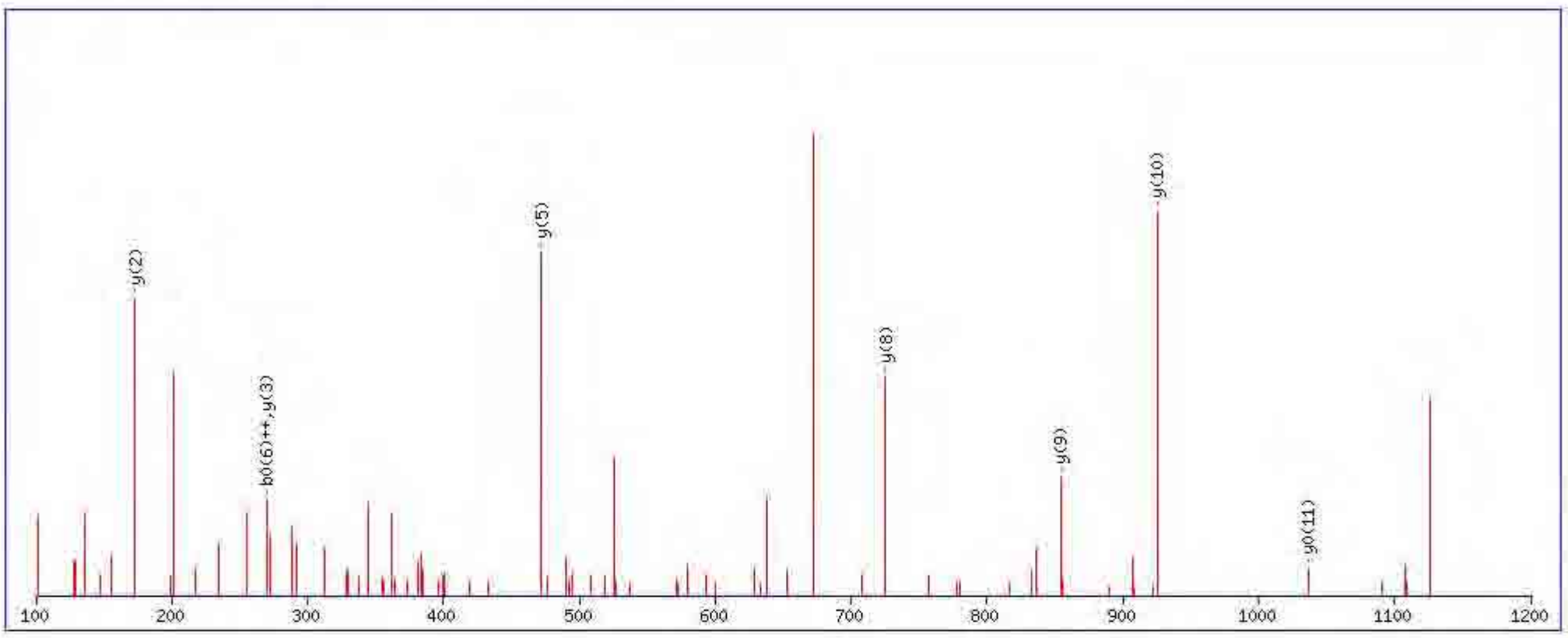
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAEGVPTTPGP**
Found in **F134C_HUMAN**, Protein FAM134C OS=Homo sapiens GN=FAM134C PE=1 SV=1

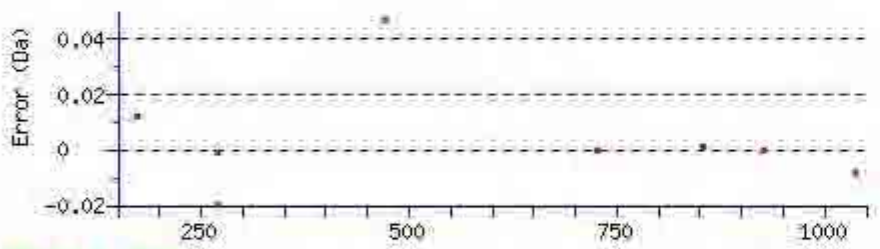
Match to Query 7745: 1124.536728 from(563.275640,2+) rtinseconds(816) index(2952)
Title: Locus:1.1.1.1437.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

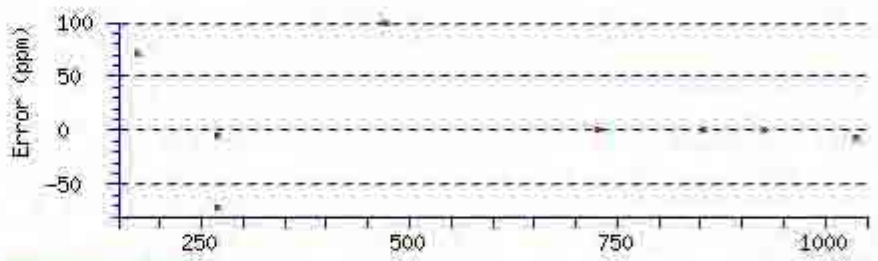
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1124.534973
Ions Score: 46 Expect: 0.0011
Matches : 8/80 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A					12
2	201.086983	101.047130	183.076418	92.041847	E	1054.505133	527.756205	1036.494568	518.750922	11
3	272.124097	136.565687	254.113532	127.560404	A	*925.462540*	463.234908	907.451975	454.229626	10
4	401.166690	201.086983	383.156125	192.081701	E	*854.425426*	427.716351	836.414861	418.711069	9
5	458.188154	229.597715	440.177589	220.592433	G	*725.382833*	363.195055	707.372268	354.189772	8
6	557.256568	279.131922	539.246003	270.126640	V	668.361369	334.684323	650.350804	325.679040	7
7	654.309332	327.658304	636.298767	318.653022	P	569.292955	285.150116	551.282390	276.144833	6
8	755.357011	378.182144	737.346446	369.176861	T	*472.240191*	236.623733	454.229626	227.618451	5
9	856.404690	428.705983	838.394125	419.700701	T	371.192512	186.099894	353.181947	177.094611	4
10	953.457454	477.232365	935.446889	468.227083	P	*270.144833*	135.576054			3
11	1010.478918	505.743097	992.468353	496.737815	G	*173.092069*	87.049672			2
12					P	116.070605	58.538940			1





NCBI **BLAST** search of AEAEGVPTTPGP
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1124.534973	0.001755	AEAEGVPTTPGP
43.5	1124.534927	0.001801	AEAESLYQSK
13.5	1124.534973	0.001755	VTTADPYASGK
12.8	1124.546204	-0.009476	EAAPPGPGPLR
12.7	1124.546188	-0.009460	SLAESFTNTR
11.8	1124.532288	0.004440	GDDGAGRAGPPR
10.6	1124.546219	-0.009491	SPQPVPSPRP
9.9	1124.546188	-0.009460	PDGAPALESPR
8.9	1124.539658	-0.002930	EARPCPPAPR
8.4	1124.528427	0.008301	SLAEQFQRM

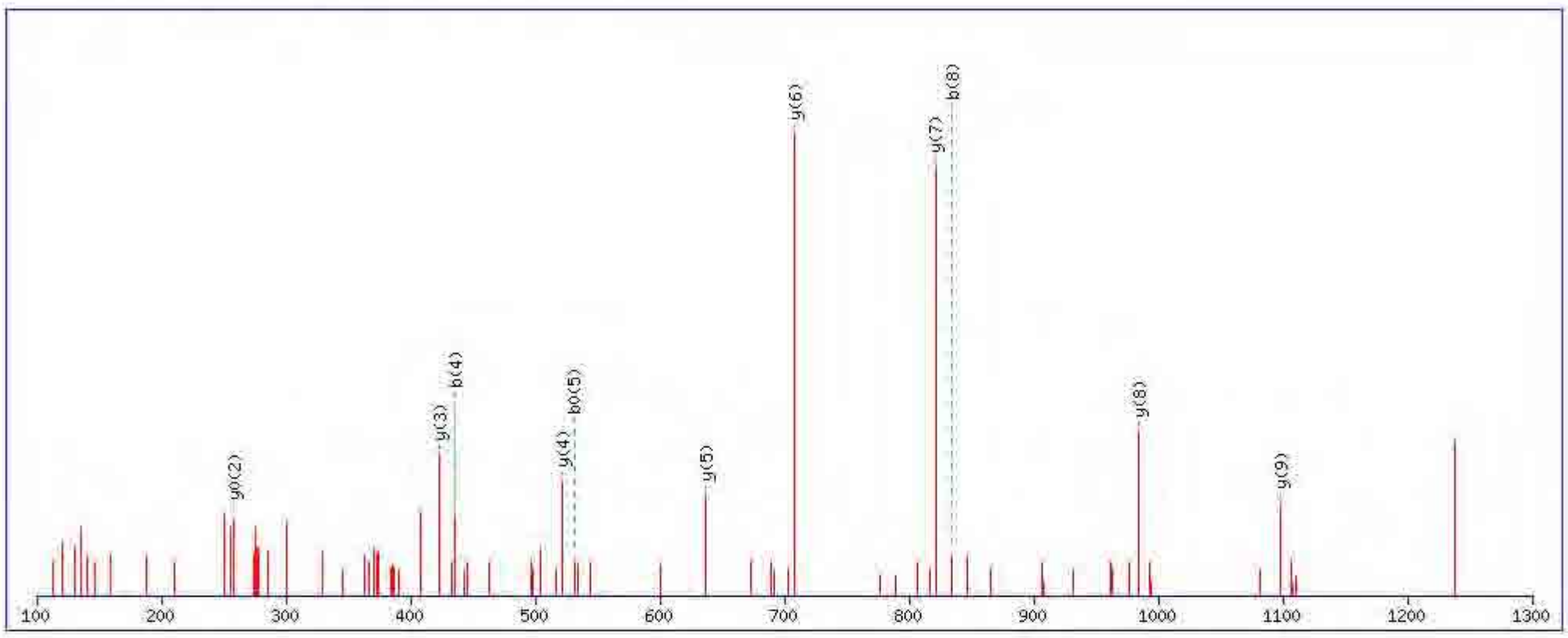
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTNYLADVFEK**
Found in **S10A7_HUMAN**, Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4

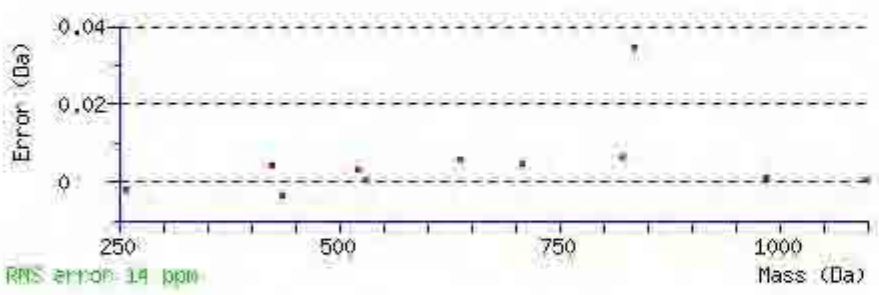
Match to Query 11332: 1255.602248 from(628.808400,2+) rtinseconds(1926) index(14958)
Title: Locus:1.1.1.2056.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

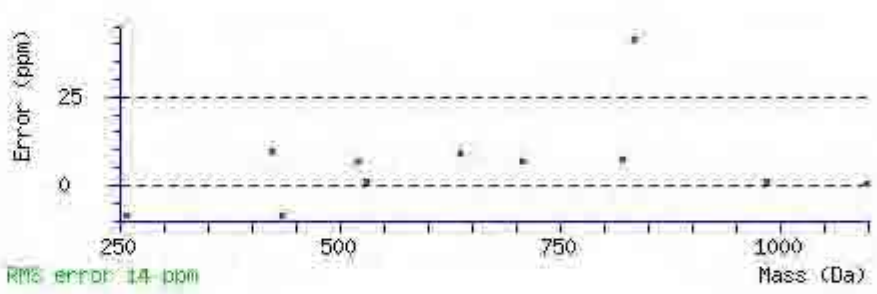
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1255.608459
Ions Score: 46 **Expect:** 0.00028
Matches : 11/112 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	159.076419	80.041847			141.065854	71.036565	T	1199.594281	600.300778	1182.567732	591.787504	1181.583716	591.295496	10
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	N	*1098.546602*	549.776939	1081.520053	541.263665	1080.536037	540.771656	9
4	**436.182675**	218.594976	419.156126	210.081701	418.172110	209.589693	Y	*984.503675*	492.755475	967.477126	484.242201	966.493110	483.750193	8
5	549.266739	275.137008	532.240190	266.623733	531.256174	266.131725	L	*821.440346*	411.223811	804.413797	402.710536	803.429781	402.218528	7
6	620.303853	310.655565	603.277304	302.142290	602.293288	301.650282	A	*708.356282*	354.681779	691.329733	346.168504	690.345717	345.676496	6
7	735.330796	368.169036	718.304247	359.655761	717.320231	359.163753	D	*637.319168*	319.163222	620.292619	310.649947	619.308603	310.157939	5
8	**834.399210**	417.703243	817.372661	409.189968	816.388645	408.697960	V	*522.292225*	261.649750	505.265676	253.136476	504.281660	252.644468	4
9	981.467624	491.237450	964.441075	482.724175	963.457059	482.232167	F	*423.223811*	212.115543	406.197262	203.602269	405.213246	203.110261	3
10	1110.510217	555.758746	1093.483668	547.245472	1092.499652	546.753464	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GTNYLADVFEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	1255.608459	-0.006211	GTNYLADVFEK
7.7	1255.604462	-0.002214	SPHTTLSPAGSTT
6.5	1255.597916	0.004332	GTYNGTRGLSCK
4.5	1255.611862	-0.009614	ISGPNPVVPMPT
4.5	1255.611862	-0.009614	ISGPNPVVPMPT
2.8	1255.605301	-0.003053	YNVLMSLRGCT
2.4	1255.605301	-0.003053	GTFRQMLMEK
2.2	1255.611816	-0.009568	TEYQISVSAMK
1.7	1255.590714	0.011534	EQPWPLPVQM
1.1	1255.605286	-0.003038	SYLIGCAIASCR

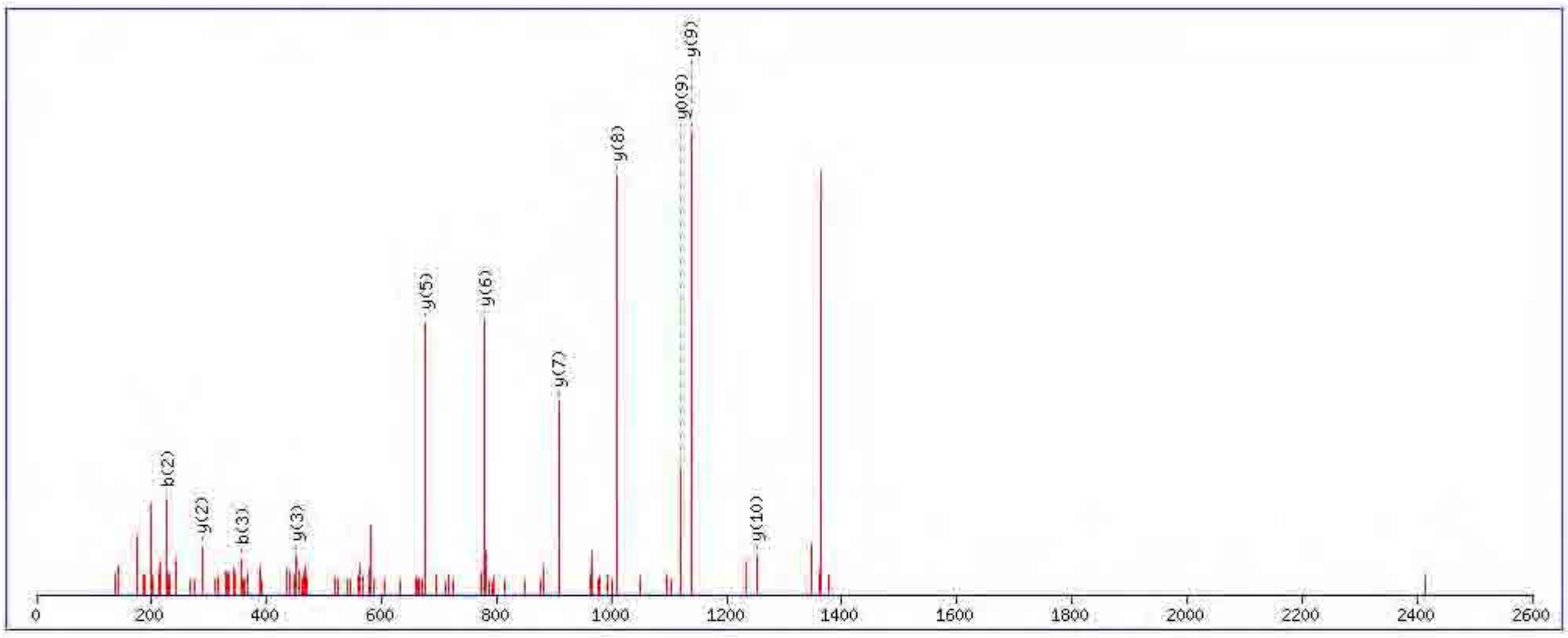
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **S10A8_HUMAN**, Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1

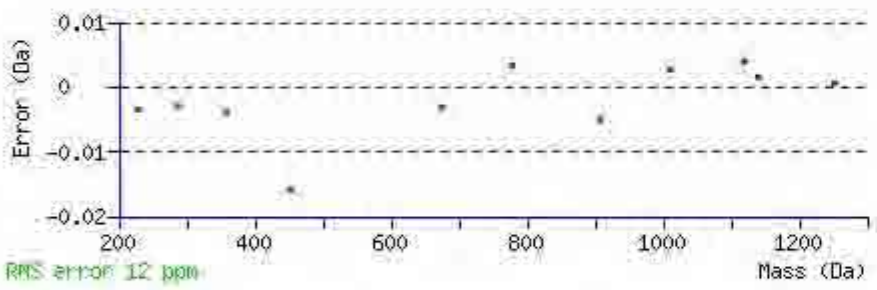
Match to Query 13508: 1363.682088 from(682.848320,2+) rtinseconds(1562) index(10569)
Title: Locus:1.1.1.1856.23
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

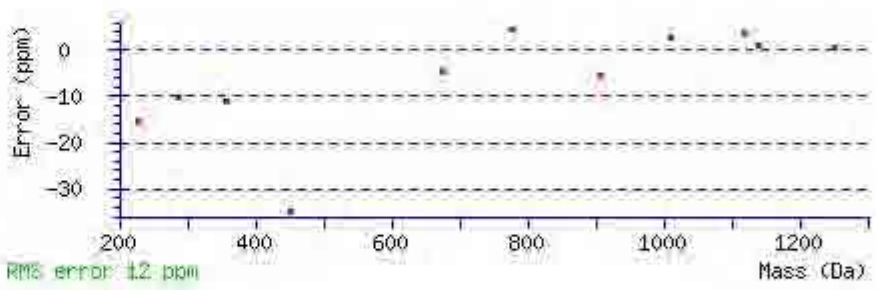
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1363.680557
Ions Score: 80 **Expect:** 4.1e-006
Matches : 11/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	227.175404	114.091340					L	1251.603801	626.305539	1234.577252	617.792264	1233.593236	617.300256	10
3	356.217997	178.612637			338.207432	169.607354	E	1138.519737	569.763507	1121.493188	561.250232	1120.509172	560.758224	9
4	457.265676	229.136476			439.255111	220.131194	T	1009.477144	505.242210	992.450595	496.728936	991.466579	496.236928	8
5	586.308269	293.657773			568.297704	284.652490	E	908.429465	454.718371	891.402916	446.205096	890.418900	445.713088	7
6	689.317454	345.162365			671.306889	336.157083	C	779.386872	390.197074	762.360323	381.683800			6
7	786.370218	393.688747			768.359653	384.683465	P	676.377687	338.692482	659.351138	330.179207			5
8	914.428796	457.718036	897.402247	449.204762	896.418231	448.712754	Q	579.324923	290.166100	562.298374	281.652825			4
9	1077.492125	539.249701	1060.465576	530.736426	1059.481560	530.244418	Y	451.266345	226.136810	434.239796	217.623536			3
10	1190.576189	595.791733	1173.549640	587.278458	1172.565624	586.786450	I	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLETECPQYIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.1	1363.680557	0.001531	LLETECPQYIR
25.2	1363.673203	0.008885	LPERPGPSNPPVG
25.2	1363.673203	0.008885	LPERPGPSNPPVG
23.3	1363.691788	-0.009700	PEEVLSCRYLR
21.1	1363.677200	0.004888	PIEADFSWQKK
20.4	1363.680573	0.001515	LPEDPAIPMPPR
20.4	1363.673203	0.008885	LPERPGPSNPPVG
17.1	1363.673203	0.008885	LPERPGPSNPPVG
17.1	1363.673203	0.008885	LPERPGPSNPPVG
16.7	1363.671844	0.010244	IPTEETTISTEK

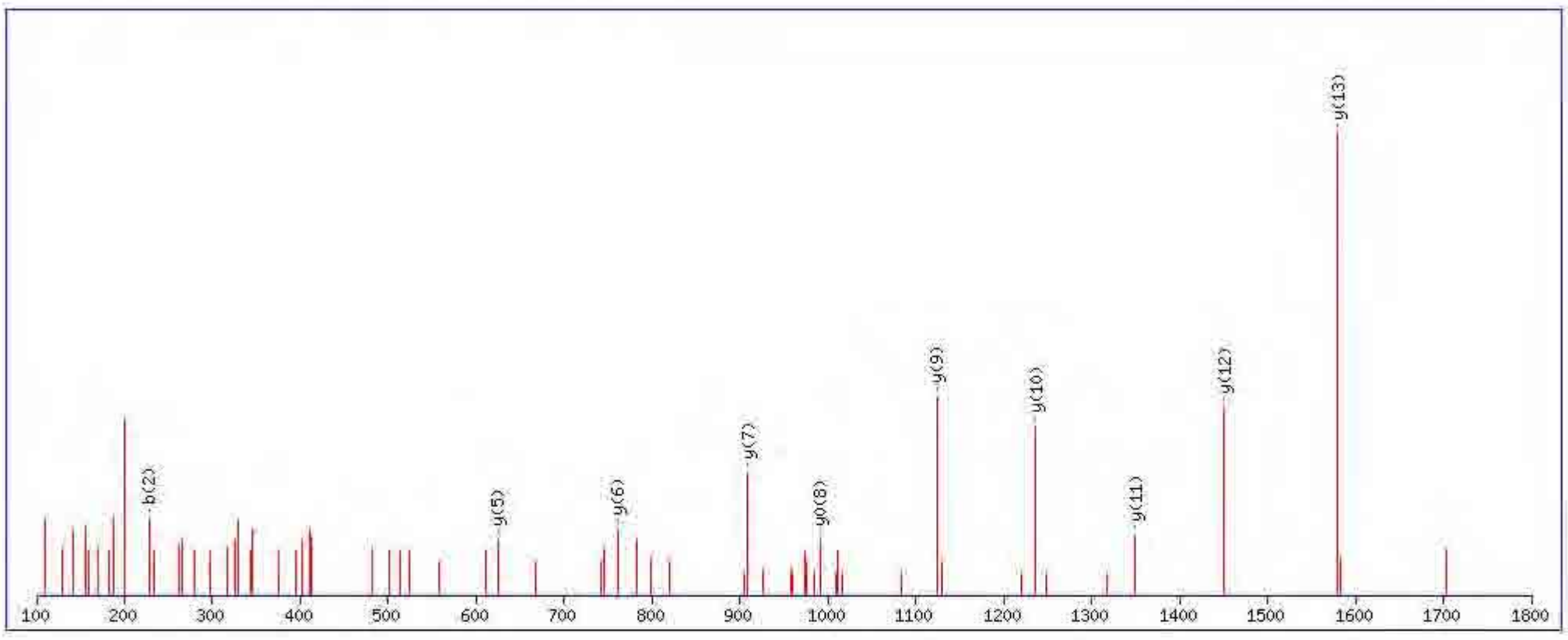
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **S10A9_HUMAN**, Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1

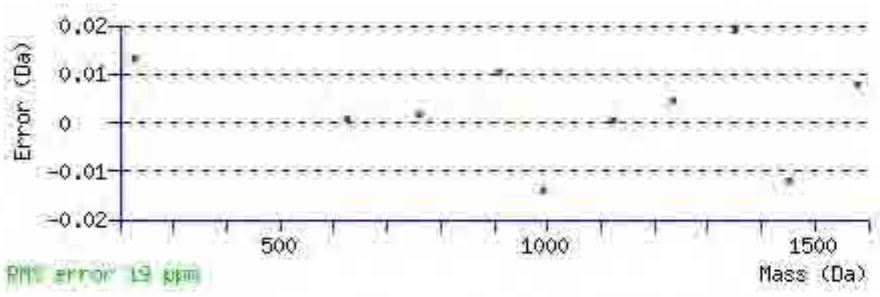
Match to Query 19519: 1805.928312 from(602.983380,3+) rtinseconds(2154) index(17820)
Title: Locus:1.1.1.2181.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

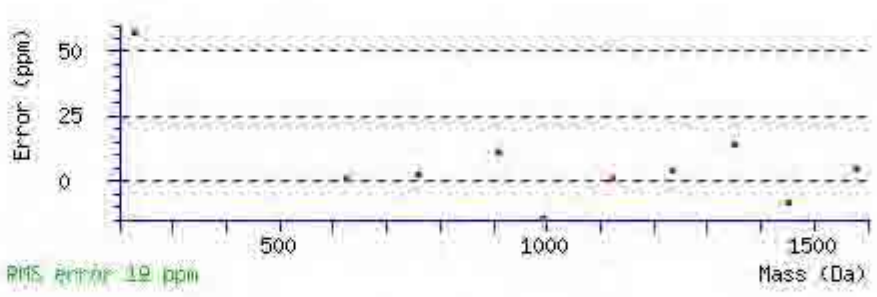
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1805.931183
Ions Score: 51 **Expect:** 9.3e-005
Matches : 10/160 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							15
2	228.134267	114.570771	211.107718	106.057497			I	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	14
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	E	*1579.811485*	790.409381	1562.784936	781.896106	1561.800920	781.404098	13
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	T	*1450.768892*	725.888084	1433.742343	717.374810	1432.758327	716.882802	12
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	I	*1349.721213*	675.364245	1332.694664	666.850970	1331.710648	666.358962	11
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	I	*1236.637149*	618.822213	1219.610600	610.308938	1218.626584	609.816930	10
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	N	*1123.553085*	562.280181	1106.526536	553.766906	1105.542520	553.274898	9
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	T	1009.510158	505.258717	992.483609	496.745443	991.499593	496.253435	8
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	F	*908.462479*	454.734878	891.435930	446.221603	890.451914	445.729595	7
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	H	*761.394065*	381.200671	744.367516	372.687396	743.383500	372.195388	6
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	Q	*624.335153*	312.671215	607.308604	304.157940	606.324588	303.665932	5
12	1474.732506	737.869891	1457.705957	729.356617	1456.721941	728.864609	Y	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	4
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	S	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	1660.832948	830.920112	1643.806399	822.406838	1642.822383	821.914830	V	246.181218	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NIETIINTFHQYSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.1	1805.931183	-0.002871	NIETIINTFHQYSVK
7.6	1805.913437	0.014875	CIQPPPYPGNIFRLK
4.4	1805.934570	-0.006258	RLMLPPPSTPALSGAPPG
2.8	1805.915466	0.012846	IKDLTLPELIGIMDTC
2.4	1805.915939	0.012373	TPSERQLTPLPPSAPPS
0.2	1805.941086	-0.012774	NLETVLSQSVQSIPLY
0.2	1805.931183	-0.002871	VGAEFQALRAFLVEQE
0.1	1805.931229	-0.002917	FDPVGPLPGPNPILPGR
0.1	1805.934570	-0.006258	LGGQTPYLMDQLGLRL
0.1	1805.941101	-0.012789	NLLEVSGPETVPLPNVP

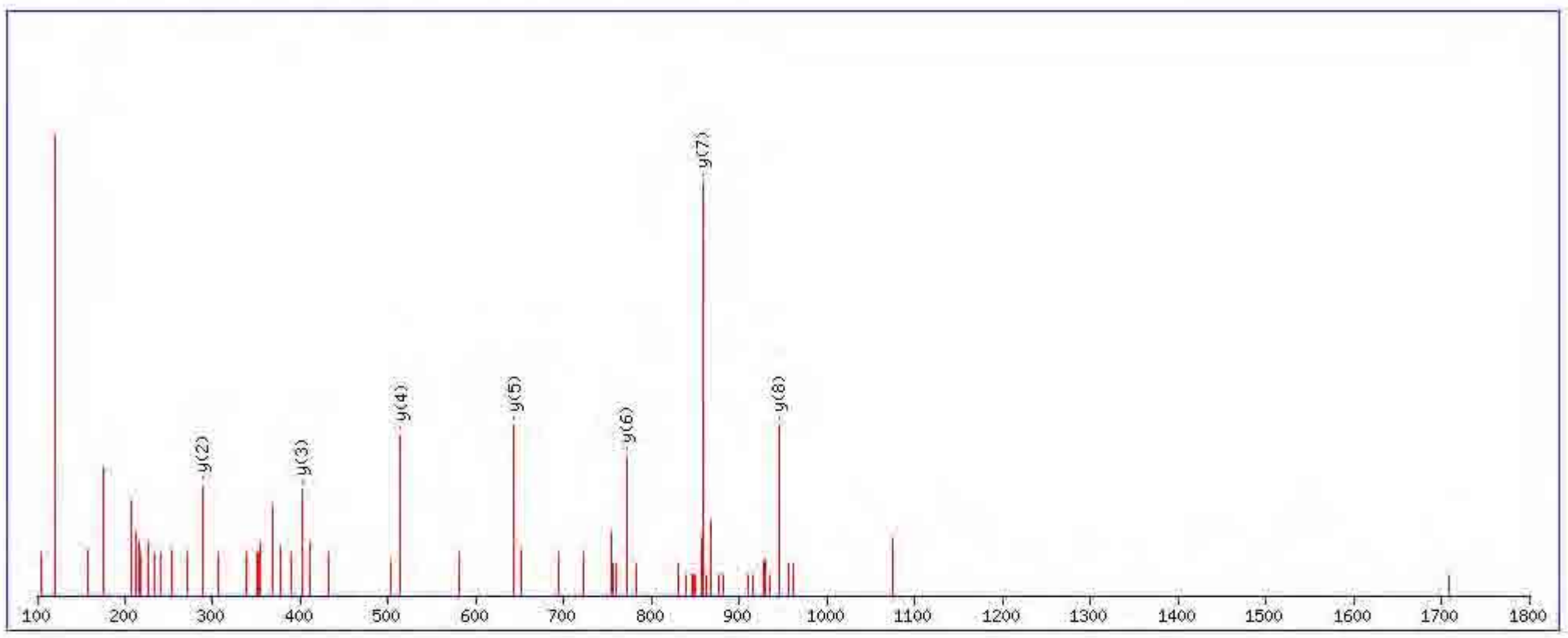
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSSQELILR**
Found in **TGM3_HUMAN**, Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4

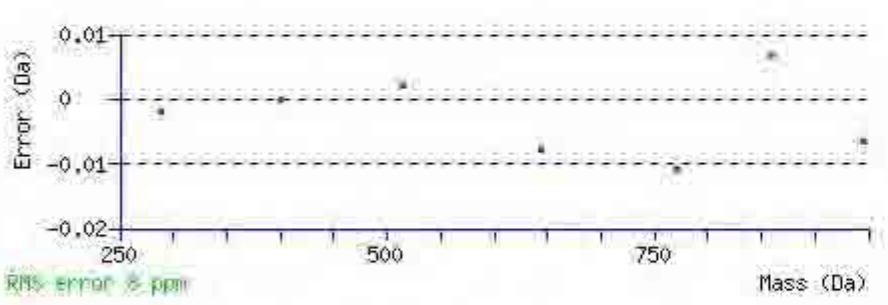
Match to Query 6946: 1091.594808 from(546.804680,2+) rtinseconds(1576) index(10755)
Title: Locus:1.1.1.1864.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

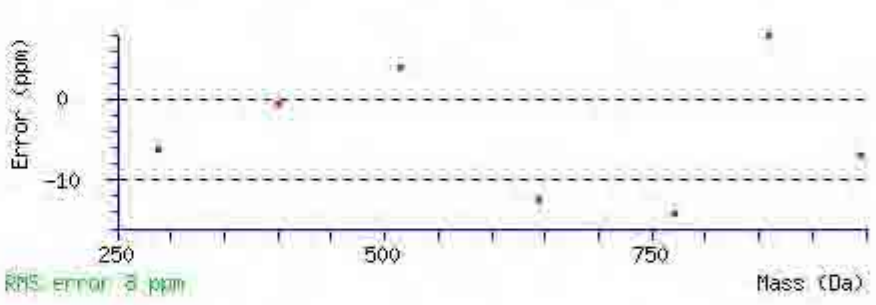
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1091.597488
Ions Score: 65 **Expect:** 4.1e-005
Matches : 7/80 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							9
2	235.107718	118.057497			217.097153	109.052214	S	*945.536371*	473.271824	928.509822	464.758549	927.525806	464.266541	8
3	322.139746	161.573511			304.129181	152.568229	S	*858.504343*	429.755810	841.477794	421.242535	840.493778	420.750527	7
4	450.198324	225.602800	433.171775	217.089526	432.187759	216.597518	Q	*771.472315*	386.239796	754.445766	377.726521	753.461750	377.234513	6
5	579.240917	290.124097	562.214368	281.610822	561.230352	281.118814	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	L	*514.371144*	257.689210	497.344595	249.175936			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	*401.287080*	201.147178	384.260531	192.633904			3
8	918.493109	459.750193	901.466560	451.236918	900.482544	450.744910	L	*288.203016*	144.605146	271.176467	136.091872			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FSSQELILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.2	1091.597488	-0.002680	FSSQELILR
19.1	1091.597488	-0.002680	FSLASADLLR
19.0	1091.597473	-0.002665	YSAKPEILR
9.1	1091.597504	-0.002696	FSTLDIQLR
8.7	1091.597473	-0.002665	AYSQSPAIKK
8.7	1091.597504	-0.002696	SFSQKGNLVL
8.5	1091.597519	-0.002711	VDSVLFGSLR
8.3	1091.586258	0.008550	ALPEALPPPAT
7.3	1091.597504	-0.002696	FKSTPDLLR
7.2	1091.597488	-0.002680	NLSTYLIPR

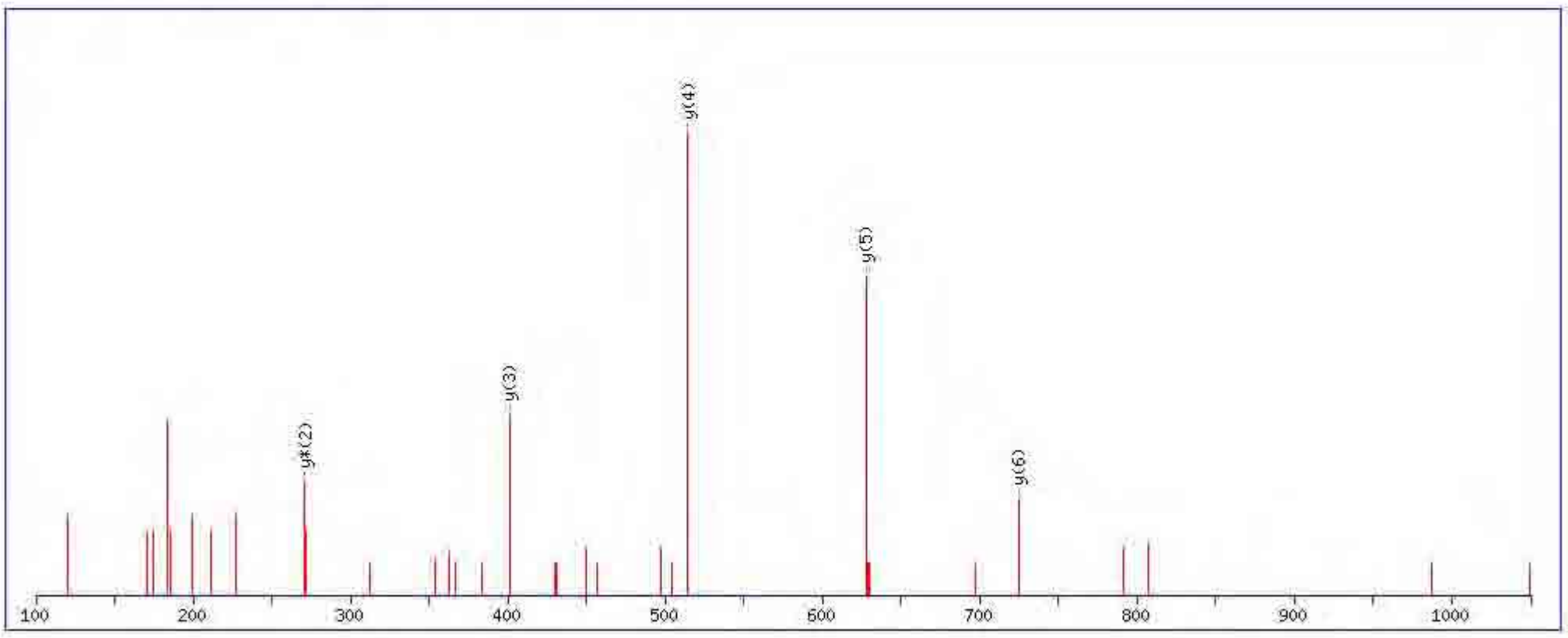
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPILLIR**
Found in **LYOX_HUMAN**, Protein-lysine 6-oxidase OS=Homo sapiens GN=LOX PE=1 SV=2

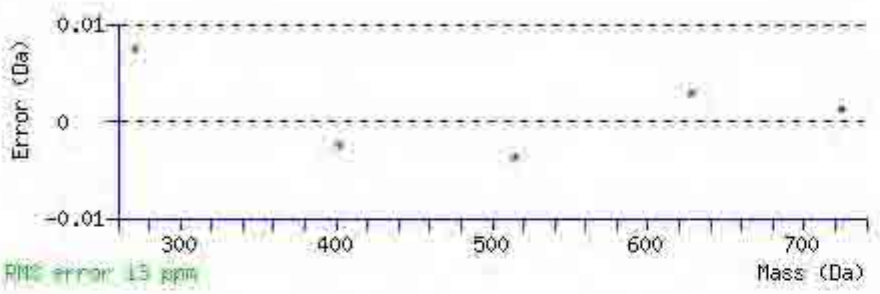
Match to Query 1329: 824.548368 from(413.281460,2+) rtinseconds(1603) index(11124)
Title: Locus:1.1.1.1879.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

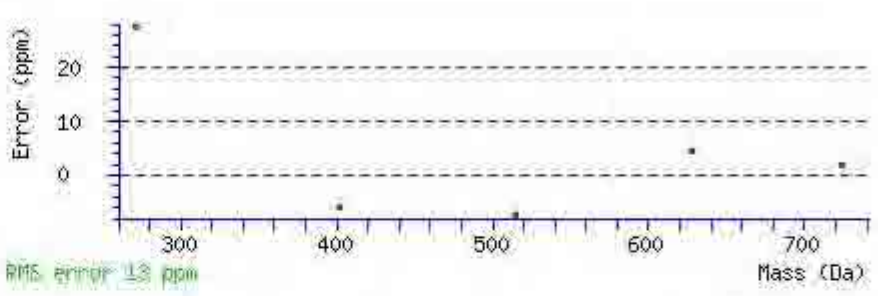
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 824.548355
Ions Score: 35 **Expect:** 0.0027
Matches : 5/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.054955	51.531116	84.044390	42.525833	T					7
2	199.107719	100.057497	181.097154	91.052215	P	*724.507972*	362.757624	707.481423	354.244350	6
3	312.191783	156.599529	294.181218	147.594247	I	*627.455208*	314.231242	610.428659	305.717968	5
4	425.275847	213.141561	407.265282	204.136279	L	*514.371144*	257.689210	497.344595	249.175936	4
5	538.359911	269.683594	520.349346	260.678311	L	*401.287080*	201.147178	384.260531	192.633904	3
6	651.443975	326.225626	633.433410	317.220343	I	288.203016	144.605146	271.176467	136.091872	2
7					R	175.118952	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of TPILLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	824.548355	0.000013	TPILLIR
19.9	824.548355	0.000013	PTLLLLR
19.9	824.548370	-0.000002	VVIILPR
18.9	824.548355	0.000013	TLPLIIR
7.2	824.548355	0.000013	LTPLLLR
7.2	824.548355	0.000013	PITLLLR
7.2	824.548370	-0.000002	VLVPLLR

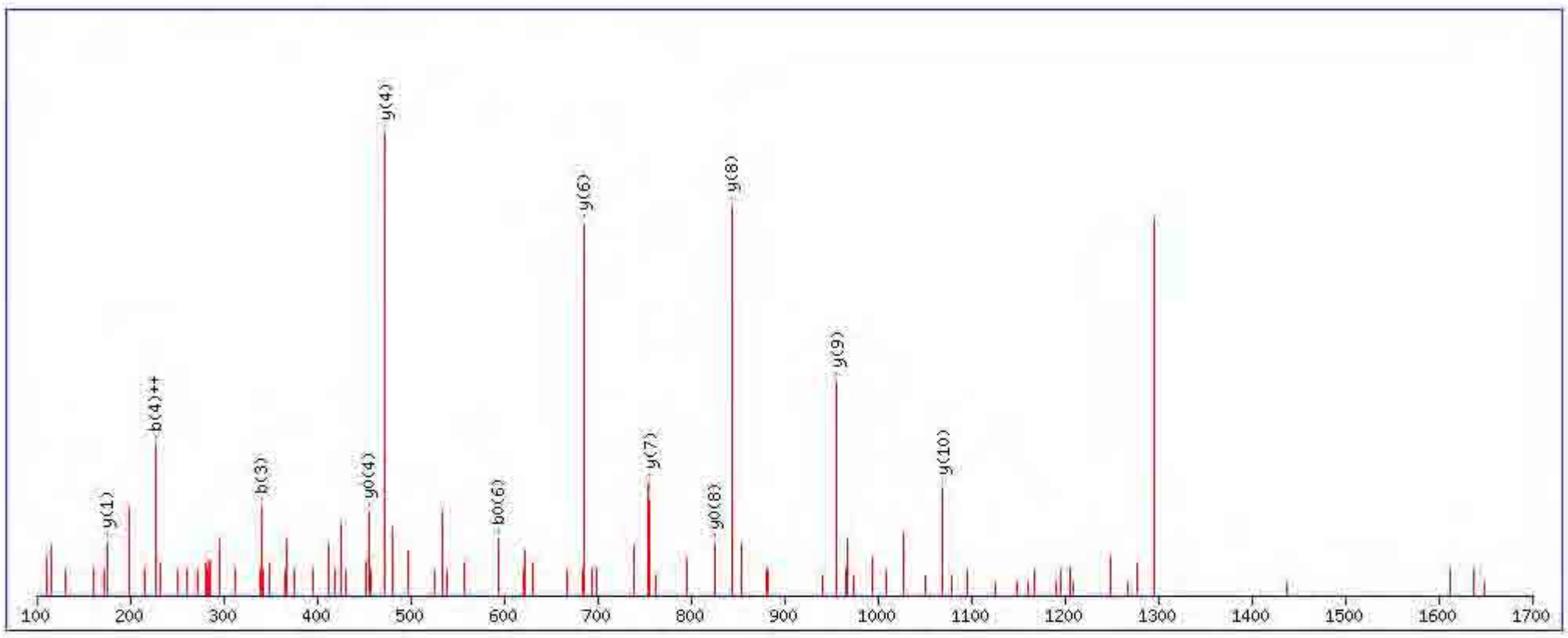
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIISAPDPSNR**
Found in **SRPX2_HUMAN**, Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRPX2 PE=1 SV=1

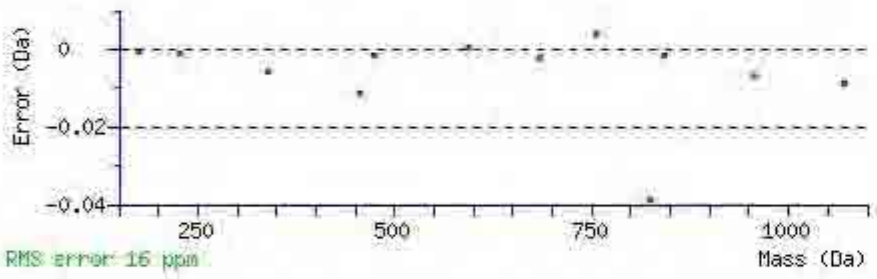
Match to Query 12119: 1294.727368 from(648.370960,2+) rtinseconds(1637) index(11556)
Title: Locus:1.1.1.1897.16
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

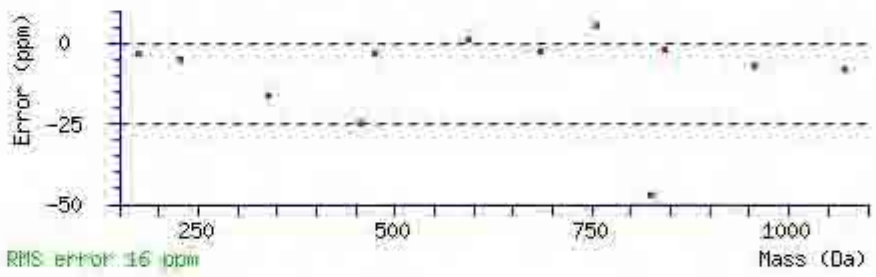
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1294.724472
Ions Score: 44 **Expect:** 0.0038
Matches : 13/100 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							12
2	227.175404	114.091340					L	1182.647712	591.827494	1165.621163	583.314220	1164.637147	582.822212	11
3	340.259468	170.633372					I	*1069.563648*	535.285462	1052.537099	526.772188	1051.553083	526.280180	10
4	453.343532	227.175404					I	*956.479584*	478.743430	939.453035	470.230156	938.469019	469.738148	9
5	540.375560	270.691418			522.364995	261.686136	S	*843.395520*	422.201398	826.368971	413.688124	825.384955	413.196116	8
6	611.412674	306.209975			593.402109	297.204693	A	*756.363492*	378.685384	739.336943	370.172110	738.352927	369.680102	7
7	708.465438	354.736357			690.454873	345.731075	P	*685.326378*	343.166827	668.299829	334.653553	667.315813	334.161545	6
8	823.492381	412.249829			805.481816	403.244546	D	588.273614	294.640445	571.247065	286.127171	570.263049	285.635163	5
9	920.545145	460.776211			902.534580	451.770928	P	*473.246671*	237.126973	456.220122	228.613699	455.236106	228.121691	4
10	1007.577173	504.292225			989.566608	495.286942	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
11	1121.620100	561.313688	1104.593551	552.800414	1103.609535	552.308406	N	289.161879	145.084577	272.135330	136.571303			2
12							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIISAPDPSNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	1294.724472	0.002896	LLIISAPDPSNR
27.5	1294.724503	0.002865	PPLLSPGLGLQR
11.2	1294.724503	0.002865	PLLLGPNTPVSR
10.4	1294.738388	-0.011020	IILPKEEEVLP
10.4	1294.735718	-0.008350	IIPPAAPLSGRR
9.8	1294.724487	0.002881	PILALSGGLGEPR
9.5	1294.735916	-0.008548	LLLLALSFCGFV
9.5	1294.735718	-0.008350	LPLLARPRGSPA
9.5	1294.724503	0.002865	PPPIARAVVPSK
9.1	1294.732529	-0.005161	ILLISFLWGAY

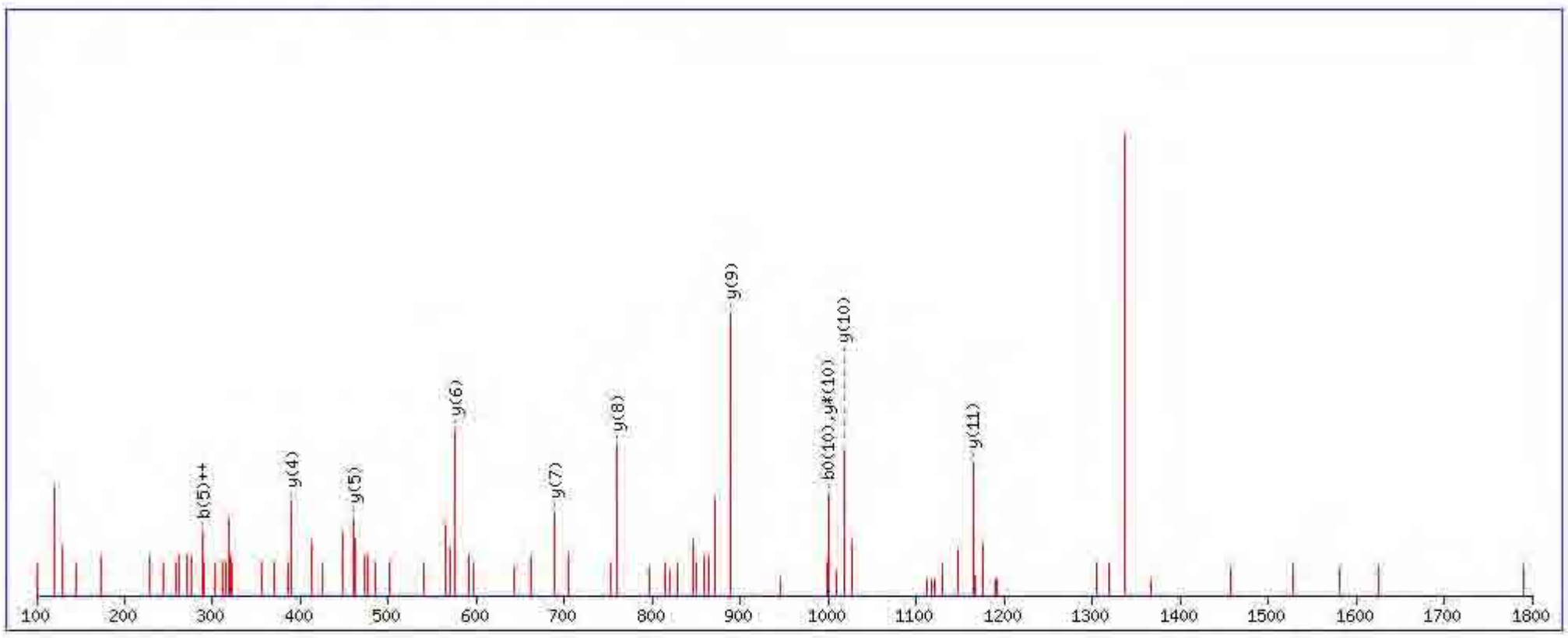
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAFQEALDAAGDK**
Found in **THIO_HUMAN**, Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

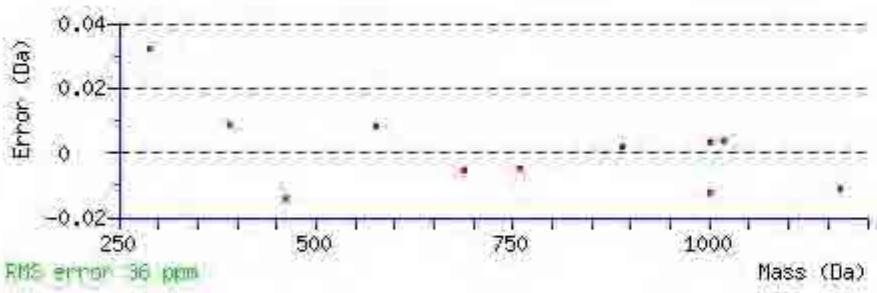
Match to Query 13034: 1335.634748 from(668.824650,2+) rtinseconds(1600) index(11091)
Title: Locus:1.1.1.1877.20
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

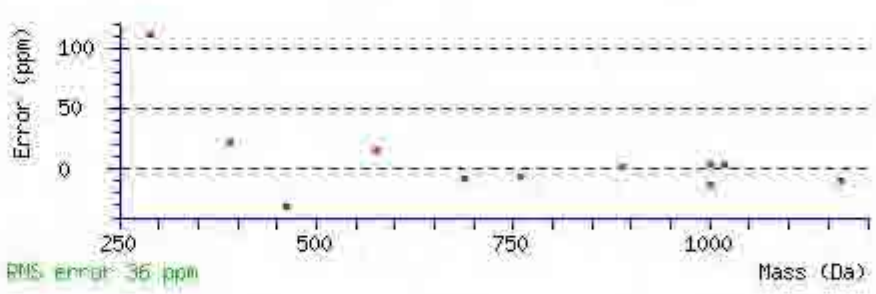
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1335.630646
Ions Score: 69 **Expect:** 5.4e-006
Matches : 11/136 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	1235.590259	618.298768	1218.563710	609.785493	1217.579694	609.293485	12
3	320.160483	160.583879			302.149918	151.578597	F	*1164.553145*	582.780211	1147.526596	574.266936	1146.542580	573.774928	11
4	448.219061	224.613168	431.192512	216.099894	430.208496	215.607886	Q	*1017.484731*	509.246004	1000.458182	500.732729	999.474166	500.240721	10
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	E	*889.426153*	445.216715	872.399604	436.703440	871.415588	436.211432	9
6	648.298768	324.653022	631.272219	316.139748	630.288203	315.647740	A	*760.383560*	380.695418	743.357011	372.182144	742.372995	371.690136	8
7	761.382832	381.195054	744.356283	372.681780	743.372267	372.189772	L	*689.346446*	345.176861	672.319897	336.663587	671.335881	336.171579	7
8	876.409775	438.708526	859.383226	430.195251	858.399210	429.703243	D	*576.262382*	288.634829	559.235833	280.121555	558.251817	279.629547	6
9	947.446889	474.227082	930.420340	465.713808	929.436324	465.221800	A	*461.235439*	231.121358	444.208890	222.608083	443.224874	222.116075	5
10	1018.484003	509.745639	1001.457454	501.232365	1000.473438	500.740357	A	*390.198325*	195.602801	373.171776	187.089526	372.187760	186.597518	4
11	1075.505467	538.256372	1058.478918	529.743097	1057.494902	529.251089	G	319.161211	160.084244	302.134662	151.570969	301.150646	151.078961	3
12	1190.532410	595.769843	1173.505861	587.256569	1172.521845	586.764561	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAFQEALDAAGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.6	1335.630646	0.004102	TAFQEALDAAGDK
11.6	1335.638031	-0.003283	FIDISPAEMANL
5.8	1335.645233	-0.010485	STMQELNSRLAS
4.0	1335.645264	-0.010516	MSTSQIPGRVASS
3.8	1335.635376	-0.000628	MGDKPPGFRGSR
3.8	1335.635376	-0.000628	MGDKPPGFRGSR
2.1	1335.634689	0.000059	KFASVPEPEFPG
0.8	1335.634018	0.000730	CLQSLEKSQDVS
0.2	1335.645905	-0.011157	HFYLSPLDNSK

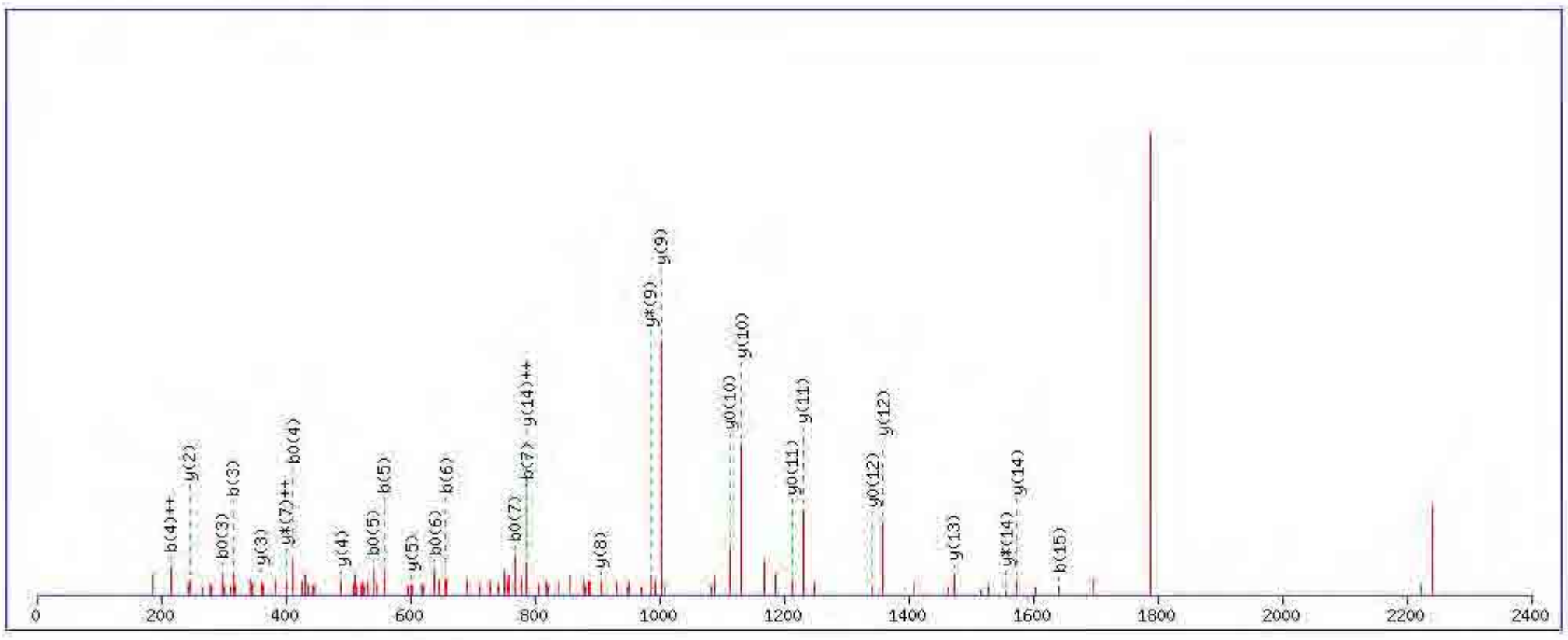
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TITLEVEPSDTIENVK**
Found in **RL40_HUMAN**, Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2

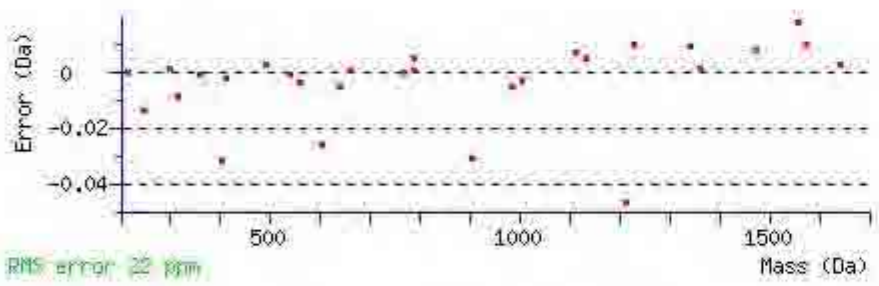
Match to Query 19201: 1786.925868 from(894.470210,2+) rtinseconds(1776) index(13369)
Title: Locus:1.1.1.1972.26
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling1_4.mgf

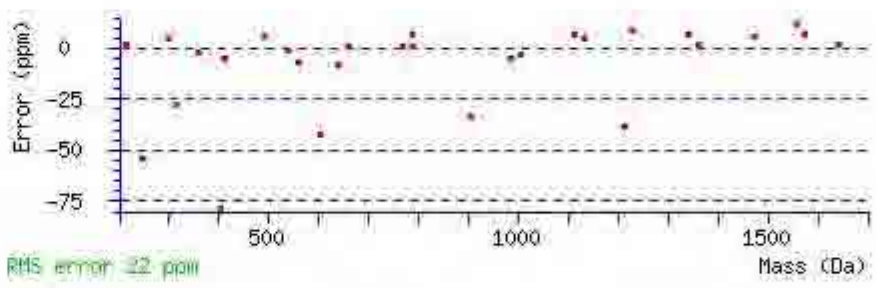
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1786.920013
Ions Score: 53 **Expect:** 9.5e-005
Matches : 30/148 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							16
2	215.139019	108.073147			197.128454	99.067865	I	1686.879623	843.943450	1669.853074	835.430175	1668.869058	834.938167	15
3	316.186698	158.596987			298.176133	149.591704	T	*1573.795559*	787.401418	1556.769010	778.888143	1555.784994	778.396135	14
4	429.270762	215.139019			411.260197	206.133737	L	*1472.747880*	736.877578	1455.721331	728.364304	1454.737315	727.872296	13
5	558.313355	279.660316			540.302790	270.655033	E	*1359.663816*	680.335546	1342.637267	671.822272	1341.653251	671.330264	12
6	657.381769	329.194523			639.371204	320.189240	V	*1230.621223*	615.814250	1213.594674	607.300975	1212.610658	606.808967	11
7	786.424362	393.715819			768.413797	384.710536	E	*1131.552809*	566.280043	1114.526260	557.766768	1113.542244	557.274760	10
8	883.477126	442.242201			865.466561	433.236919	P	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	9
9	970.509154	485.758215			952.498589	476.752932	S	*905.457452*	453.232364	888.430903	444.719090	887.446887	444.227082	8
10	1085.536097	543.271686			1067.525532	534.266404	D	818.425424	409.716350	801.398875	401.203076	800.414859	400.711068	7
11	1186.583776	593.795526			1168.573211	584.790243	T	703.398481	352.202879	686.371932	343.689604	685.387916	343.197596	6
12	1299.667840	650.337558			1281.657275	641.332275	I	*602.350802*	301.679039	585.324253	293.165765	584.340237	292.673757	5
13	1428.710433	714.858855			1410.699868	705.853572	E	*489.266738*	245.137007	472.240189	236.623733	471.256173	236.131725	4
14	1542.753360	771.880318	1525.726811	763.367044	1524.742795	762.875035	N	*360.224145*	180.615711	343.197596	172.102436			3
15	1641.821774	821.414525	1624.795225	812.901251	1623.811209	812.409243	V	*246.181218*	123.594247	229.154669	115.080973			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TITLEVEPSDTIENVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	1786.920013	0.005855	TITLEVEPSDTIENVK
9.2	1786.917511	0.008357	VIFSIPCEPNLDALIQ
7.8	1786.925415	0.000453	TVDELVRHFFPDVTI
7.2	1786.936142	-0.010274	TPPMPVMFIKAIPADK
7.2	1786.931229	-0.005361	SVELSEQSLQELQAVK
6.4	1786.932770	-0.006902	LAIFVPSYGCYAKPVK
6.0	1786.928726	-0.002858	SNNIMILVDLKNEVW
5.6	1786.910126	0.015742	PPAPAPPAPSAPAPGTLAK
4.8	1786.924713	0.001155	ADMIKEGAAVIDVGINR
3.4	1786.932098	-0.006230	LILALMLSMTGADSHAK

Sibling 2 – technical replicate # 1

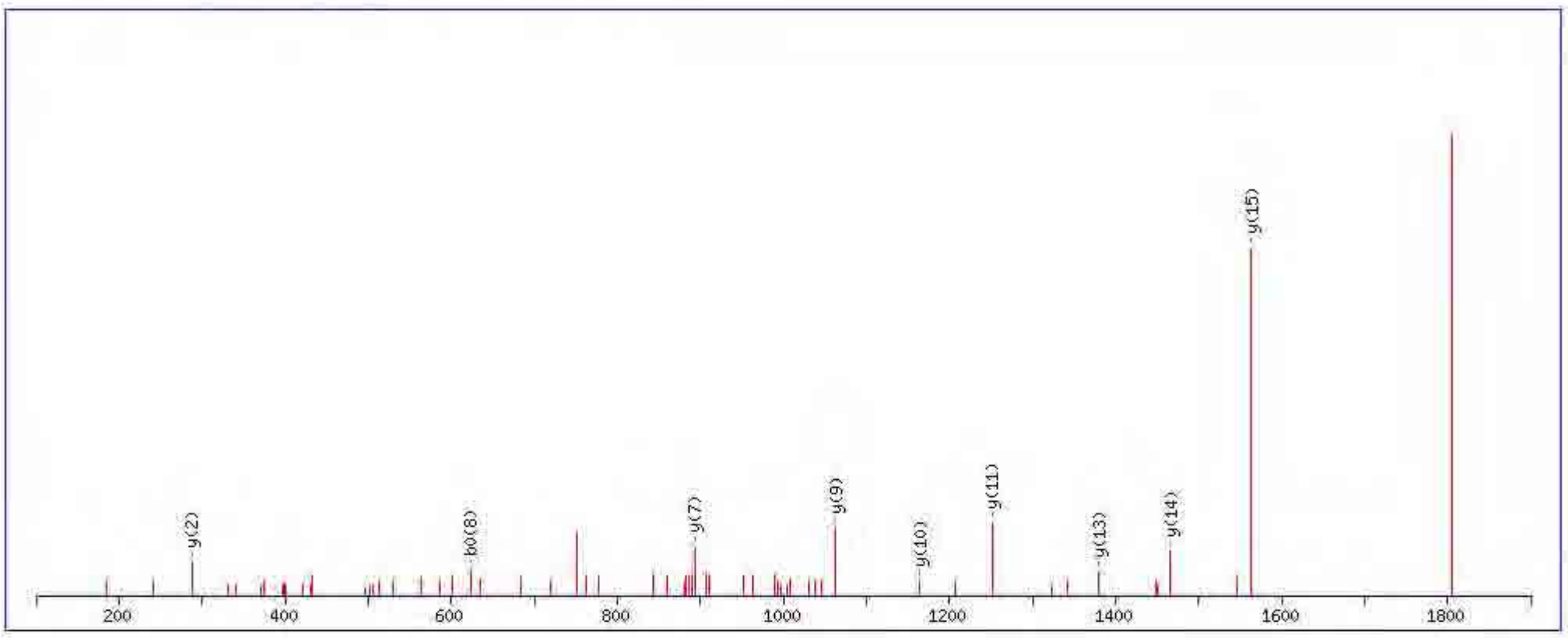
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAVPSGASTGIYEALELR**
Found in **ENOA_HUMAN**, Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2

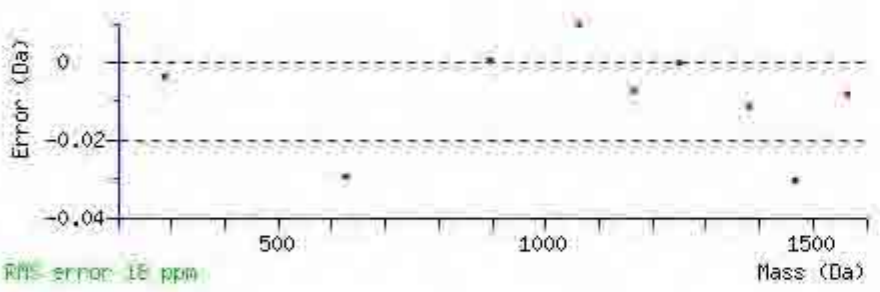
Match to Query 16558: 1803.950088 from(902.982320,2+) rtinseconds(2067) index(14663)
Title: Locus:1.1.1.1932.22
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

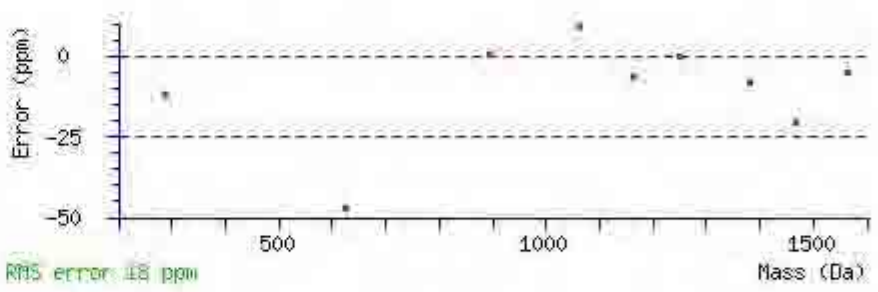
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1803.936646
Ions Score: 52 **Expect:** 3.5e-005
Matches : 9/158 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							18
2	143.081504	72.044390			A	1733.906842	867.457059	1716.880293	858.943785	1715.896277	858.451777	17
3	242.149918	121.578597			V	1662.869728	831.938502	1645.843179	823.425228	1644.859163	822.933220	16
4	339.202682	170.104979			P	*1563.801314*	782.404295	1546.774765	773.891021	1545.790749	773.399013	15
5	426.234710	213.620993	408.224145	204.615711	S	*1466.748550*	733.877913	1449.722001	725.364639	1448.737985	724.872631	14
6	483.256174	242.131725	465.245609	233.126443	G	*1379.716522*	690.361899	1362.689973	681.848625	1361.705957	681.356616	13
7	554.293288	277.650282	536.282723	268.645000	A	1322.695058	661.851167	1305.668509	653.337893	1304.684493	652.845885	12
8	641.325316	321.166296	*623.314751*	312.161014	S	*1251.657944*	626.332610	1234.631395	617.819336	1233.647379	617.327328	11
9	742.372995	371.690136	724.362430	362.684853	T	*1164.625916*	582.816596	1147.599367	574.303322	1146.615351	573.811314	10
10	799.394459	400.200868	781.383894	391.195585	G	*1063.578237*	532.292757	1046.551688	523.779482	1045.567672	523.287474	9
11	912.478523	456.742900	894.467958	447.737617	I	1006.556773	503.782025	989.530224	495.268750	988.546208	494.776742	8
12	1075.541852	538.274564	1057.531287	529.269282	Y	*893.472709*	447.239993	876.446160	438.726718	875.462144	438.234710	7
13	1204.584445	602.795861	1186.573880	593.790578	E	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	6
14	1275.621559	638.314418	1257.610994	629.309135	A	601.366787	301.187031	584.340238	292.673757	583.356222	292.181749	5
15	1388.705623	694.856450	1370.695058	685.851167	L	530.329673	265.668475	513.303124	257.155200	512.319108	256.663192	4
16	1517.748216	759.377746	1499.737651	750.372464	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
17	1630.832280	815.919778	1612.821715	806.914496	L	*288.203016*	144.605146	271.176467	136.091871			2
18					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AAVPSGASTGIYEALELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1803.936646	0.013442	AAVPSGASTGIYEALELR
4.6	1803.947922	0.002166	PSGLAGEPGKPGIPGLPGR
4.1	1803.951950	-0.001862	IQKLTGAPHTPVPAPDF
3.9	1803.941376	0.008712	RCLLPSHPDPGLAGSLR
3.1	1803.947891	0.002197	PQPAPGAAAASKPNSTVPK
2.8	1803.959122	-0.009034	QILAEQQLQQSHLPR
2.8	1803.961792	-0.011704	LKEELEGLNISVGIYQ
2.7	1803.944931	0.005157	IALKMVMMVGVNPAWL
2.7	1803.944931	0.005157	IALKMVMMVGVNPAWL
2.7	1803.944931	0.005157	IALKMVMMVGVNPAWL

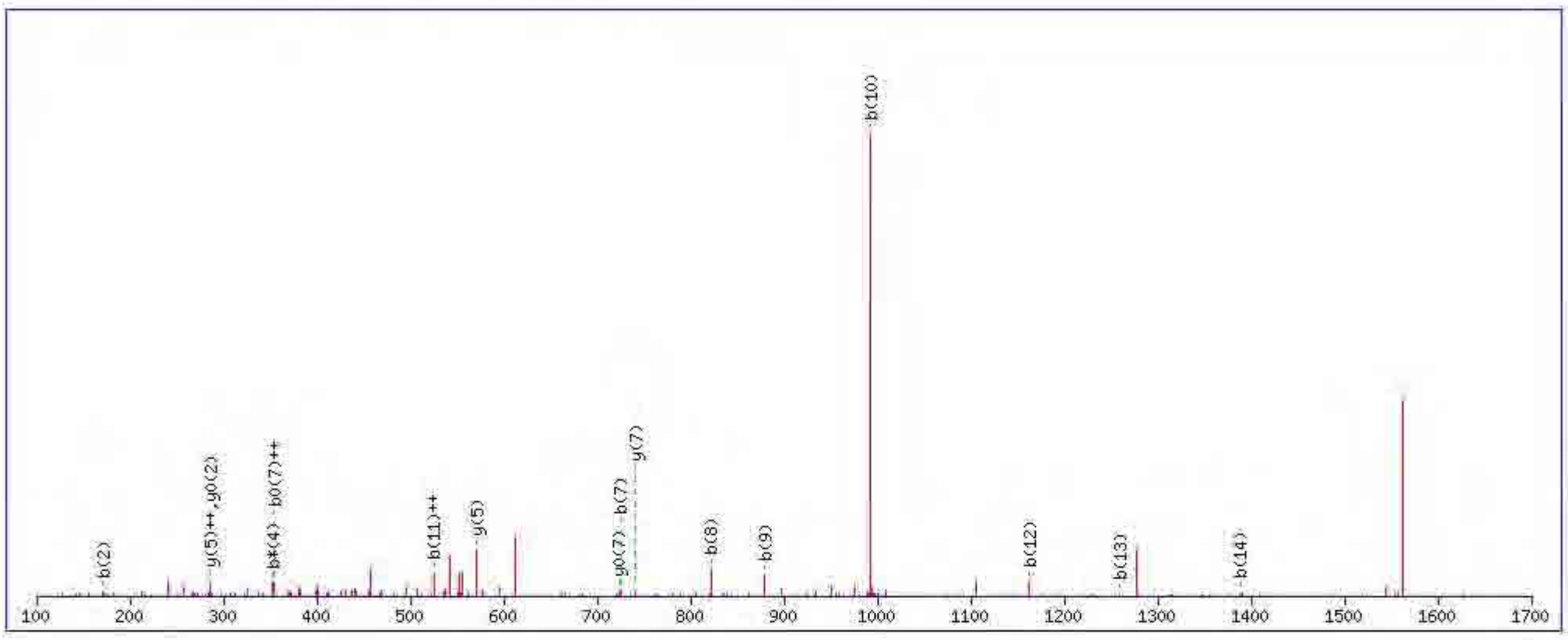
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVAQPLEPGPGPPER**
Found in **KCTD2_HUMAN**, BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens GN=KCTD2 PE=1 SV=3

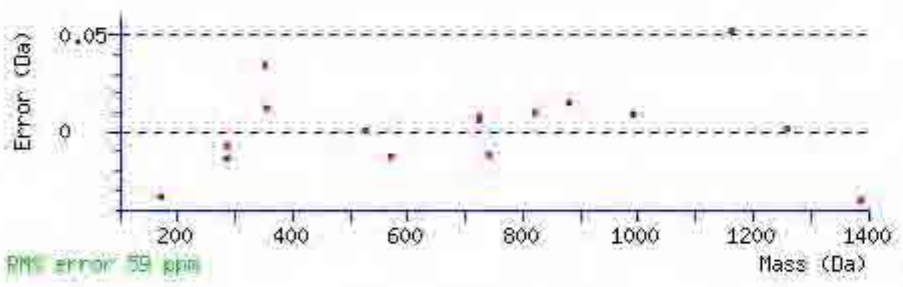
Match to Query 14053: 1561.788248 from(781.901400,2+) rtinseconds(1501) index(8416)
Title: Locus:1.1.1.1621.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

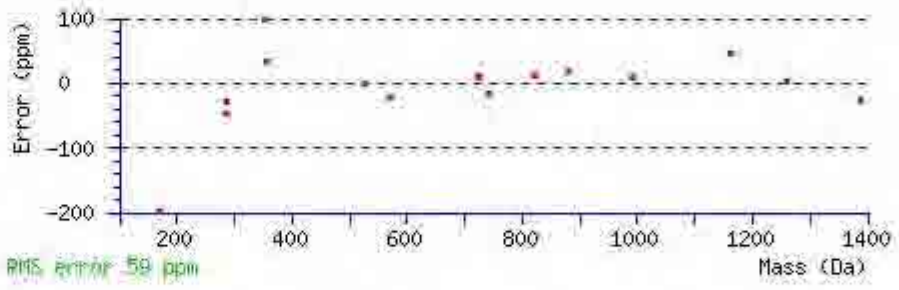
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1561.773636
Variable modifications:
P5 : Oxidation (P)
P10 : Oxidation (P)
P12 : Oxidation (P)
Ions Score: 45 **Expect:** 0.008
Matches : 16/148 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	*171.112804*	86.060040					V	1491.743801	746.375539	1474.717252	737.862264	1473.733236	737.370256	14
3	242.149918	121.578597					A	1392.675387	696.841332	1375.648838	688.328057	1374.664822	687.836049	13
4	370.208496	185.607886	353.181947	177.094612			Q	1321.638273	661.322775	1304.611724	652.809500	1303.627708	652.317492	12
5	483.256175	242.131726	466.229626	233.618451			P	1193.579695	597.293486	1176.553146	588.780211	1175.569130	588.288203	11
6	596.340239	298.673758	579.313690	290.160483			L	1080.532016	540.769646	1063.505467	532.256372	1062.521451	531.764363	10
7	*725.382832*	363.195054	708.356283	354.681780	707.372267	354.189772	E	967.447952	484.227614	950.421403	475.714339	949.437387	475.222332	9
8	*822.435596*	411.721436	805.409047	403.208162	804.425031	402.716154	P	838.405359	419.706318	821.378810	411.193043	820.394794	410.701035	8
9	*879.457060*	440.232168	862.430511	431.718894	861.446495	431.226886	G	741.352595	371.179936	724.326046	362.666661	723.342030	362.174653	7
10	*992.504739*	496.756008	975.478190	488.242733	974.494174	487.750725	P	684.331131	342.669203	667.304582	334.155929	666.320566	333.663921	6
11	1049.526203	525.266740	1032.499654	516.753465	1031.515638	516.261457	G	571.283452	286.145364	554.256903	277.632089	553.272887	277.140081	5
12	*1162.573882*	581.790579	1145.547333	573.277305	1144.563317	572.785297	P	514.261988	257.634632	497.235439	249.121357	496.251423	248.629349	4
13	*1259.626646*	630.316961	1242.600097	621.803687	1241.616081	621.311679	P	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
14	*1388.669239*	694.838258	1371.642690	686.324983	1370.658674	685.832975	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AVAQPLEPGPGPPER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1561.773636	0.014612	AVAQPLEPGPGPPER
34.3	1561.773636	0.014612	AVAQPLEPGPGPPER
32.7	1561.773636	0.014612	AVAQPLEPGPGPPER
29.2	1561.798782	-0.010534	ATLPDTAAPPGLPPAAA
24.0	1561.773636	0.014612	AVAQPLEPGPGPPER
23.6	1561.773636	0.014612	AVAQPLEPGPGPPER
17.7	1561.798782	-0.010534	ATLPDTAAPPGLPPAAA
17.7	1561.798782	-0.010534	ATLPDTAAPPGLPPAAA
17.2	1561.784882	0.003366	SLEQLRGPHGVSPGP
16.7	1561.784897	0.003351	KGLNGPTGPPGPPGPR

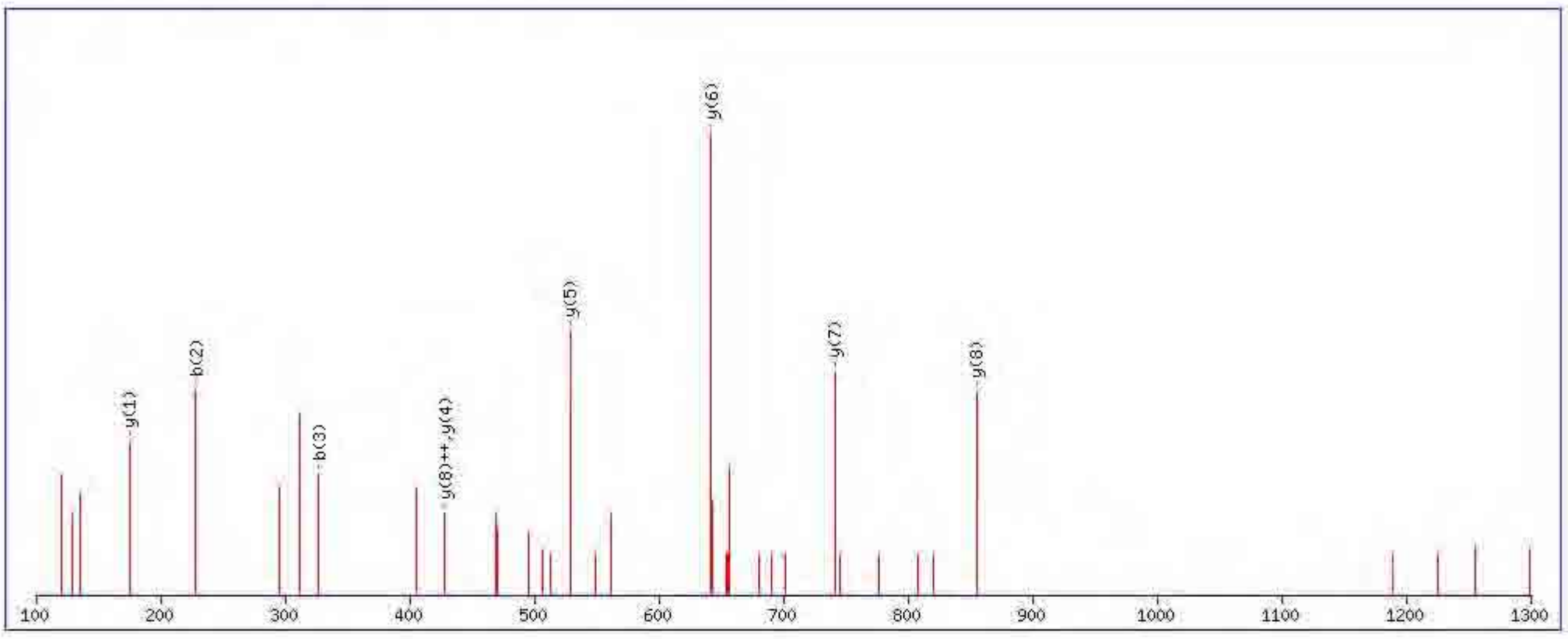
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNVITVGPR**
Found in **CATA_HUMAN**, Catalase OS=Homo sapiens GN=CAT PE=1 SV=3

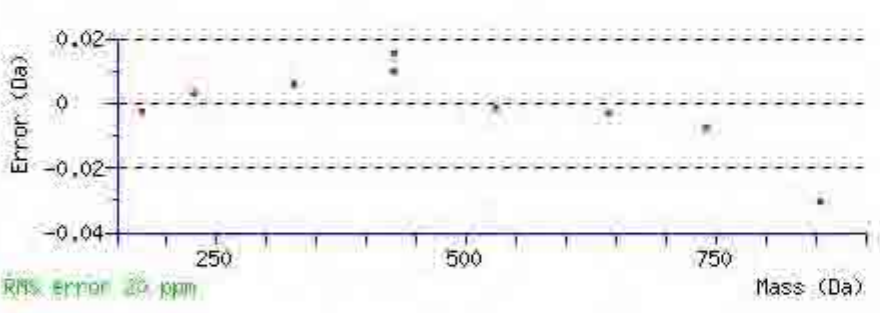
Match to Query 3768: 967.579288 from(484.796920,2+) rtinseconds(1324) index(6500)
Title: Locus:1.1.1.1524.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

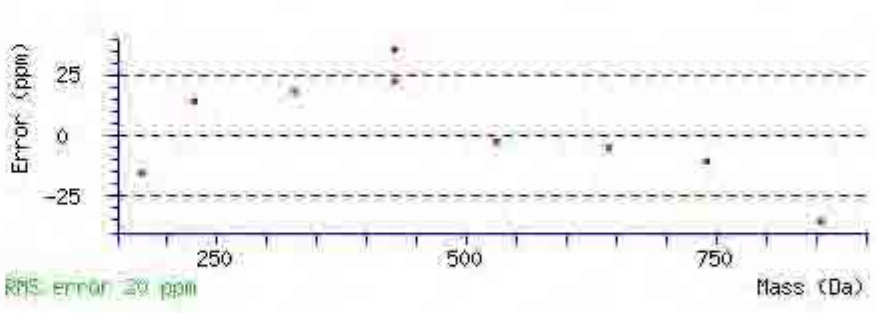
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 967.581467
Ions Score: 66 **Expect:** 1.7e-005
Matches : 9/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	228.134267	114.570771	211.107718	106.057497			N	855.504678	428.255977	838.478129	419.742703	837.494113	419.250695	8
3	327.202681	164.104978	310.176132	155.591704			V	741.461751	371.234514	724.435202	362.721239	723.451186	362.229231	7
4	440.286745	220.647010	423.260196	212.133736			I	642.393337	321.700307	625.366788	313.187032	624.382772	312.695024	6
5	541.334424	271.170850	524.307875	262.657576	523.323859	262.165568	T	529.309273	265.158275	512.282724	256.645000	511.298708	256.152992	5
6	640.402838	320.705057	623.376289	312.191782	622.392273	311.699774	V	428.261594	214.634435	411.235045	206.121161			4
7	697.424302	349.215789	680.397753	340.702515	679.413737	340.210507	G	329.193180	165.100228	312.166631	156.586954			3
8	794.477066	397.742171	777.450517	389.228897	776.466501	388.736889	P	272.171716	136.589496	255.145167	128.076222			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LNVITVGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	967.581467	-0.002179	LNVITVGPR
16.9	967.581451	-0.002163	LNVAIVRPS
16.9	967.570221	0.009067	LNVVLEGPK
16.5	967.581467	-0.002179	VQVSPLGIR
16.2	967.581467	-0.002179	RAVTPVPTK
15.8	967.581482	-0.002194	KVVLGGPGGGK
13.2	967.581451	-0.002163	LPKTKPPR
12.6	967.581436	-0.002148	LALAAGPALR
12.1	967.570206	0.009082	PNSIIPALK
11.8	967.581467	-0.002179	LRGLPGQLV

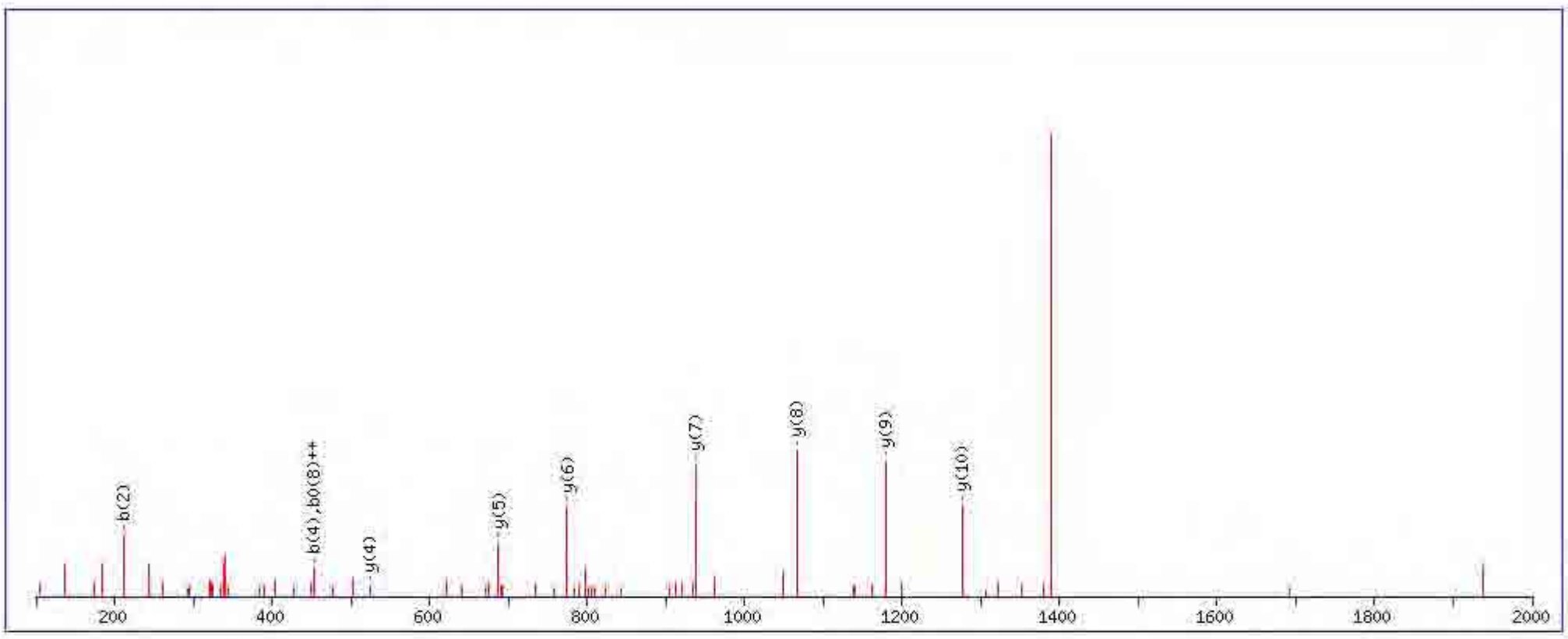
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

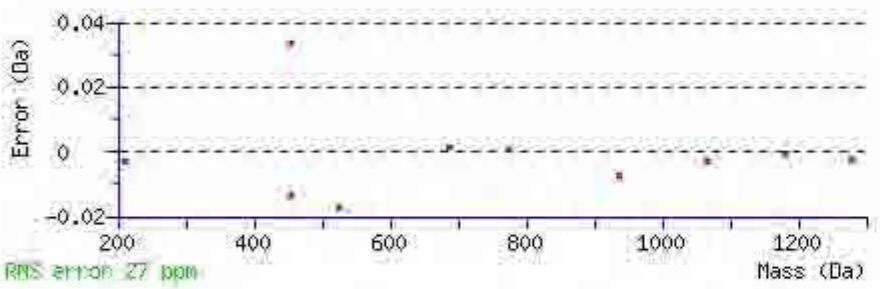
Match to Query 11800: 1388.672748 from(695.343650,2+) rtinseconds(1599) index(9401)
Title: Locus:1.1.1.1674.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

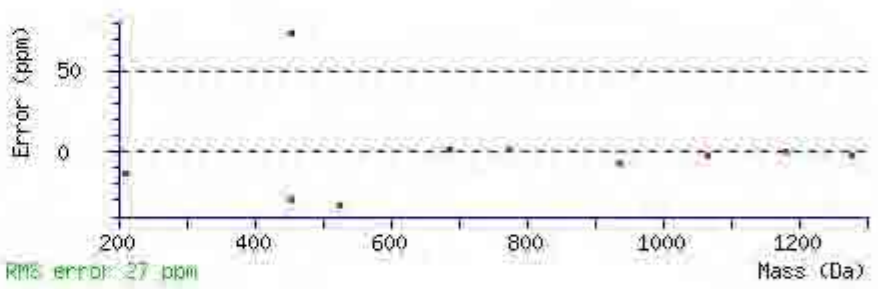
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 55 **Expect:** 0.00078
Matches : 10/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	1276.584445	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	1179.531681	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	1066.447617	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	937.405024	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	774.341695	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	687.309667	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	524.246338	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.8	1388.661194	0.011554	LPLEYSYGEYR
27.6	1388.667114	0.005634	PPPELTDTATSTK
20.1	1388.667953	0.004795	IPELLASGMVDNM
16.6	1388.667114	0.005634	PPPELTDTATSTK
13.0	1388.682373	-0.009625	PPEPQPPVTPDAL
11.9	1388.667114	0.005634	PPPELTDTATSTK
11.3	1388.671082	0.001666	IPELEEAELFAE
9.9	1388.685730	-0.012982	PPPLLLGSASDMK
9.1	1388.675812	-0.003064	QKMPAFLHEEK
7.5	1388.679703	-0.006955	LPGQGVHSQGQGPGA

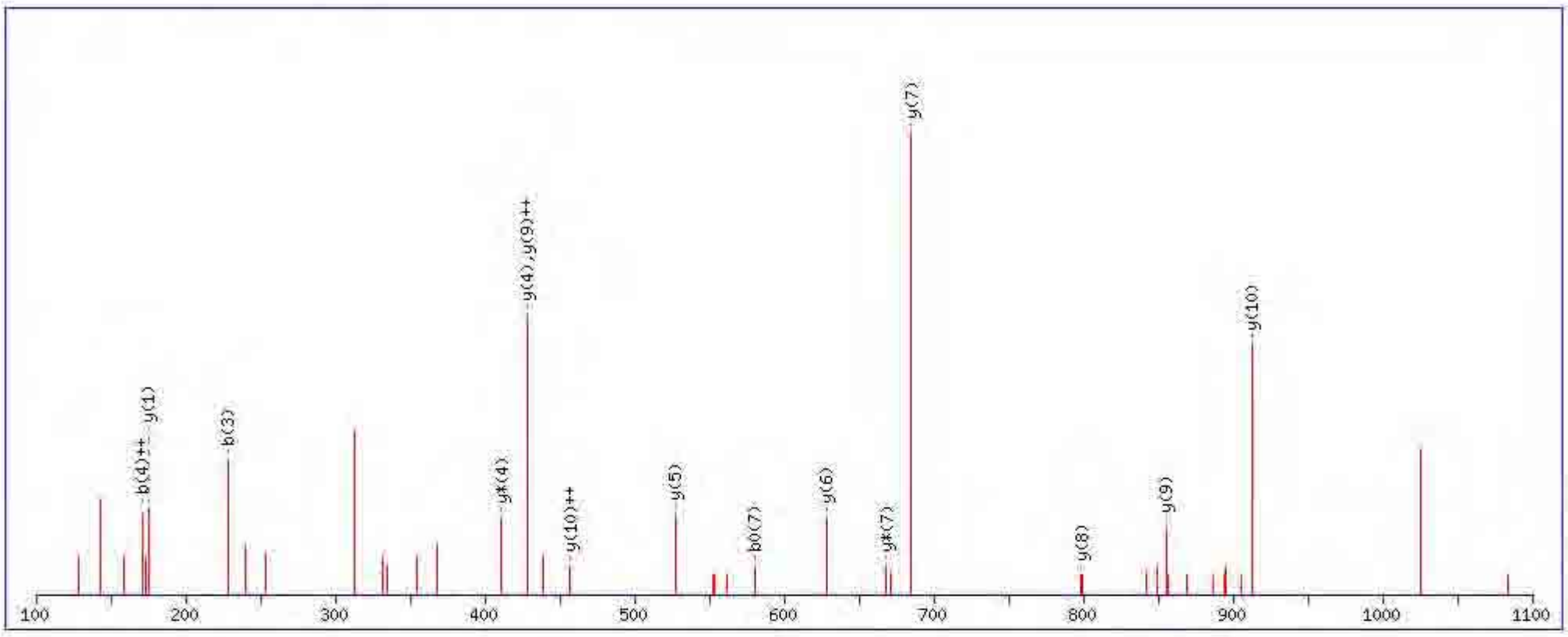
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

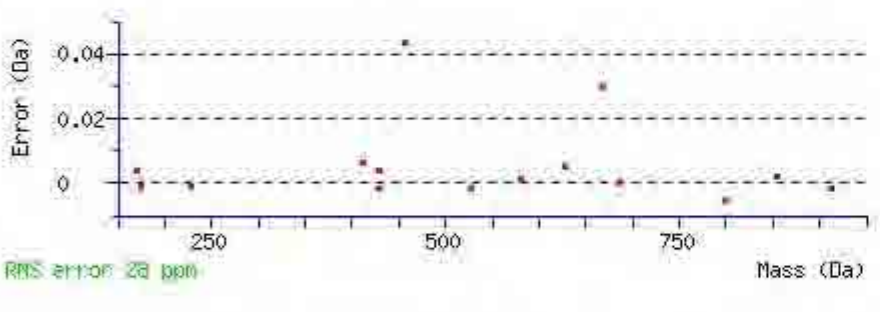
Match to Query 4709: 1024.595368 from(513.304960,2+) rtinseconds(1278) index(6022)
Title: Locus:1.1.1.1498.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

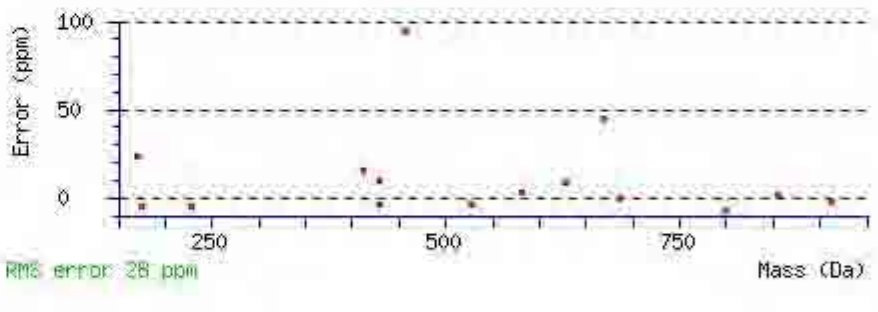
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 55 **Expect:** 0.00022
Matches : 16/80 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	912.526143	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	228.134268	114.570772			G	855.504679	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	341.218332	171.112804			I	798.483215	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	685.399151	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	628.377687	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	527.330008	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	428.261594	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	232.140416	116.573846	215.113867	108.060572			2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.9	1024.602951	-0.007583	IGGIGTVPVGR
29.9	1024.591690	0.003678	LGGPSALPKGL
14.8	1024.591690	0.003678	LGGINNILVP
13.7	1024.602905	-0.007537	PGAVAAAAILR
11.9	1024.591675	0.003693	LINSQPLPK
11.9	1024.591675	0.003693	LINSQPLPK
11.4	1024.585144	0.010224	LLNHMRLL
11.4	1024.602905	-0.007537	PLNANVLLR
10.9	1024.602921	-0.007553	IVQGPREVK
10.5	1024.595703	-0.000335	ILGGLVYYK

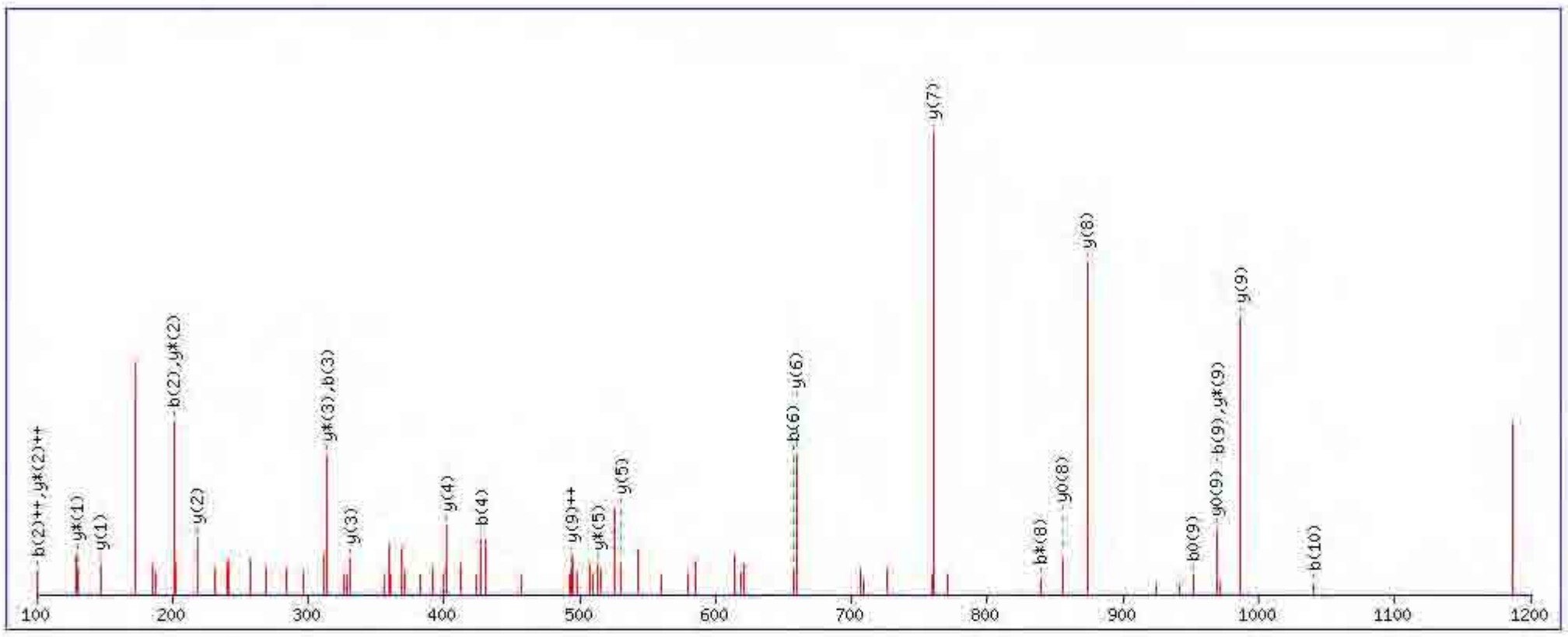
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILLTEQALAK**
Found in **LACRT_HUMAN**, Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1

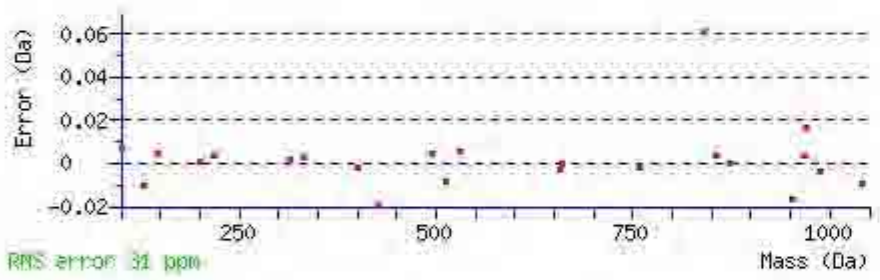
Match to Query 8213: 1185.700788 from(593.857670,2+) rtinseconds(1589) index(9321)
Title: Locus:1.1.1.1669.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

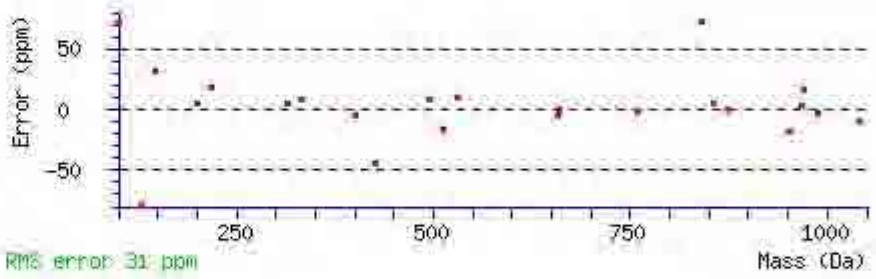
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1185.696854
Ions Score: 53 **Expect:** 0.00023
Matches : 27/98 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	201.123368	101.065322			183.112803	92.060039	I	1099.672138	550.339707	1082.645589	541.826433	1081.661573	541.334425	10
3	314.207432	157.607354			296.196867	148.602071	L	986.588074	493.797675	969.561525	485.284401	968.577509	484.792393	9
4	427.291496	214.149386			409.280931	205.144104	L	873.504010	437.255643	856.477461	428.742369	855.493445	428.250361	8
5	528.339175	264.673226			510.328610	255.667943	T	760.419946	380.713611	743.393397	372.200337	742.409381	371.708329	7
6	657.381768	329.194522			639.371203	320.189240	E	659.372267	330.189772	642.345718	321.676497	641.361702	321.184489	6
7	785.440346	393.223811	768.413797	384.710537	767.429781	384.218529	Q	530.329674	265.668475	513.303125	257.155201			5
8	856.477460	428.742368	839.450911	420.229094	838.466895	419.737086	A	402.271096	201.639186	385.244547	193.125912			4
9	969.561524	485.284400	952.534975	476.771126	951.550959	476.279118	L	331.233982	166.120629	314.207433	157.607355			3
10	1040.598638	520.802957	1023.572089	512.289683	1022.588073	511.797675	A	218.149918	109.578597	201.123369	101.065323			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SILLTEQALAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	1185.696854	0.003934	SILLTEQALAK
23.6	1185.698212	0.002576	LSILTPRHHL
18.9	1185.708084	-0.007296	ISLLNLTERK
18.9	1185.712128	-0.011340	PSLIFKQLPK
18.9	1185.708099	-0.007311	SIIPRGSLSLK
18.9	1185.696854	0.003934	SILILQEKDK
18.8	1185.696869	0.003919	TVLTELQAKIA
18.4	1185.696869	0.003919	EAIKLETGVVK
17.2	1185.708084	-0.007296	ISASALLKQQK
15.3	1185.696899	0.003889	TVLKDEGVVVK

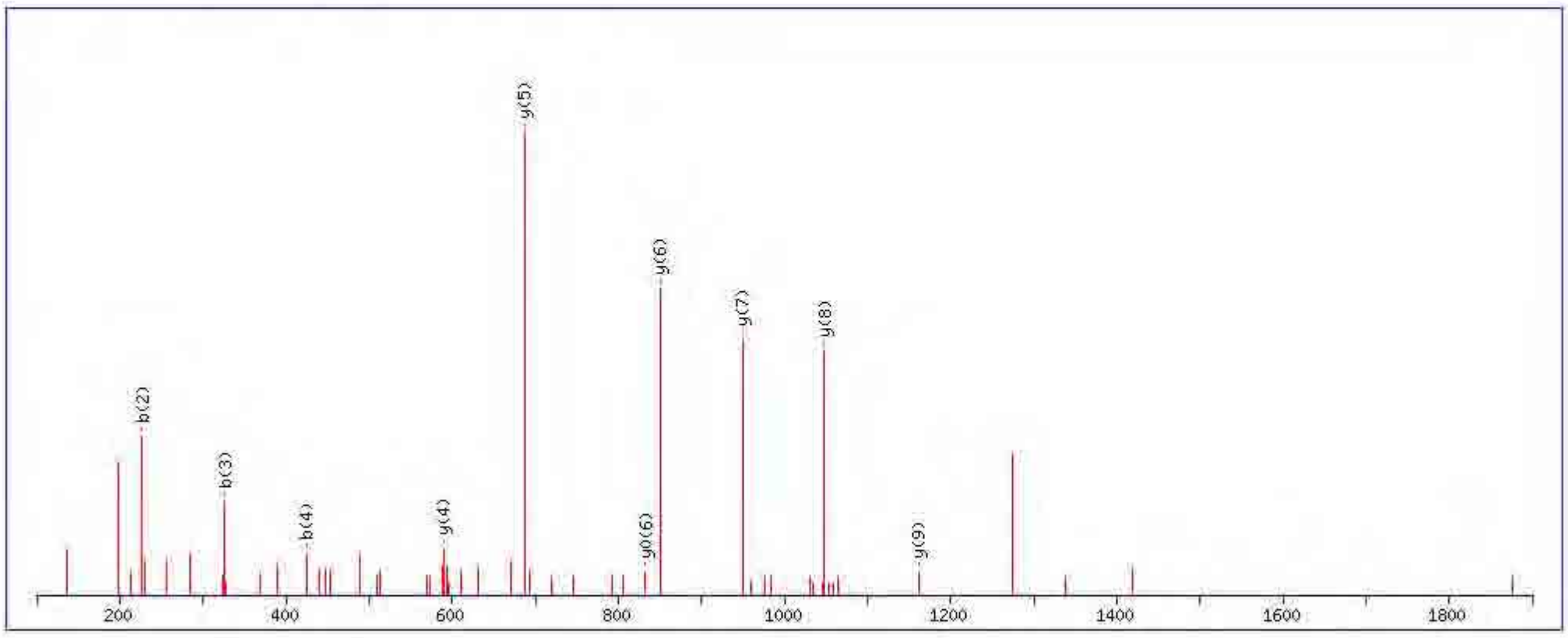
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLVVYPWTQR**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

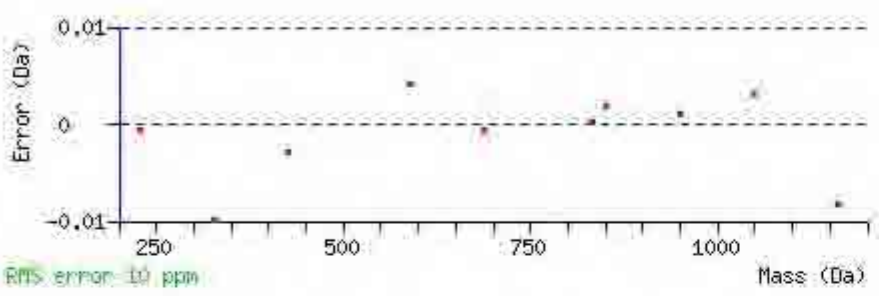
Match to Query 9962: 1273.724188 from(637.869370,2+) rtinseconds(2013) index(13932)
Title: Locus:1.1.1.1903.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

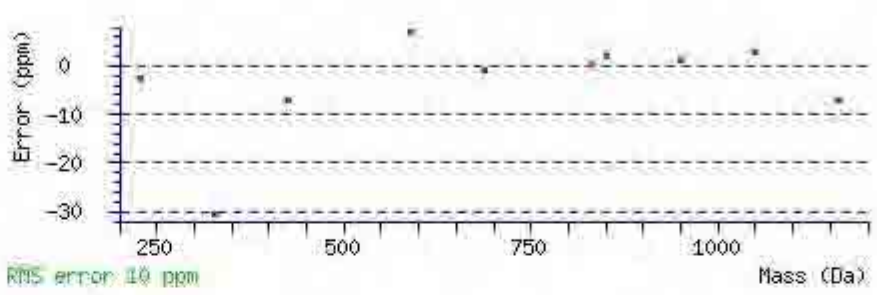
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1273.718292
Ions Score: 56 **Expect:** 0.00016
Matches : 10/74 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					L	*1161.641507*	581.324392	1144.614958	572.811117	1143.630942	572.319109	9
3	326.243818	163.625547					V	*1048.557443*	524.782360	1031.530894	516.269085	1030.546878	515.777077	8
4	425.312232	213.159754					V	*949.489029*	475.248153	932.462480	466.734878	931.478464	466.242870	7
5	588.375561	294.691419					Y	*850.420615*	425.713946	833.394066	417.200671	832.410050	416.708663	6
6	685.428325	343.217801					P	*687.357286*	344.182281	670.330737	335.669007	669.346721	335.176999	5
7	871.507638	436.257457					W	*590.304522*	295.655899	573.277973	287.142625	572.293957	286.650617	4
8	972.555317	486.781297			954.544752	477.776014	T	404.225209	202.616243	387.198660	194.102968	386.214644	193.610960	3
9	1100.613895	550.810586	1083.587346	542.297311	1082.603330	541.805303	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLVVYPWTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.3	1273.718292	0.005896	LLVVYPWTQR
14.8	1273.731537	-0.007349	ILESMVKPLTK
13.7	1273.728195	-0.004007	LIVTQTPPYVK
11.9	1273.716949	0.007239	IIVELVEFISP
11.9	1273.728195	-0.004007	LIVTQTPPYVK
10.1	1273.728180	-0.003992	ILVQYGADLLAV
10.1	1273.714249	0.009939	LLVESHHLQAK
9.8	1273.731567	-0.007379	ILVTLGILSVCSG
8.0	1273.714264	0.009924	SRHLLDQVIPP
6.7	1273.714264	0.009924	IPAQLPHPLTR

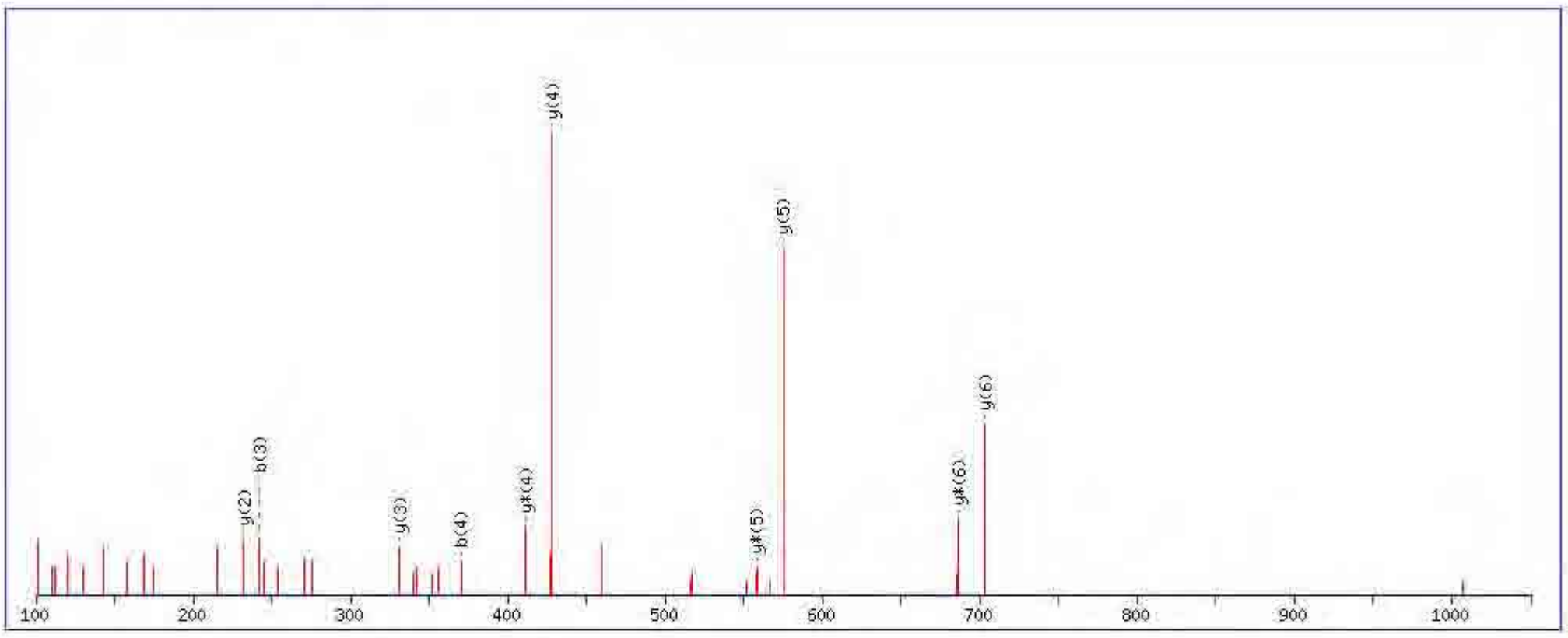
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

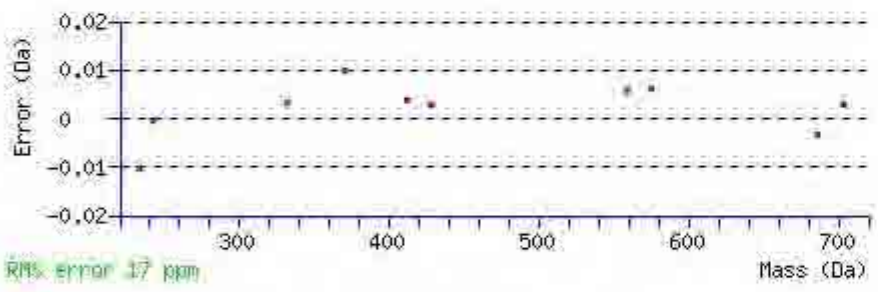
Match to Query 3405: 943.525428 from(472.769990,2+) rtinseconds(1475) index(8185)
Title: Locus:1.1.1.1607.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

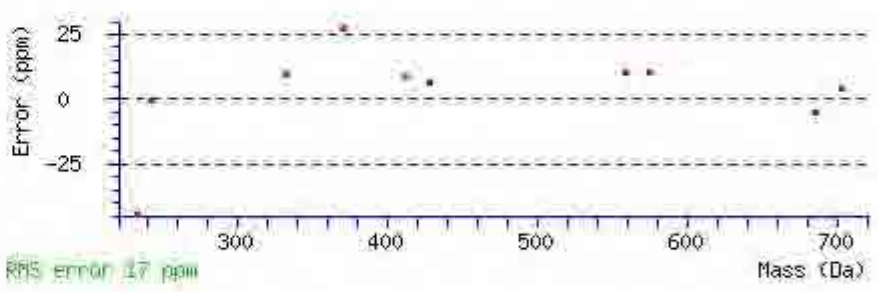
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Ions Score: 42 **Expect:** 0.0085
Matches : 10/58 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	873.494114	437.250695	856.467565	428.737421	8
3	**242.149918**	121.578597			L	816.472650	408.739963	799.446101	400.226689	7
4	**370.208496**	185.607886	353.181947	177.094612	Q	*703.388586*	352.197931	686.362037	343.684657	6
5	517.276910	259.142093	500.250361	250.628819	F	*575.330008*	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	*428.261594*	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	*331.208830*	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	*232.140416*	116.573846	215.113867	108.060571	2
9					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	943.523956	0.001472	AGLQFPVGR
18.4	943.516068	0.009360	PSGKLMSPK
17.0	943.516068	0.009360	KLLQMQPA
13.9	943.533829	-0.008401	KIGEVSSPK
13.8	943.533813	-0.008385	KLGEEQLK
13.5	943.533813	-0.008385	LKQENLSL
13.3	943.527313	-0.001885	GLAKGMPVR
13.1	943.516068	0.009360	AAVQKAIPM
13.1	943.516068	0.009360	AAVQKAIPM
12.9	943.516068	0.009360	GSPQLAMLK

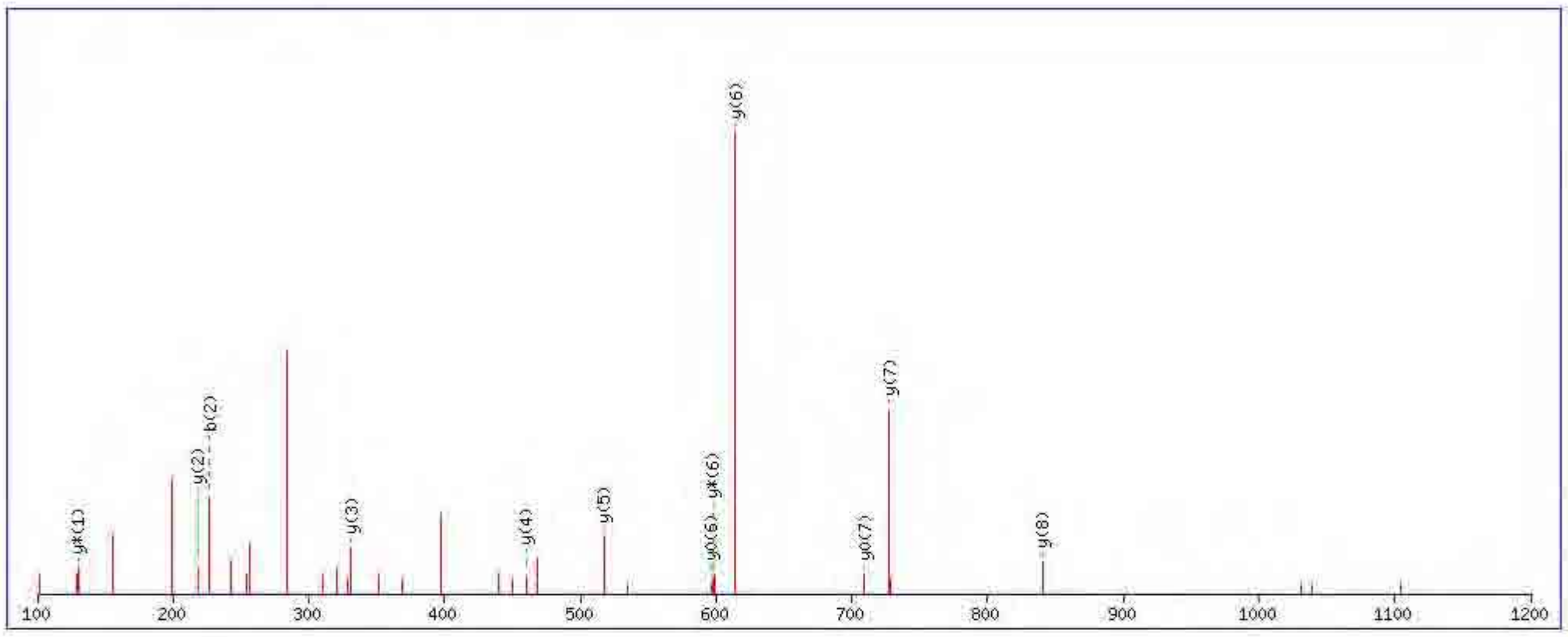
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLPGELAK**
Found in **H2B1A_HUMAN**, Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

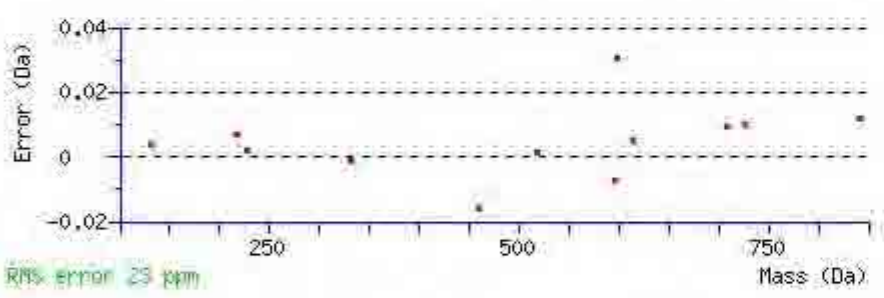
Match to Query 3555: 952.587768 from(477.301160,2+) rtinseconds(1634) index(9742)
Title: Locus:1.1.1.1694.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

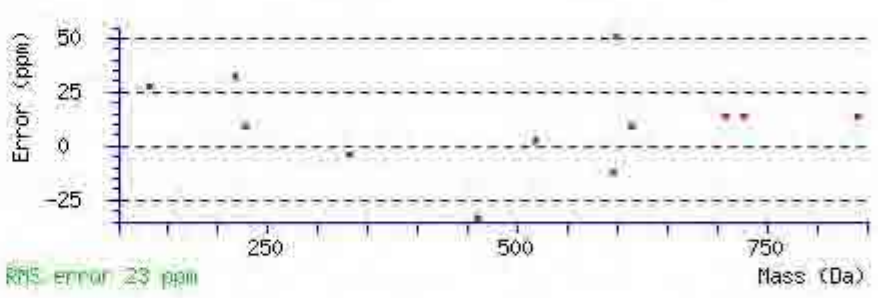
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 952.595688
Ions Score: 41 **Expect:** 0.0035
Matches : 12/64 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*840.518931*	420.763104	823.492382	412.249829	822.508366	411.757821	8
3	340.259468	170.633372			L	*727.434867*	364.221072	710.408318	355.707797	709.424302	355.215789	7
4	437.312232	219.159754			P	*614.350803*	307.679040	597.324254	299.165765	596.340238	298.673757	6
5	494.333696	247.670486			G	*517.298039*	259.152658	500.271490	250.639383	499.287474	250.147375	5
6	623.376289	312.191783	605.365724	303.186500	E	*460.276575*	230.641926	443.250026	222.128651	442.266010	221.636643	4
7	736.460353	368.733815	718.449788	359.728532	L	*331.233982*	166.120629	314.207433	157.607354			3
8	807.497467	404.252372	789.486902	395.247089	A	*218.149918*	109.578597	201.123369	101.065322			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLLPGELAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	952.595688	-0.007920	LLLPGELAK
27.0	952.595688	-0.007920	IIIPEIQK
27.0	952.595703	-0.007935	ILPPKSLGI
27.0	952.595688	-0.007920	LILPKPEK
27.0	952.581787	0.005981	LPLPVRSR
23.9	952.597031	-0.009263	LLIPRWR
20.4	952.595703	-0.007935	ILGILPPSK
19.1	952.581787	0.005981	LPPGLLRR
18.3	952.595688	-0.007920	ILLLEAGPK
18.3	952.595703	-0.007935	ILLILVANP

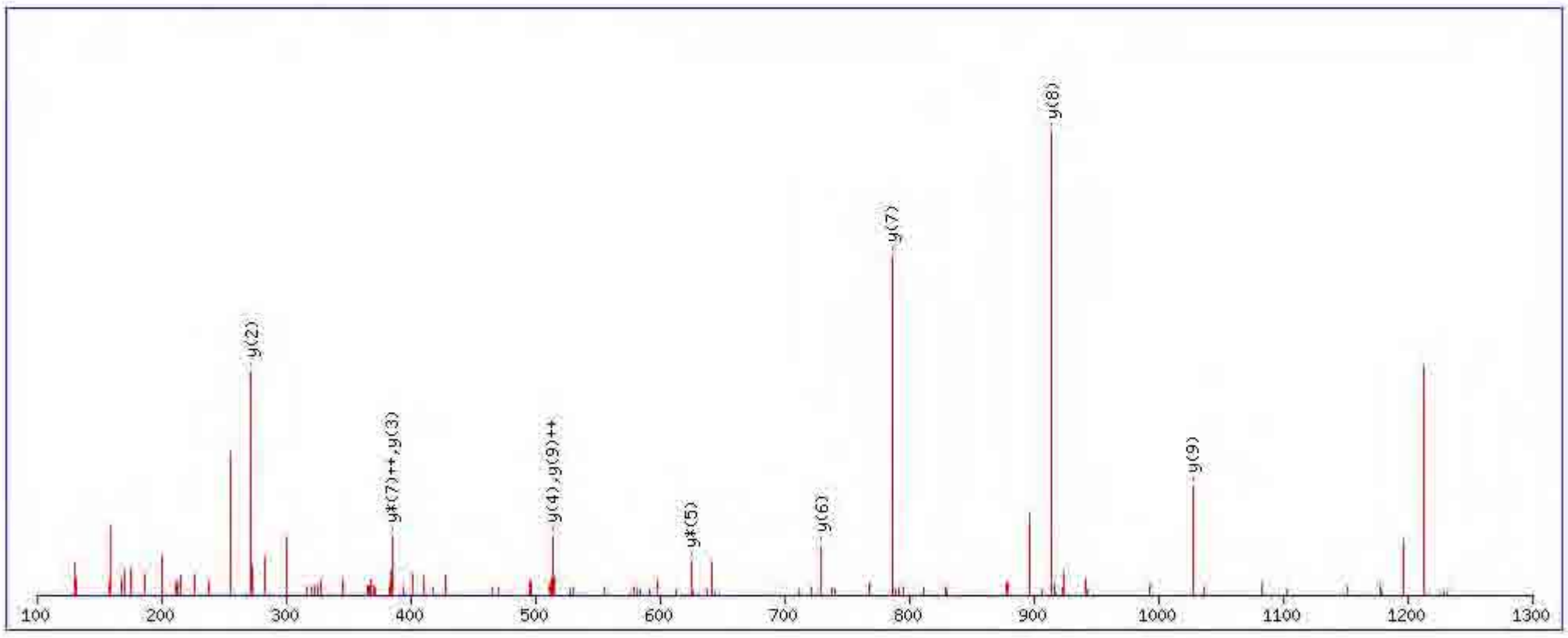
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

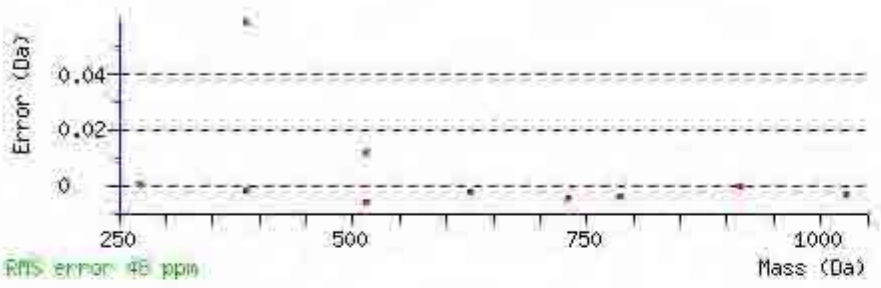
Match to Query 8840: 1212.630628 from(607.322590,2+) rtinseconds(1356) index(6861)
Title: Locus:1.1.1.1541.21
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

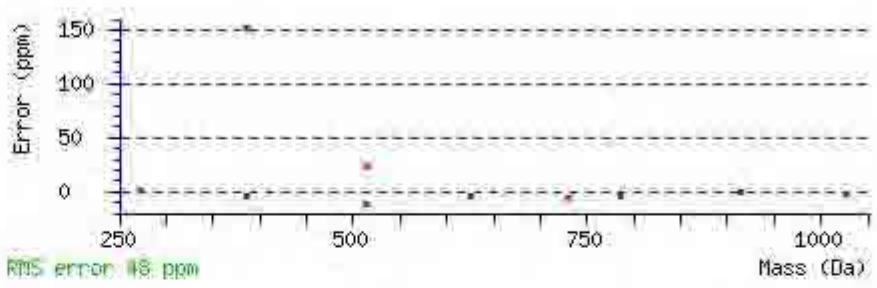
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1212.625107
Ions Score: 65 **Expect:** 3.6e-005
Matches : 10/90 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							10
2	300.170653	150.588965					L	*1027.553085*	514.280181	1010.526536	505.766906	1009.542520	505.274898	9
3	428.229231	214.618254	411.202682	206.104979			Q	*914.469021*	457.738148	897.442472	449.224874	896.458456	448.732866	8
4	485.250695	243.128986	468.224146	234.615711			G	*786.410443*	393.708860	769.383894	385.195585	768.399878	384.703577	7
5	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	S	*729.388979*	365.198128	712.362430	356.684853	711.378414	356.192845	6
6	700.341301	350.674289	683.314752	342.161014	682.330736	341.669006	Q	642.356951	321.682114	625.330402	313.168839	624.346386	312.676831	5
7	829.383894	415.195585	812.357345	406.682311	811.373329	406.190303	E	*514.298373*	257.652825	497.271824	249.139550	496.287808	248.647542	4
8	942.467958	471.737617	925.441409	463.224343	924.457393	462.732335	L	*385.255780*	193.131528	368.229231	184.618253			3
9	1039.520722	520.263999	1022.494173	511.750724	1021.510157	511.258716	P	*272.171716*	136.589496	255.145167	128.076221			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WLQGSQELPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.2	1212.625107	0.005521	WLQGSQELPR
17.0	1212.636353	-0.005725	GTIRYHTPPR
12.8	1212.635025	-0.004397	SALPTQKQVPP
12.3	1212.636353	-0.005725	DRFGPGAPKPR
12.0	1212.625107	0.005521	QWGSPEKLPR
11.7	1212.636337	-0.005709	DRWTAAGALPR
11.7	1212.623795	0.006833	ASPLPSGLLTPP
11.3	1212.636353	-0.005725	LWQGQQVQAR
11.1	1212.632507	-0.001879	MAPKPKPWVQ
11.0	1212.636353	-0.005725	DRFGPGAPKPR

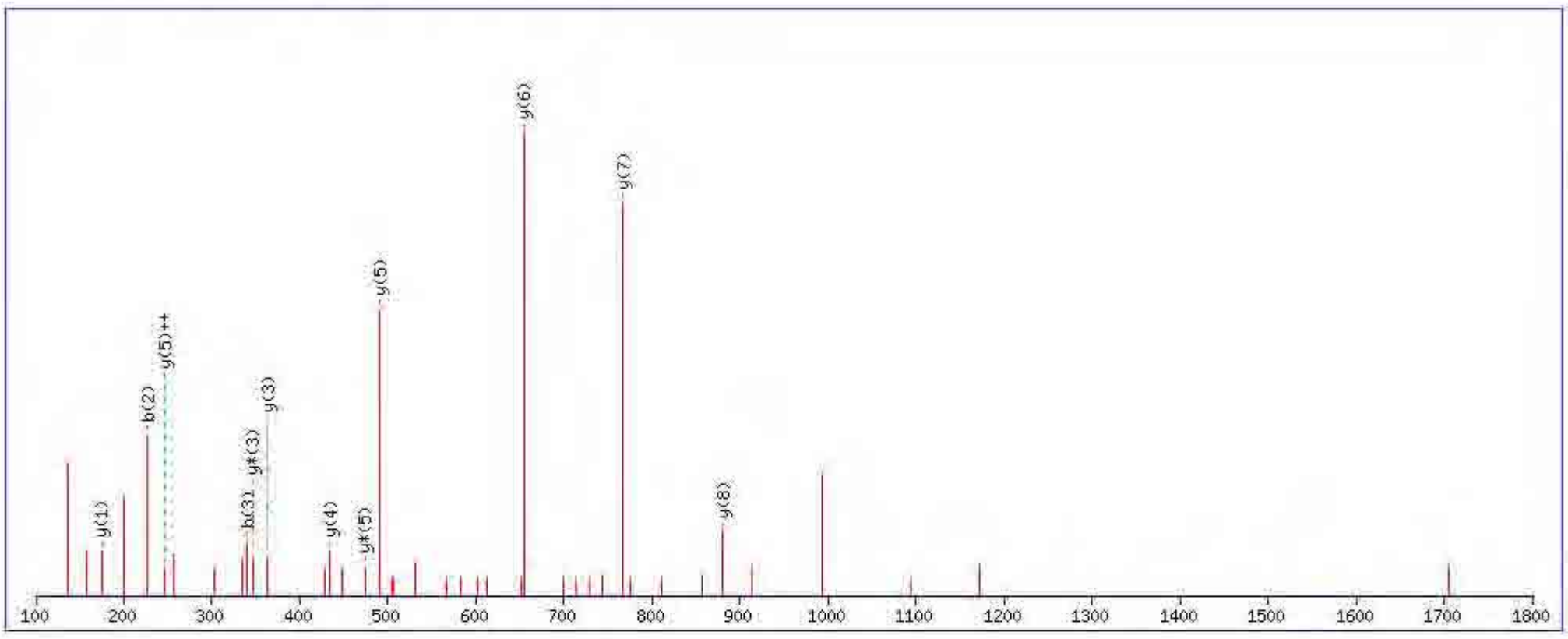
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

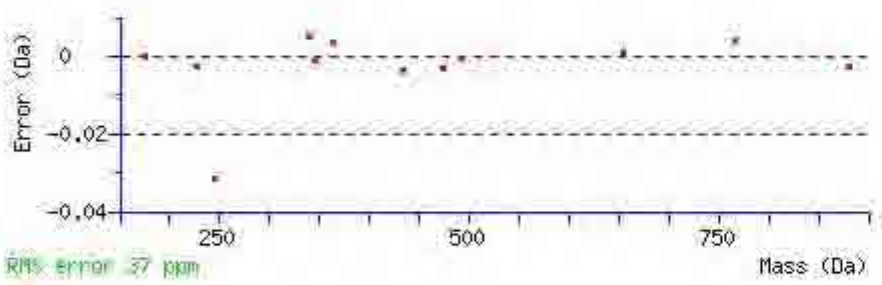
Match to Query 4193: 992.564348 from(497.289450,2+) rtinseconds(1300) index(6258)
Title: Locus:1.1.1.1510.13
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

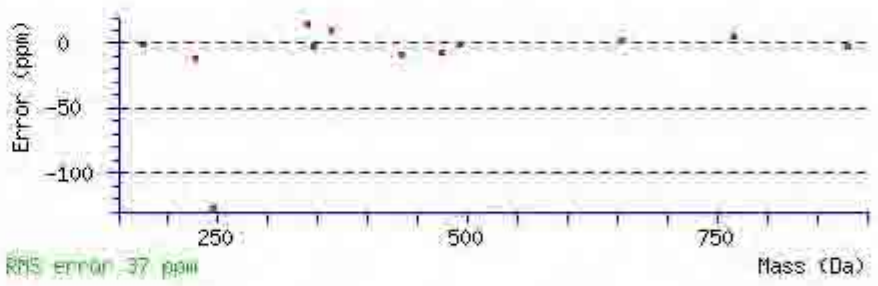
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 39 **Expect:** 0.0074
Matches : 12/66 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	*434.235773*	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	*363.198659*	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	992.565460	-0.001112	LLIYGASTR
38.7	992.565460	-0.001112	LLIYGATSR
25.5	992.555588	0.008760	IPLGWHVR
17.9	992.569504	-0.005156	IILNAVFGF
17.9	992.566803	-0.002455	ILPHWRR
17.9	992.565475	-0.001127	ILPSVSHKP
17.9	992.565460	-0.001112	LIINSSPHL
17.9	992.565460	-0.001112	LILGPHESK
17.9	992.565460	-0.001112	LLLDPASHK
17.9	992.572861	-0.008513	LLLFICGSK

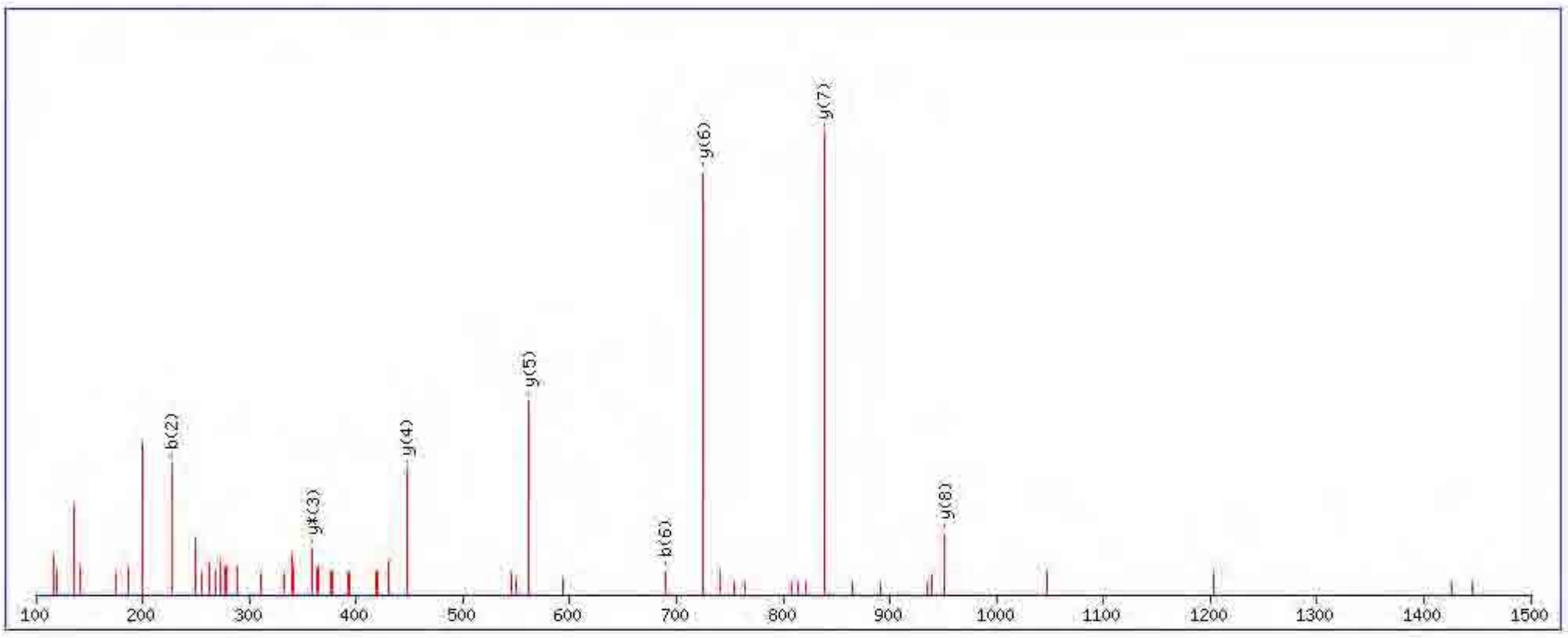
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

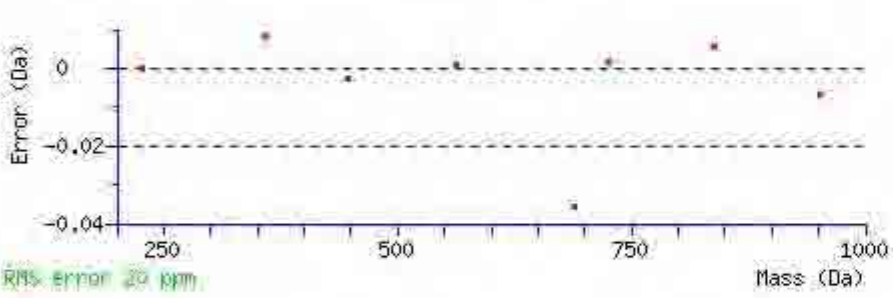
Match to Query 5441: 1063.568348 from(532.791450,2+) rtinseconds(1325) index(6504)
Title: Locus:1.1.1.1524.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

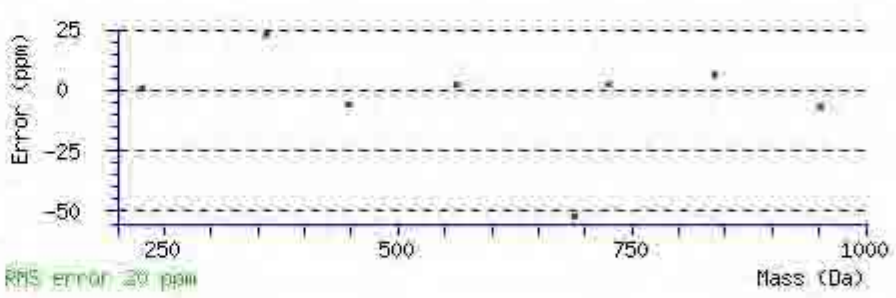
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 46 **Expect:** 0.0018
Matches : 8/70 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*951.489421*	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	*838.405357*	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	*725.321293*	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	*562.257964*	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	*447.231021*	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	1063.566177	0.002171	LLIYDASNR
15.8	1063.566208	0.002140	LPLAQVSAHP
14.5	1063.577423	-0.009075	PLHSSPAALR
14.1	1063.566208	0.002140	LLLQHGADPT
13.2	1063.570221	-0.001873	IIYIPPPDH
12.6	1063.566193	0.002155	EPLLPQDPR
12.4	1063.577438	-0.009090	IIPGGIADRH
12.4	1063.577438	-0.009090	IIPGGVAERH
12.3	1063.573593	-0.005245	ILMFLSNGLG
12.3	1063.573593	-0.005245	LLPNFGKML

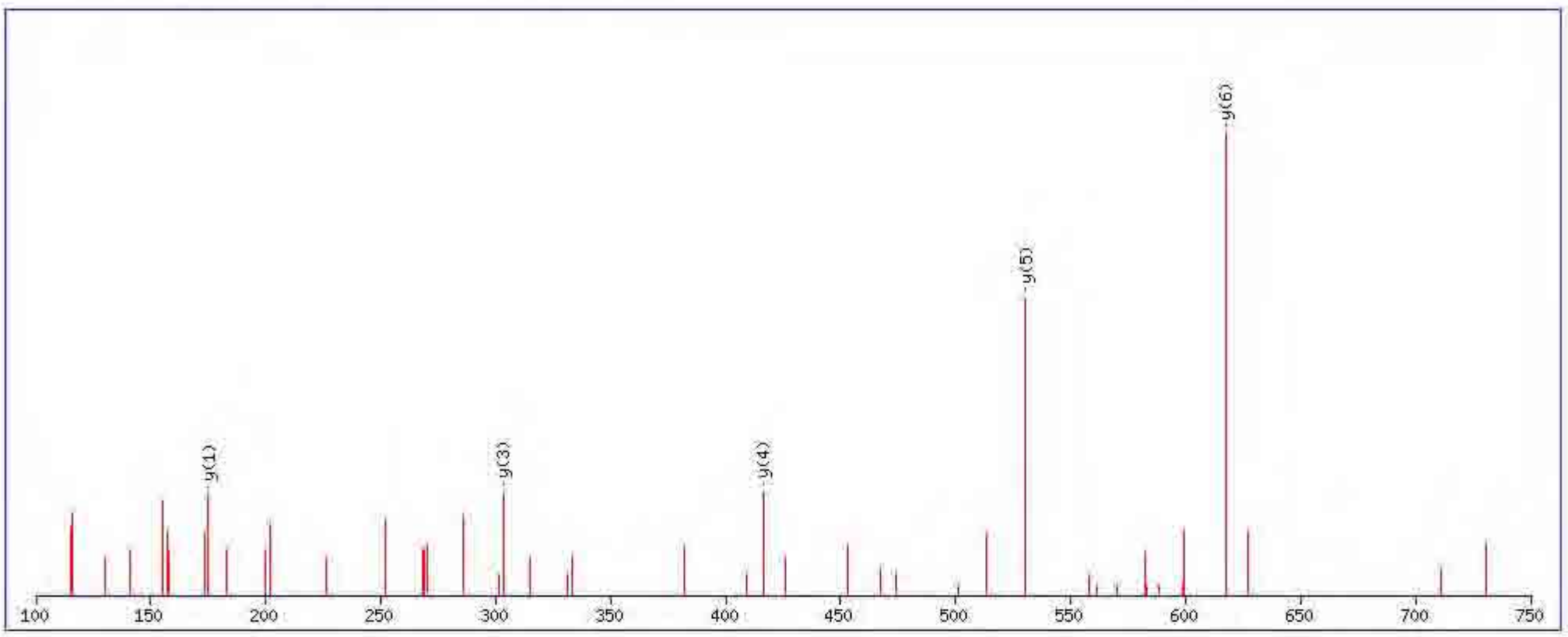
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSNPAGR**
Found in **ULK1_HUMAN**, Serine/threonine-protein kinase ULK1 OS=Homo sapiens GN=ULK1 PE=1 SV=2

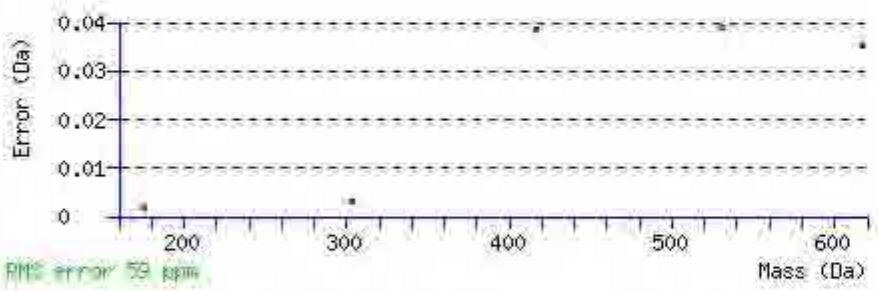
Match to Query 226: 729.380968 from(365.697760,2+) rtinseconds(416) index(346)
Title: Locus:1.1.1.1009.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

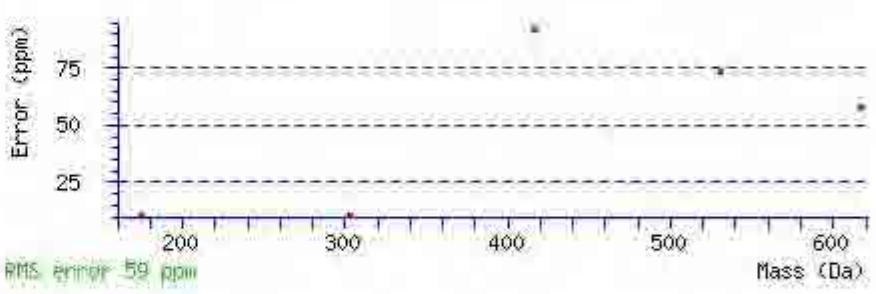
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 729.376938
Variable modifications:
P4 : Oxidation (P)
Ions Score: 49 **Expect:** 0.0027
Matches : 5/56 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							7
2	201.123368	101.065322			183.112803	92.060039	S	*617.300164*	309.153720	600.273615	300.640446	599.289599	300.148438	6
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	N	*530.268136*	265.637706	513.241587	257.124432			5
4	428.213974	214.610625	411.187425	206.097350	410.203409	205.605342	P	*416.225209*	208.616243	399.198660	200.102968			4
5	499.251088	250.129182	482.224539	241.615907	481.240523	241.123899	A	*303.177530*	152.092403	286.150981	143.579129			3
6	556.272552	278.639914	539.246003	270.126640	538.261987	269.634632	G	232.140416	116.573846	215.113867	108.060572			2
7							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LSNPAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	729.376938	0.004030	LSNPAGR
48.8	729.376938	0.004030	LSNPQR
48.8	729.376938	0.004030	PSNLQR
31.1	729.376938	0.004030	PSNPRK
31.1	729.376953	0.004015	LSPGGQR
31.1	729.376953	0.004015	PSGAVQR
31.1	729.376938	0.004030	PSINQR
31.1	729.376938	0.004030	PSLNQR
31.1	729.376938	0.004030	PSPNKR
31.1	729.388168	-0.007200	PSRAAGR

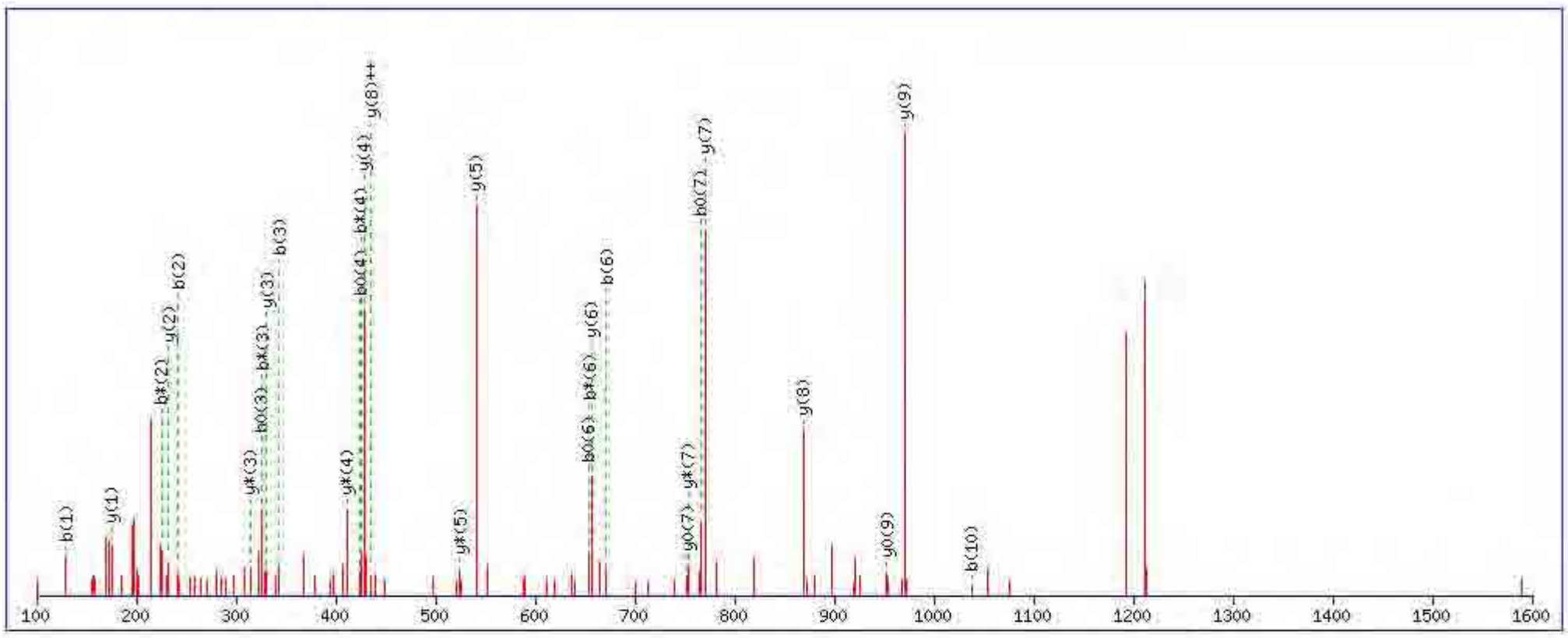
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QITVNDLPVGR**
Found in **PRDX1_HUMAN**, Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

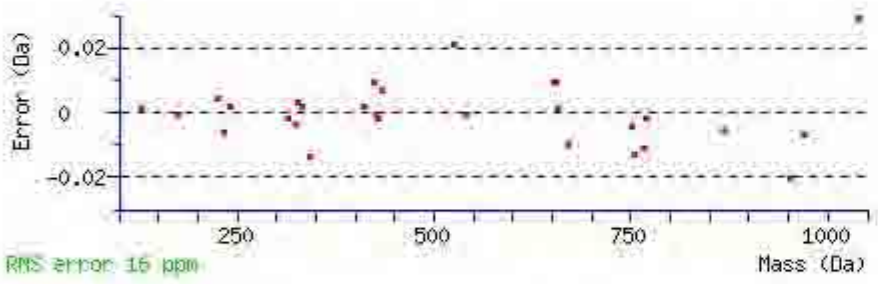
Match to Query 8801: 1210.664388 from(606.339470,2+) rtinseconds(1497) index(8392)
Title: Locus:1.1.1.1619.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

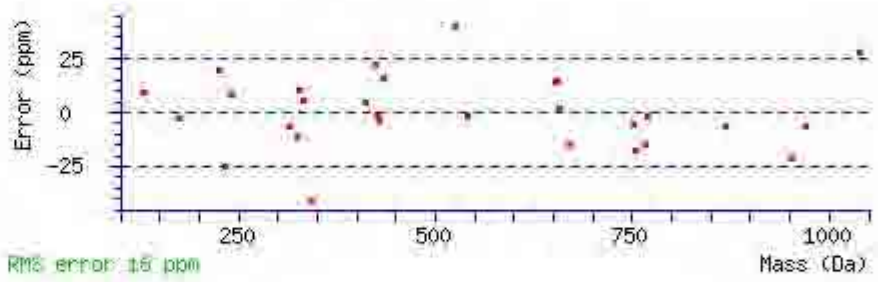
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1210.666992
Ions Score: 47 **Expect:** 0.00051
Matches : 29/106 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	242.149918	121.578597	225.123369	113.065323			I	1083.615685	542.311481	1066.589136	533.798206	1065.605120	533.306198	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	*970.531621*	485.769449	953.505072	477.256174	952.521056	476.764166	9
4	442.266011	221.636644	425.239462	213.123369	424.255446	212.631361	V	*869.483942*	435.245609	852.457393	426.732335	851.473377	426.240327	8
5	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	N	*770.415528*	385.711402	753.388979	377.198128	752.404963	376.706120	7
6	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	D	*656.372601*	328.689939	639.346052	320.176664	638.362036	319.684656	6
7	784.419945	392.713611	767.393396	384.200336	766.409380	383.708328	L	*541.345658*	271.176467	524.319109	262.663193			5
8	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	P	*428.261594*	214.634435	411.235045	206.121160			4
9	980.541123	490.774200	963.514574	482.260925	962.530558	481.768917	V	*331.208830*	166.108053	314.182281	157.594778			3
10	1037.562587	519.284932	1020.536038	510.771657	1019.552022	510.279649	G	*232.140416*	116.573846	215.113867	108.060571			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QITVNDLPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	1210.666992	-0.002604	QITVNDLPVGR
11.1	1210.653046	0.011342	ASRPEPQVRR
10.7	1210.666977	-0.002589	LGKELQTGTHK
10.7	1210.666992	-0.002604	QLTPGGGPLSLR
9.2	1210.671005	-0.006617	VPQPNITWLK
8.8	1210.653046	0.011342	RTSPRPASPAR
8.5	1210.653046	0.011342	ASRPEPQVRR
8.1	1210.666977	-0.002589	ALGVSLSRPAPQ
7.6	1210.674362	-0.009974	KITEVALMGHL
7.6	1210.666977	-0.002589	ALGVSLSRPAPQ

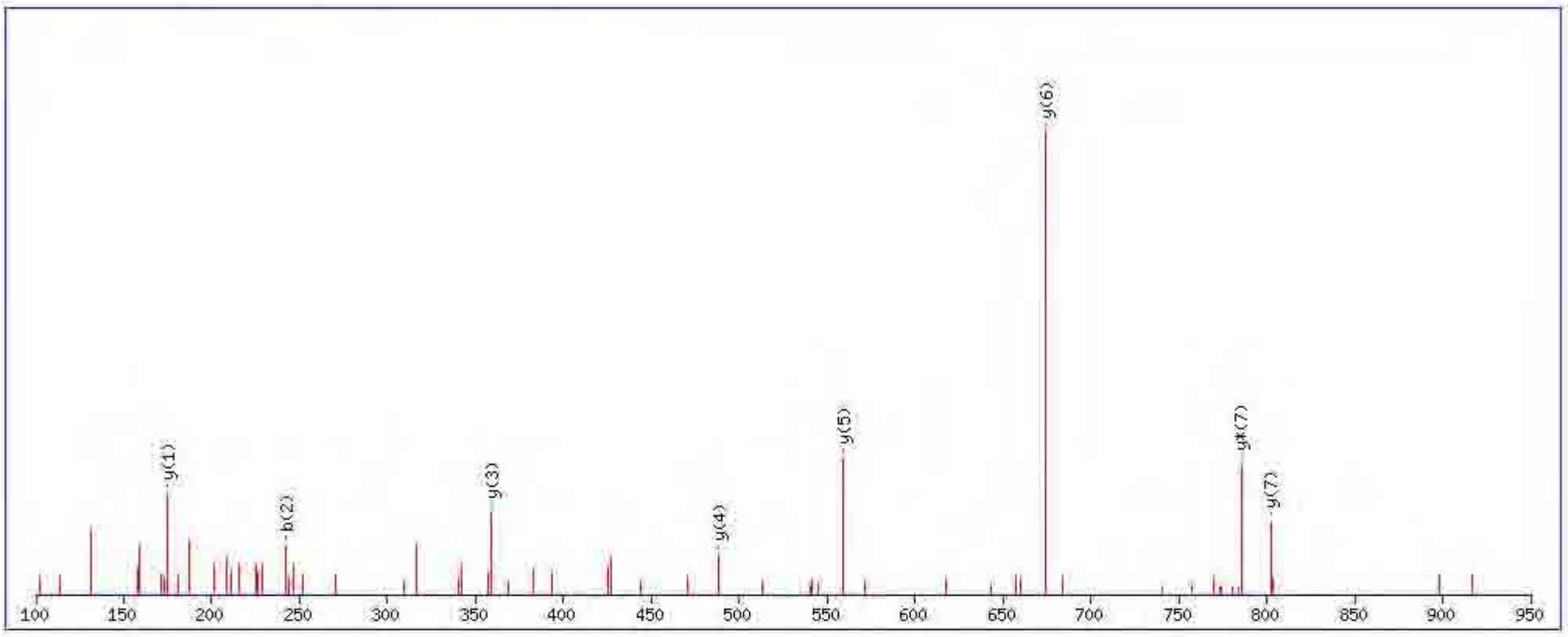
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQDAEIAR**
Found in **S10A6_HUMAN**, Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1

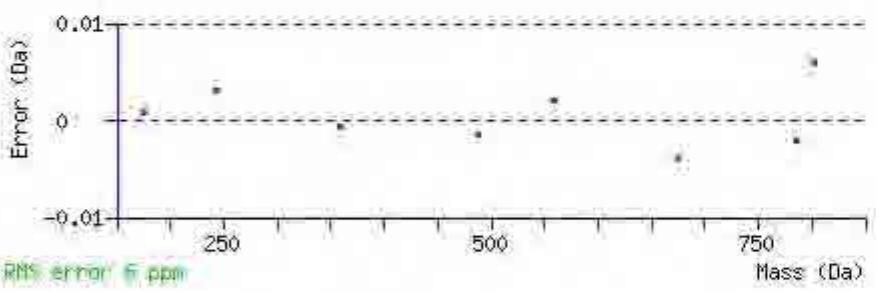
Match to Query 2947: 914.481688 from(458.248120,2+) rtinseconds(727) index(1491)
Title: Locus:1.1.1.1186.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

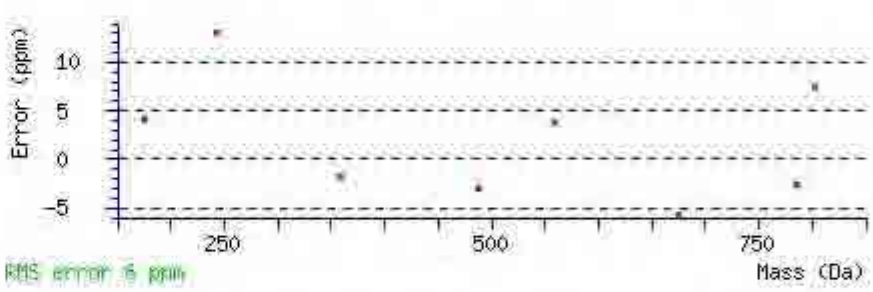
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 914.482117
Ions Score: 60 **Expect:** 0.0002
Matches : 8/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							8
2	242.149918	121.578597	225.123369	113.065323			Q	*802.405358*	401.706317	785.378809	393.193043	784.394793	392.701035	7
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	D	*674.346780*	337.677028	657.320231	329.163754	656.336215	328.671746	6
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	A	*559.319837*	280.163557	542.293288	271.650282	541.309272	271.158274	5
5	557.256568	279.131922	540.230019	270.618648	539.246003	270.126640	E	*488.282723*	244.644999	471.256174	236.131725	470.272158	235.639717	4
6	670.340632	335.673954	653.314083	327.160680	652.330067	326.668672	I	*359.240130*	180.123703	342.213581	171.610428			3
7	741.377746	371.192511	724.351197	362.679237	723.367181	362.187229	A	246.156066	123.581671	229.129517	115.068396			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LQDAEIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.7	914.482117	-0.000429	LQDAEIAR
42.3	914.482132	-0.000444	LQDLSSPR
42.1	914.482132	-0.000444	PKDAPSLR
29.2	914.482117	-0.000429	LQGEIEAR
27.3	914.482147	-0.000459	IKDPGPTR
27.3	914.482147	-0.000459	IKDVPGDR
27.0	914.482132	-0.000444	IKPSDSPR
27.0	914.482132	-0.000444	IQLDSSPR
26.8	914.482147	-0.000459	PQGEVITR
23.8	914.482117	-0.000429	LAQDEALR

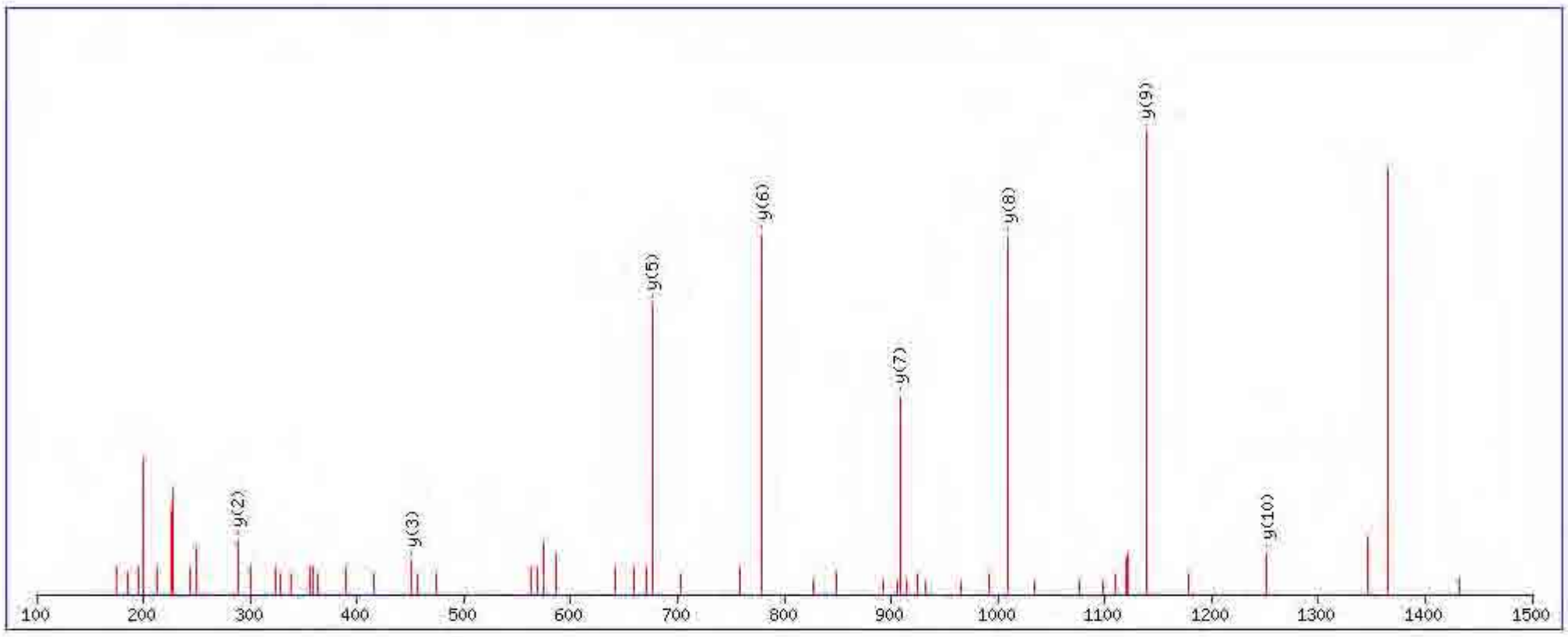
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **S10A8_HUMAN**, Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1

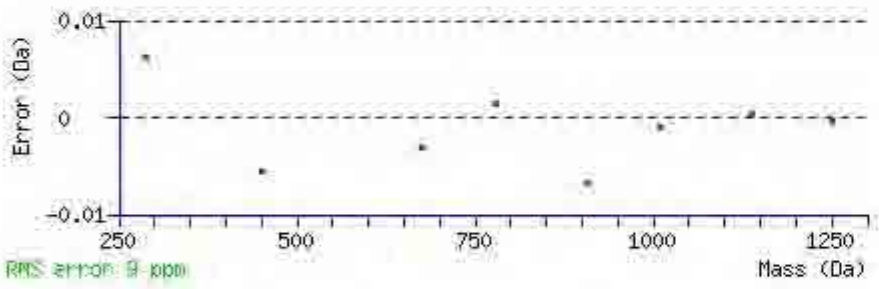
Match to Query 11467: 1363.678768 from(682.846660,2+) rtinseconds(1552) index(8929)
Title: Locus:1.1.1.1649.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

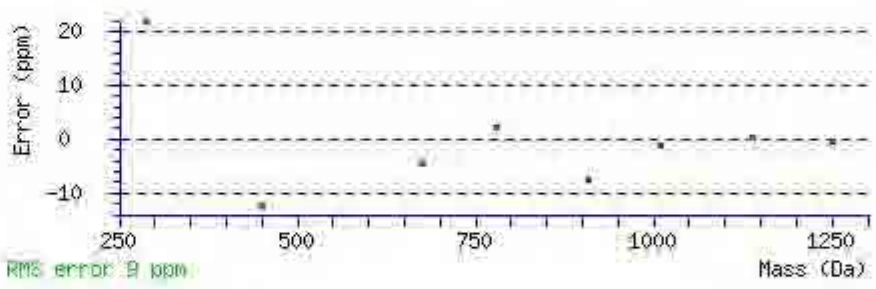
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1363.680557
Ions Score: 71 **Expect:** 3.8e-005
Matches : 8/90 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	227.175404	114.091340					L	*1251.603801*	626.305539	1234.577252	617.792264	1233.593236	617.300256	10
3	356.217997	178.612637			338.207432	169.607354	E	*1138.519737*	569.763507	1121.493188	561.250232	1120.509172	560.758224	9
4	457.265676	229.136476			439.255111	220.131194	T	*1009.477144*	505.242210	992.450595	496.728936	991.466579	496.236928	8
5	586.308269	293.657773			568.297704	284.652490	E	*908.429465*	454.718371	891.402916	446.205096	890.418900	445.713088	7
6	689.317454	345.162365			671.306889	336.157083	C	*779.386872*	390.197074	762.360323	381.683800			6
7	786.370218	393.688747			768.359653	384.683465	P	*676.377687*	338.692482	659.351138	330.179207			5
8	914.428796	457.718036	897.402247	449.204762	896.418231	448.712754	Q	579.324923	290.166100	562.298374	281.652825			4
9	1077.492125	539.249701	1060.465576	530.736426	1059.481560	530.244418	Y	*451.266345*	226.136810	434.239796	217.623536			3
10	1190.576189	595.791733	1173.549640	587.278458	1172.565624	586.786450	I	*288.203016*	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLETECPQYIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.7	1363.680557	-0.001789	LLETECPQYIR
23.9	1363.673203	0.005565	LPERPGPSNPPVG
23.9	1363.673203	0.005565	LPERPGPSNPPVG
18.9	1363.691788	-0.013020	PEEVLSCRYLR
16.4	1363.677200	0.001568	PIEADFSWQKK
16.1	1363.671844	0.006924	IPTEETTISTEK
15.4	1363.680573	-0.001805	LPEDPAIPMPPR
15.4	1363.673203	0.005565	LPERPGPSNPPVG
15.3	1363.683929	-0.005161	LIEMSEVQLMR
15.1	1363.673203	0.005565	LPERPGPSNPPVG

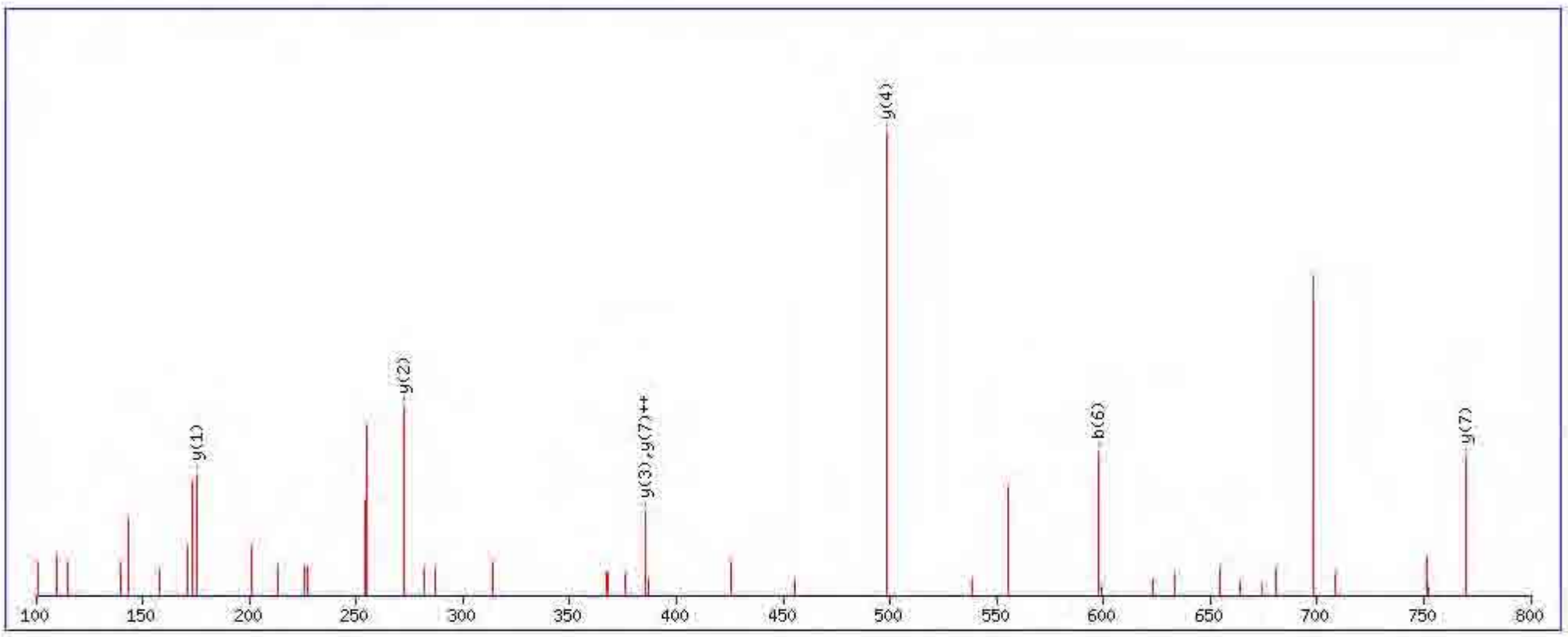
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSAILIPR**
Found in **S36A3_HUMAN**, Proton-coupled amino acid transporter 3 OS=Homo sapiens GN=SLC36A3 PE=1 SV=2

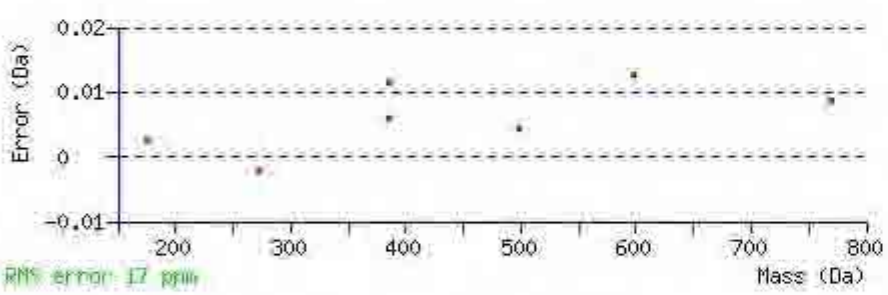
Match to Query 2022: 867.546068 from(434.780310,2+) rtinseconds(1294) index(6180)
Title: Locus:1.1.1.1507.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

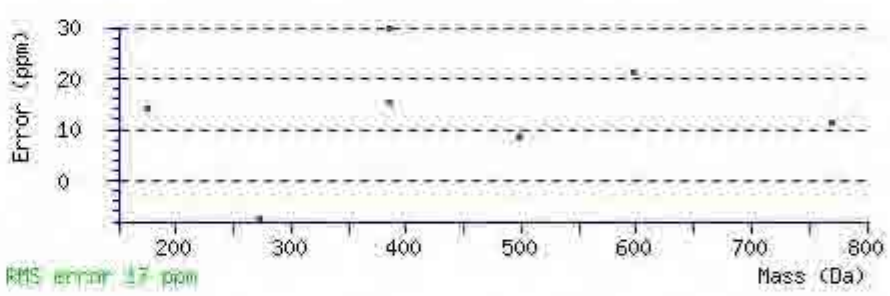
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 867.554169
Ions Score: 47 **Expect:** 0.00061
Matches : 7/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							8
2	187.107718	94.057497	169.097153	85.052214	S	*769.493050*	385.250163	752.466501	376.736889	751.482485	376.244881	7
3	258.144832	129.576054	240.134267	120.570772	A	682.461022	341.734149	665.434473	333.220875			6
4	371.228896	186.118086	353.218331	177.112804	I	611.423908	306.215592	594.397359	297.702318			5
5	484.312960	242.660118	466.302395	233.654836	L	*498.339844*	249.673560	481.313295	241.160285			4
6	597.397024	299.202150	579.386459	290.196868	I	*385.255780*	193.131528	368.229231	184.618253			3
7	694.449788	347.728532	676.439223	338.723250	P	*272.171716*	136.589496	255.145167	128.076221			2
8					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VSAILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	867.554169	-0.008101	VSAILIPR
30.2	867.554153	-0.008085	EKIILPR
30.2	867.554184	-0.008116	TLGVLPLR
26.6	867.554169	-0.008101	GLLSLPLR
22.3	867.554184	-0.008116	TLVILGPR
17.7	867.554184	-0.008116	VALTLRVP
15.7	867.554184	-0.008116	LGTPLLVR
15.1	867.554169	-0.008101	VALLALPR
15.1	867.554169	-0.008101	VALLPLAR
15.1	867.554199	-0.008131	VAVPVLVR

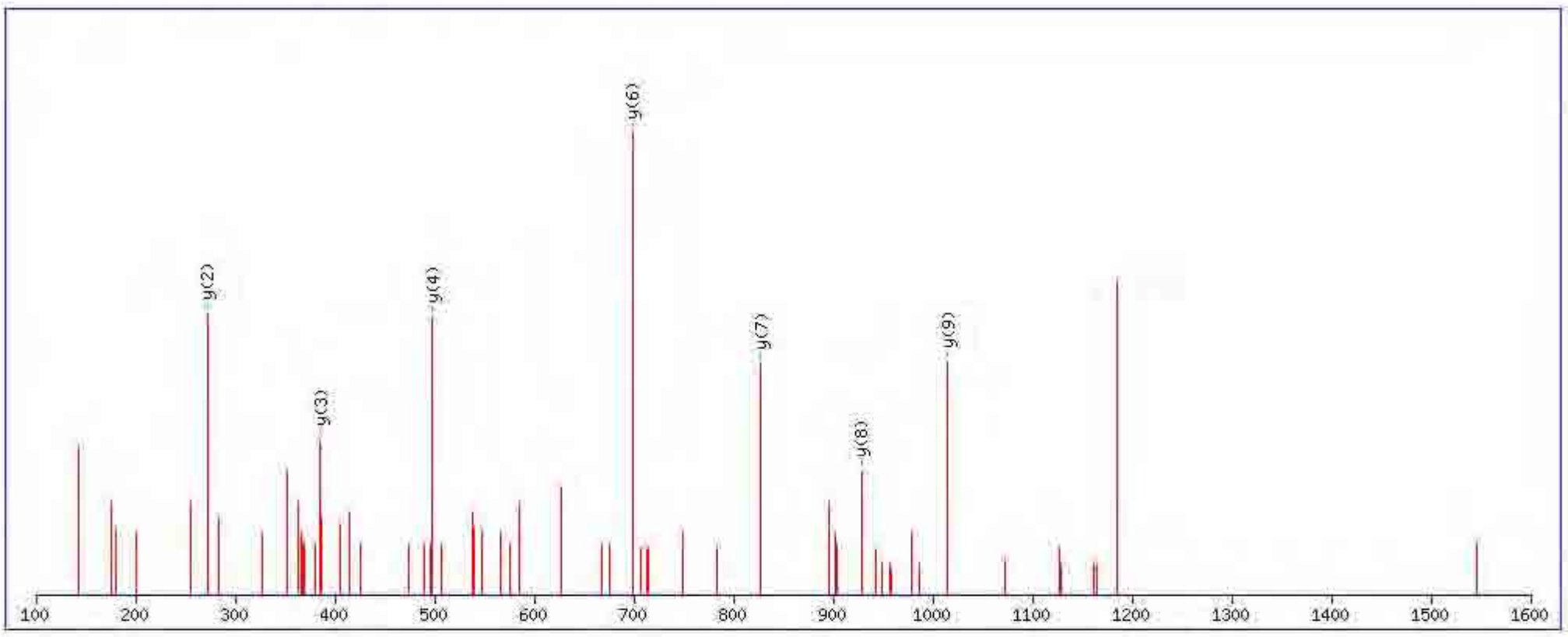
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

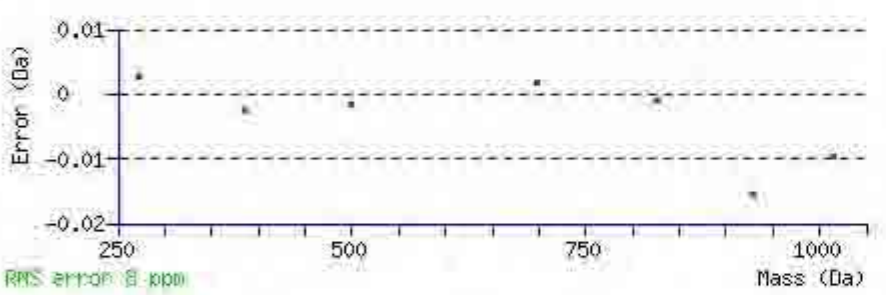
Match to Query 8195: 1184.679728 from(593.347140,2+) rtinseconds(1719) index(10634)
Title: Locus:1.1.1.1740.13
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

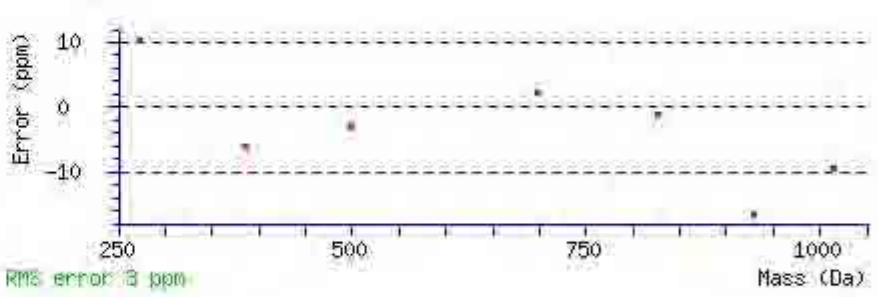
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 56 **Expect:** 0.00038
Matches : 7/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	*1015.578236*	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	*928.546208*	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	*827.498529*	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	*698.455936*	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	611.423908	306.215592	594.397359	297.702318			5
8	801.435260	401.221268	783.424695	392.215986	L	*498.339844*	249.673560	481.313295	241.160285			4
9	914.519324	457.763300	896.508759	448.758018	I	*385.255780*	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	*272.171716*	136.589496	255.145167	128.076221			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1184.676468	0.003260	GLSTESILIPR
14.9	1184.677795	0.001933	PRHPEALLPR
14.4	1184.676483	0.003245	LDSTALLVTPR
13.7	1184.676468	0.003260	KEDLTTLLPR
12.8	1184.687698	-0.007970	LGTLRELLDR
8.4	1184.676468	0.003260	IGITLSNAIVNA
6.3	1184.683868	-0.004140	LGTPLCIIVEK
6.0	1184.670609	0.009119	WPAGLFLLPR
4.7	1184.687698	-0.007970	LTSREITIPR
3.8	1184.687683	-0.007955	ISAAKAVADAIR

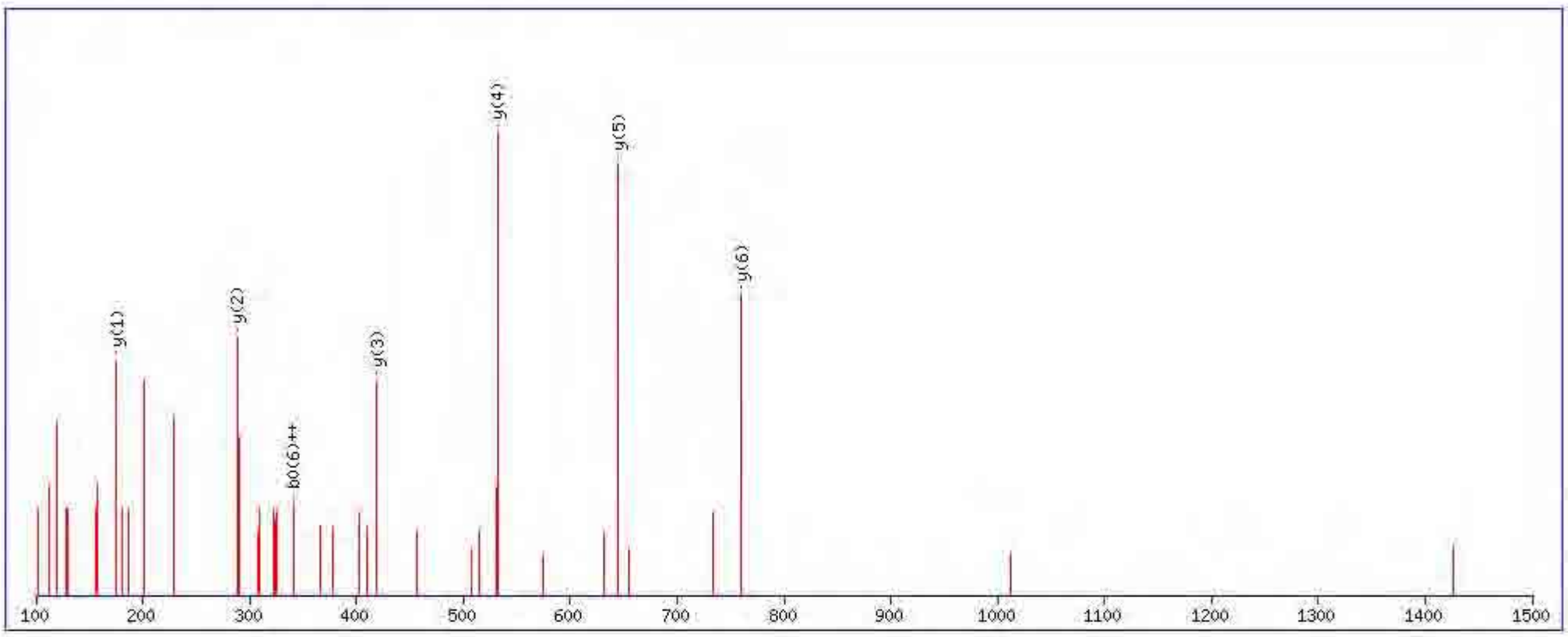
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDILMLR**
Found in **RARG_HUMAN**, Retinoic acid receptor gamma OS=Homo sapiens GN=RARG PE=1 SV=1

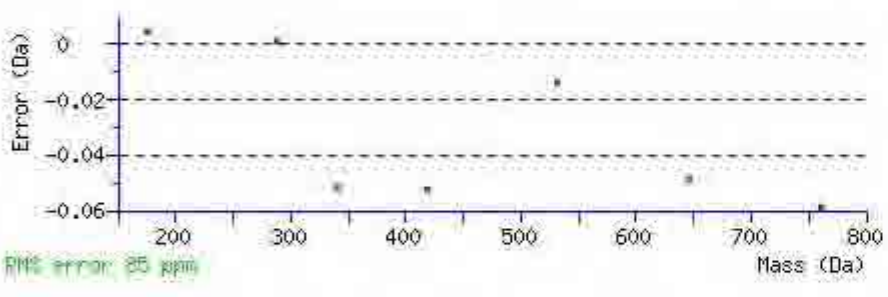
Match to Query 2134: 872.516128 from(437.265340,2+) rtinseconds(1415) index(7511)
Title: Locus:1.1.1.1574.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

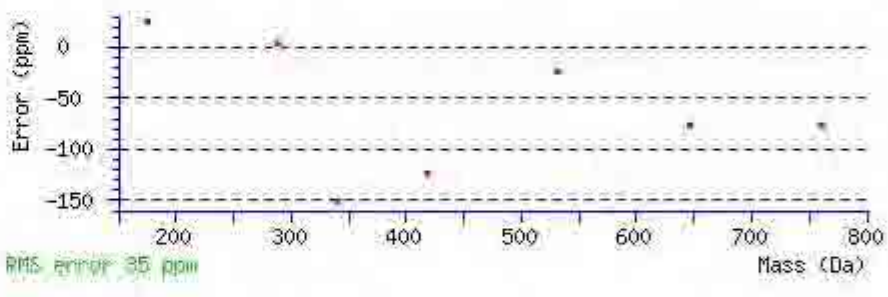
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 872.515335
Ions Score: 61 **Expect:** 0.0001
Matches : 7/48 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							7
2	229.118283	115.062779	211.107718	106.057497	D	*760.438572*	380.722924	743.412023	372.209650	742.428007	371.717642	6
3	342.202347	171.604811	324.191782	162.599529	I	*645.411629*	323.209453	628.385080	314.696178			5
4	455.286411	228.146843	437.275846	219.141561	L	*532.327565*	266.667421	515.301016	258.154146			4
5	586.326896	293.667086	568.316331	284.661804	M	*419.243501*	210.125389	402.216952	201.612114			3
6	699.410960	350.209118	681.400395	341.203836	L	*288.203016*	144.605146	271.176467	136.091872			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LDILMLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.7	872.515335	0.000793	LDILMLR
42.0	872.515335	0.000793	LDLMILR
41.8	872.515335	0.000793	DIIIMIR
41.4	872.515335	0.000793	IEVIMLR
26.1	872.515335	0.000793	LDIMIRL
25.9	872.521866	-0.005738	IDLLSSLI
25.9	872.515335	0.000793	LDILLRM
25.9	872.515335	0.000793	DLLMLLR
25.7	872.511978	0.004150	DIILPFR
25.7	872.511978	0.004150	VEIIPFR

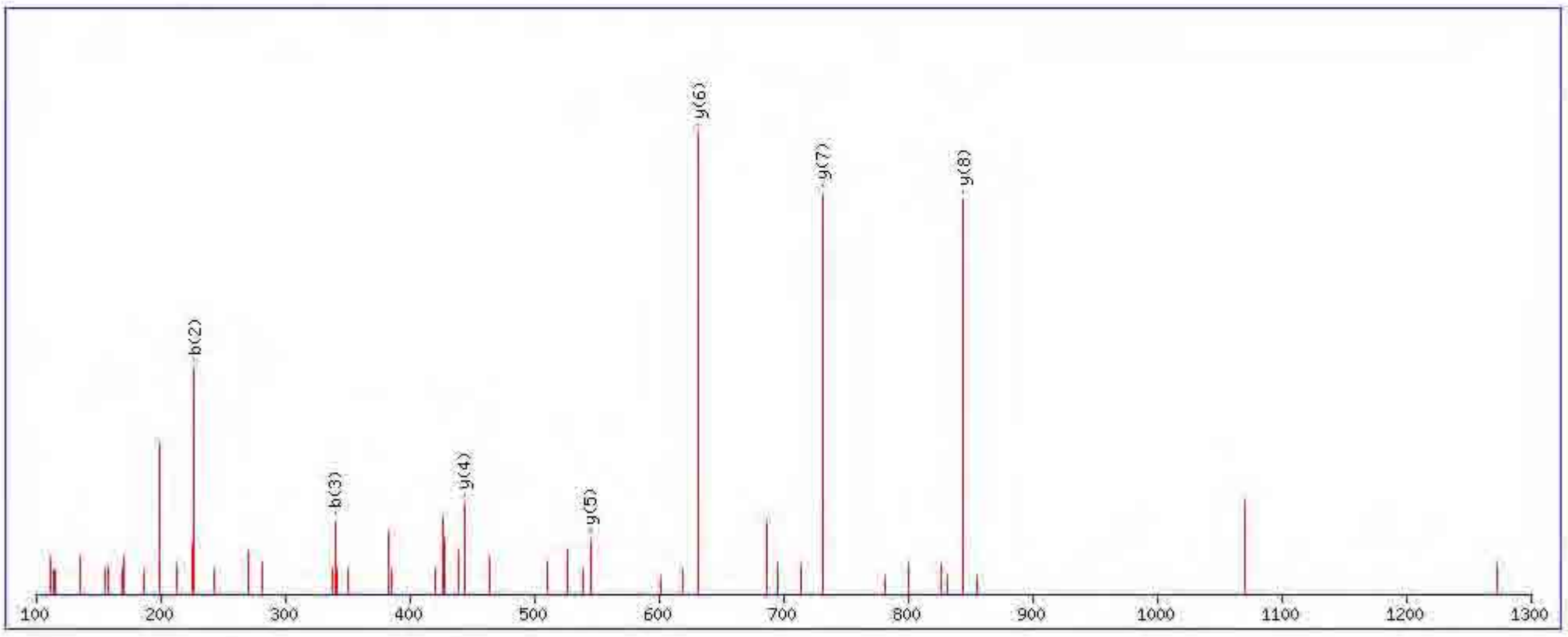
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

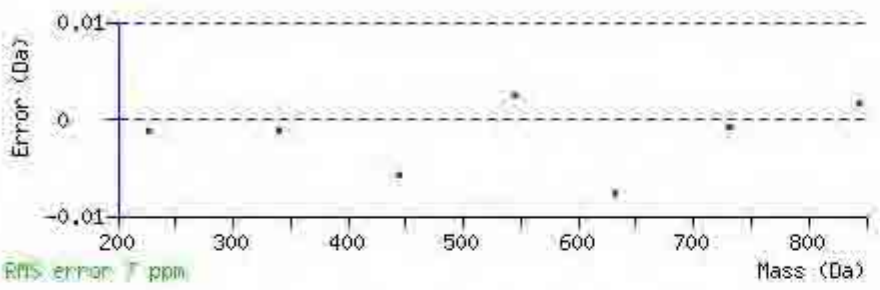
Match to Query 5556: 1069.650288 from(535.832420,2+) rtinseconds(1385) index(7134)
Title: Locus:1.1.1.1557.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

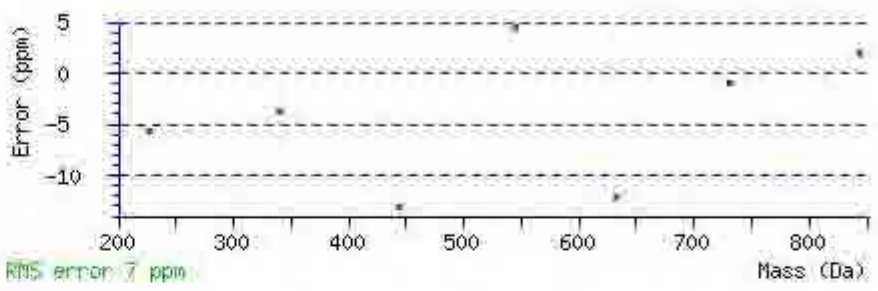
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 46 **Expect:** 0.0013
Matches : 7/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	844.488694	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	731.404630	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	632.336216	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	444.256509	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1069.649536	0.000752	LLIVSTPTAR
18.1	1069.649521	0.000767	PLLSVKELR
16.6	1069.660736	-0.010448	LILSEAIRR
16.6	1069.660751	-0.010463	PLLSSLLRR
16.4	1069.660751	-0.010463	IPILSSRLR
16.2	1069.649506	0.000782	LLLDALREK
16.2	1069.653564	-0.003276	LLLWVSVVAA
11.6	1069.660736	-0.010448	ILLSRLEAR
11.6	1069.649506	0.000782	PILSANIKAK
11.4	1069.656906	-0.006618	ILIQLCAALL

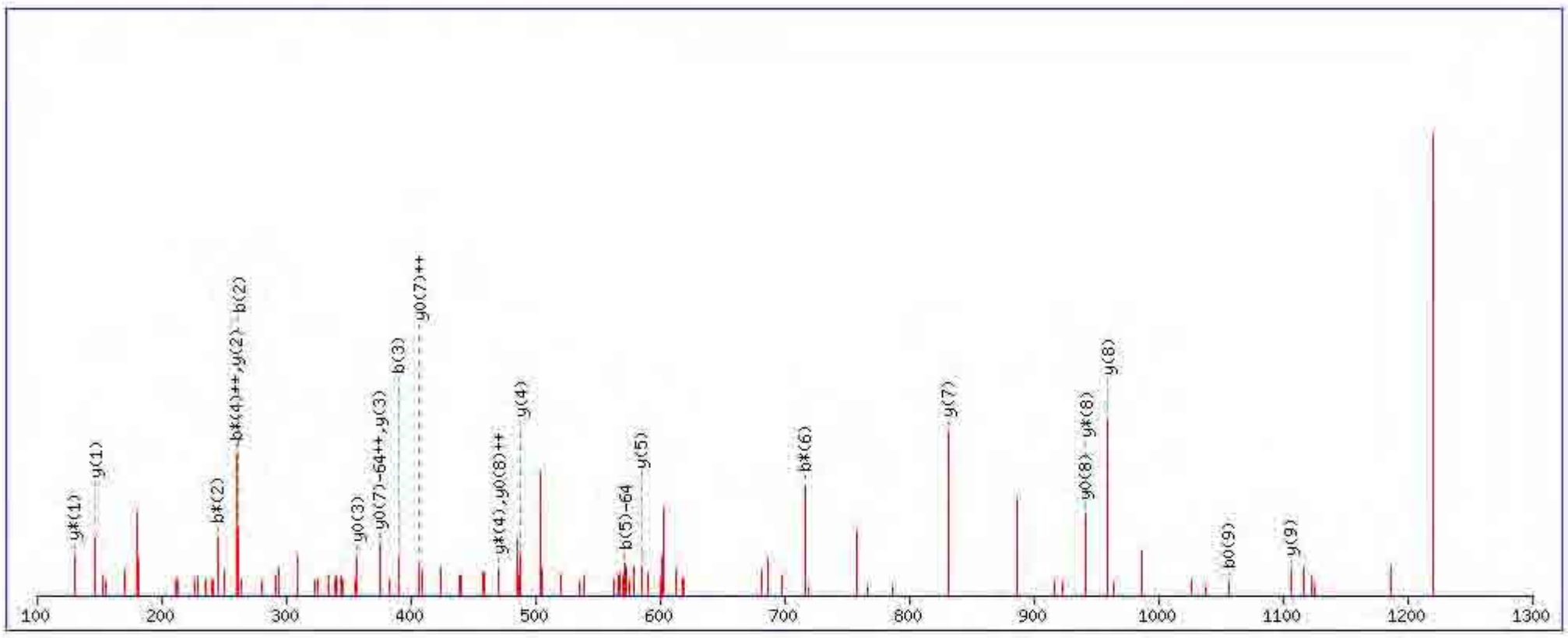
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFQMVPLDPK**
Found in **TSP2_HUMAN**, Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2

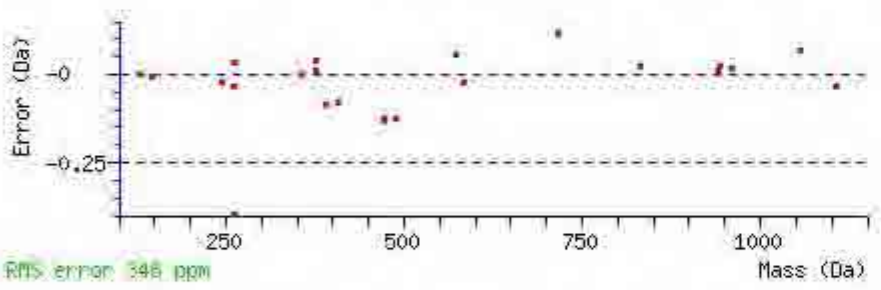
Match to Query 8957: 1219.591188 from(610.802870,2+) rtinseconds(1374) index(7031)
Title: Locus:1.1.1.1551.16
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_1.mgf

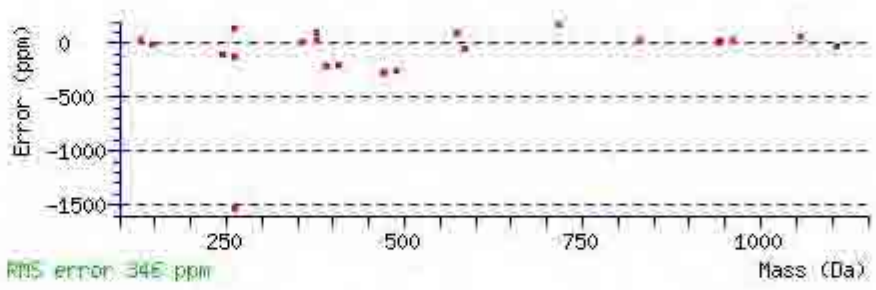
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1219.590714
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P9 : Oxidation (P)
Ions Score: 49 **Expect:** 0.002
Matches : 23/136 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**262.118617**	131.562946	245.092068	123.049672			F	*1106.555060*	553.781168	1089.528511	545.267894	1088.544495	544.775885	9
3	**390.177195**	195.592235	373.150646	187.078961			Q	*959.486646*	480.246961	942.460097	471.733686	941.476081	471.241678	8
4	537.212595	269.109936	520.186046	260.596661			M	*831.428068*	416.217672	814.401519	407.704397	813.417503	407.212389	7
5	636.281009	318.644142	619.254460	310.130868			V	684.392668	342.699972	667.366119	334.186697	666.382103	333.694689	6
6	733.333773	367.170525	716.307224	358.657250			P	*585.324254*	293.165765	568.297705	284.652491	567.313689	284.160483	5
7	846.417837	423.712557	829.391288	415.199282			L	*488.271490*	244.639383	471.244941	236.126108	470.260925	235.634100	4
8	961.444780	481.226028	944.418231	472.712753	943.434215	472.220745	D	*375.187426*	188.097351	358.160877	179.584076	357.176861	179.092068	3
9	1074.492459	537.749867	1057.465910	529.236593	1056.481894	528.744585	P	*260.160483*	130.583879	243.133934	122.070605			2
10							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NFQMVPLDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	1219.590714	0.000474	NFQMVPLDPK
44.6	1219.590714	0.000474	NFQMVPLDPK
19.2	1219.593201	-0.002013	NTETATEVDIK
18.0	1219.594070	-0.002882	NAVSDMMVPLK
17.4	1219.590714	0.000474	NFQMVPLDPK
12.9	1219.597214	-0.006026	EFIDIDENLI
12.5	1219.583298	0.007890	SWSRSIEDLQ
11.9	1219.583298	0.007890	YNQQQALIDQ
9.1	1219.579269	0.011919	SSSQENTPRSK
9.0	1219.594070	-0.002882	NAVSDMMVPLK

Sibling 2 – technical replicate # 2

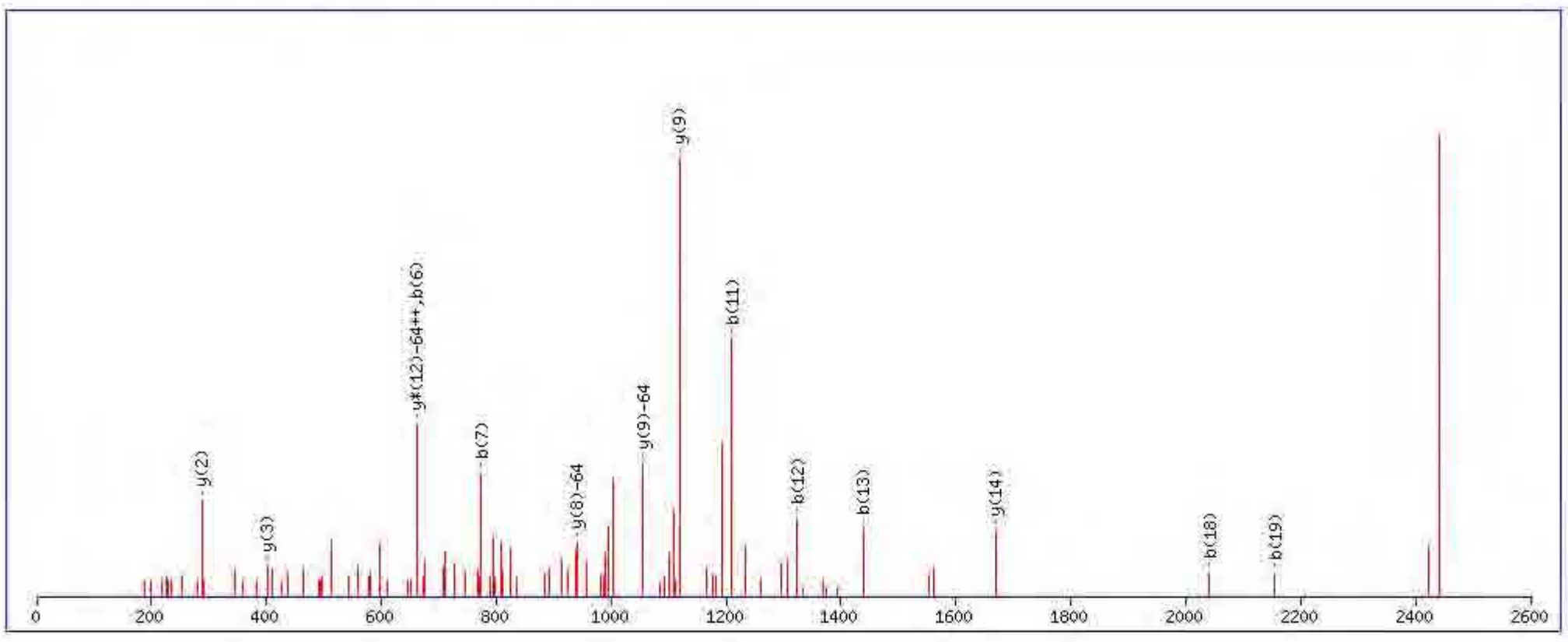
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNYGVLLHELGLDEPLMTPLR**
Found in **OGFD2_HUMAN**, 2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2 OS=Homo sapiens GN=OGFOD2 PE=2 SV=2

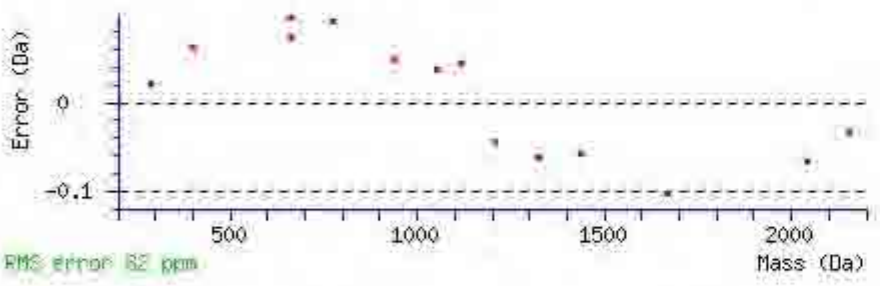
Match to Query 14666: 2441.230392 from(814.750740,3+) rtinseconds(2244) index(16843)
Title: Locus:1.1.1.2020.16
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

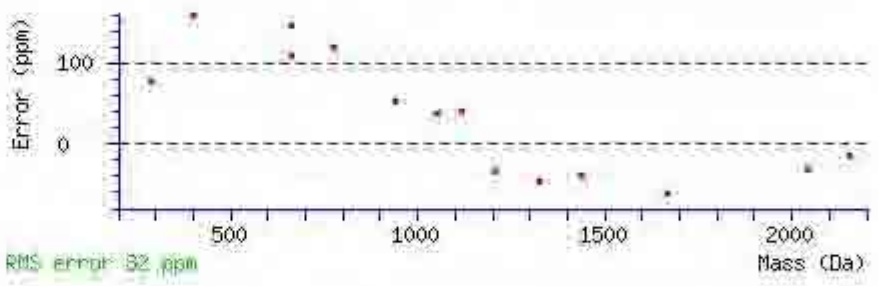
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 2441.226044
Variable modifications:
P15 : Oxidation (P)
M17 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P19 : Oxidation (P)
Ions Score: 44 **Expect:** 0.00072
Matches : 14/338 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							21
2	229.093130	115.050203	212.066581	106.536929			N	2328.190412	1164.598844	2311.163863	1156.085569	2310.179847	1155.593561	20
3	392.156459	196.581867	375.129910	188.068593			Y	2214.147485	1107.577380	2197.120936	1099.064106	2196.136920	1098.572098	19
4	449.177923	225.092599	432.151374	216.579325			G	2051.084156	1026.045716	2034.057607	1017.532441	2033.073591	1017.040433	18
5	548.246337	274.626807	531.219788	266.113532			V	1994.062692	997.534984	1977.036143	989.021710	1976.052127	988.529702	17
6	*661.330401*	331.168839	644.303852	322.655564			L	1894.994278	948.000777	1877.967729	939.487503	1876.983713	938.995495	16
7	*774.414465*	387.710871	757.387916	379.197596			L	1781.910214	891.458745	1764.883665	882.945471	1763.899649	882.453463	15
8	911.473377	456.240327	894.446828	447.727052			H	**1668.826150**	834.916713	1651.799601	826.403439	1650.815585	825.911431	14
9	1040.515970	520.761623	1023.489421	512.248349	1022.505405	511.756341	E	1531.767238	766.387257	1514.740689	757.873983	1513.756673	757.381975	13
10	1153.600034	577.303655	1136.573485	568.790381	1135.589469	568.298373	L	1402.724645	701.865961	1385.698096	693.352686	1384.714080	692.860678	12
11	*1210.621498*	605.814387	1193.594949	597.301113	1192.610933	596.809104	G	1289.640581	645.323929	1272.614032	636.810654	1271.630016	636.318646	11
12	*1323.705562*	662.356419	1306.679013	653.843144	1305.694997	653.351136	L	1232.619117	616.813197	1215.592568	608.299922	1214.608552	607.807914	10
13	*1438.732505*	719.869891	1421.705956	711.356616	1420.721940	710.864608	D	**1119.535053**	560.271165	1102.508504	551.757890	1101.524488	551.265882	9
14	1567.775098	784.391187	1550.748549	775.877912	1549.764533	775.385904	E	1004.508110	502.757693	987.481561	494.244419	986.497545	493.752411	8
15	1680.822777	840.915026	1663.796228	832.401752	1662.812212	831.909744	P	875.465517	438.236397	858.438968	429.723122	857.454952	429.231114	7
16	1793.906841	897.457058	1776.880292	888.943784	1775.896276	888.451776	L	762.417838	381.712557	745.391289	373.199283	744.407273	372.707275	6
17	1940.942241	970.974758	1923.915692	962.461484	1922.931676	961.969476	M	649.333774	325.170525	632.307225	316.657251	631.323209	316.165243	5
18	*2041.989920*	1021.498598	2024.963371	1012.985323	2023.979355	1012.493315	T	502.298374	251.652825	485.271825	243.139551	484.287809	242.647543	4
19	*2155.037599*	1078.022437	2138.011050	1069.509163	2137.027034	1069.017155	P	**401.250695**	201.128986	384.224146	192.615711			3
20	2268.121663	1134.564469	2251.095114	1126.051195	2250.111098	1125.559187	L	**288.203016**	144.605146	271.176467	136.091872			2
21							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NNYGVLLHELGLDEPLMTPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	2441.226044	0.004348	NNYGVLLHELGLDEPLMTPLR
9.4	2441.245117	-0.014725	YYHANAAVNDQSPGPLALKIAGR
8.5	2441.219498	0.010894	LMYLYGQGIRQDTEAALQCLR
7.6	2441.218140	0.012252	LLEEAQANIMKSIPNLEMPPAT
7.6	2441.218140	0.012252	LLEEAQANIMKSIPNLEMPPAT
6.2	2441.214661	0.015731	LLGDPGLRGTTEPDATGGGSGSLAAR
4.4	2441.214813	0.015579	SLEAINEPIPQPMPFPPSIIR
4.4	2441.214813	0.015579	SLEAINEPIPQPMPFPPSIIR
4.4	2441.214813	0.015579	SLEAINEPIPQPMPFPPSIIR
3.7	2441.233948	-0.003556	PRVTLAPPWNGLAPPAPPPPPR

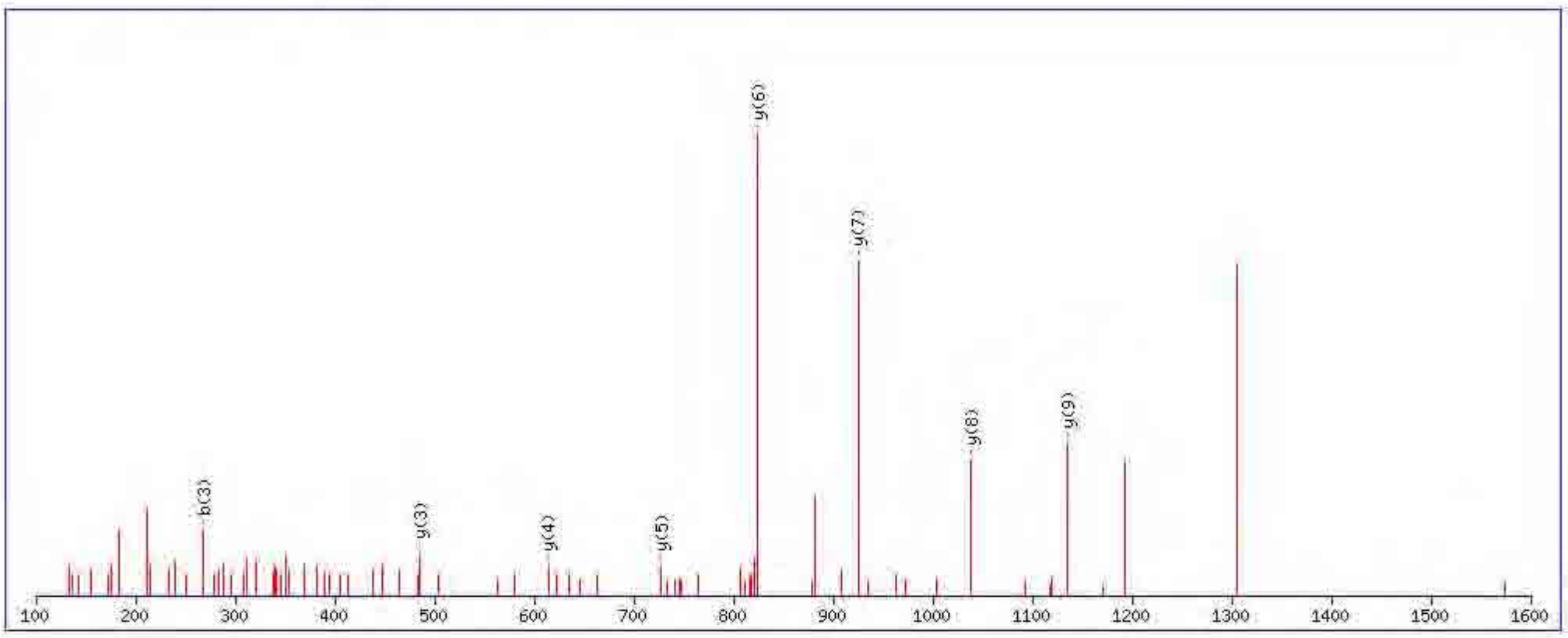
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPITPLEFYR**
Found in **BLMH_HUMAN**, Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1

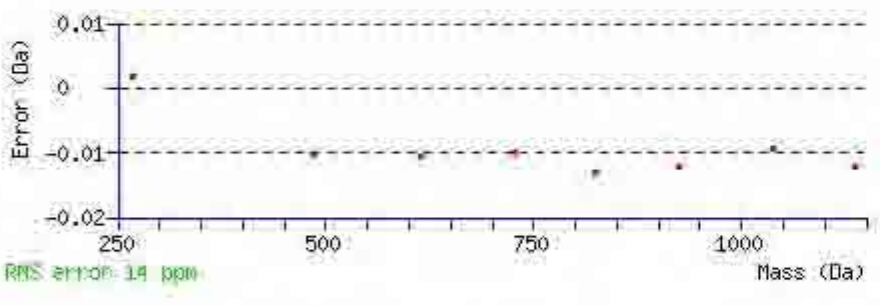
Match to Query 10371: 1304.705488 from(653.360020,2+) rtinseconds(2094) index(15243)
Title: Locus:1.1.1.1938.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

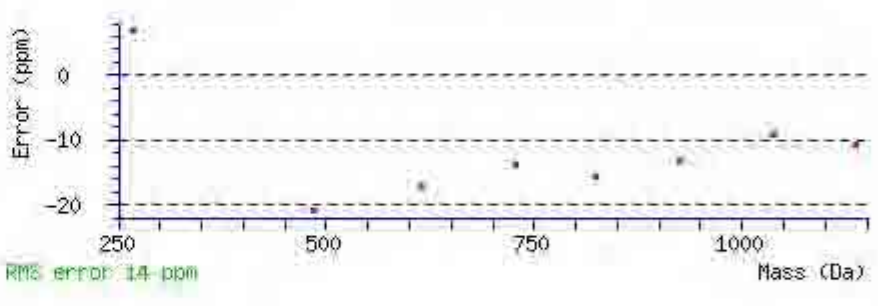
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1304.712860
Ions Score: 54 **Expect:** 0.0001
Matches : 8/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	1192.636087	596.821682	1175.609538	588.308407	1174.625522	587.816399	10
3	268.165568	134.586422			P	*1135.614623*	568.310949	1118.588074	559.797675	1117.604058	559.305667	9
4	381.249632	191.128454			I	*1038.561859*	519.784568	1021.535310	511.271293	1020.551294	510.779285	8
5	482.297311	241.652293	464.286746	232.647011	T	*925.477795*	463.242536	908.451246	454.729261	907.467230	454.237253	7
6	579.350075	290.178676	561.339510	281.173393	P	*824.430116*	412.718696	807.403567	404.205422	806.419551	403.713414	6
7	692.434139	346.720708	674.423574	337.715425	L	*727.377352*	364.192314	710.350803	355.679039	709.366787	355.187031	5
8	821.476732	411.242004	803.466167	402.236722	E	*614.293288*	307.650282	597.266739	299.137007	596.282723	298.644999	4
9	968.545146	484.776211	950.534581	475.770929	F	*485.250695*	243.128985	468.224146	234.615711			3
10	1131.608475	566.307876	1113.597910	557.302593	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGPITPLEFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.4	1304.712860	-0.007372	IGPITPLEFYR
11.3	1304.697617	0.007871	IGPPAVEAAVTPPA
5.2	1304.708832	-0.003344	PLGPGLKPPEER
3.7	1304.697617	0.007871	IGPPAVEAAVTPPA
3.7	1304.708847	-0.003359	LGSPDPPPKPLR
3.7	1304.708847	-0.003359	LGSPDPPPKPLR
3.7	1304.708847	-0.003359	LGSPDPPPKPLR
3.7	1304.708847	-0.003359	LGSPDPPPKPLR
3.2	1304.697617	0.007871	IGPPAVEAAVTPPA
1.9	1304.708862	-0.003374	PGTKPTPIPPPR

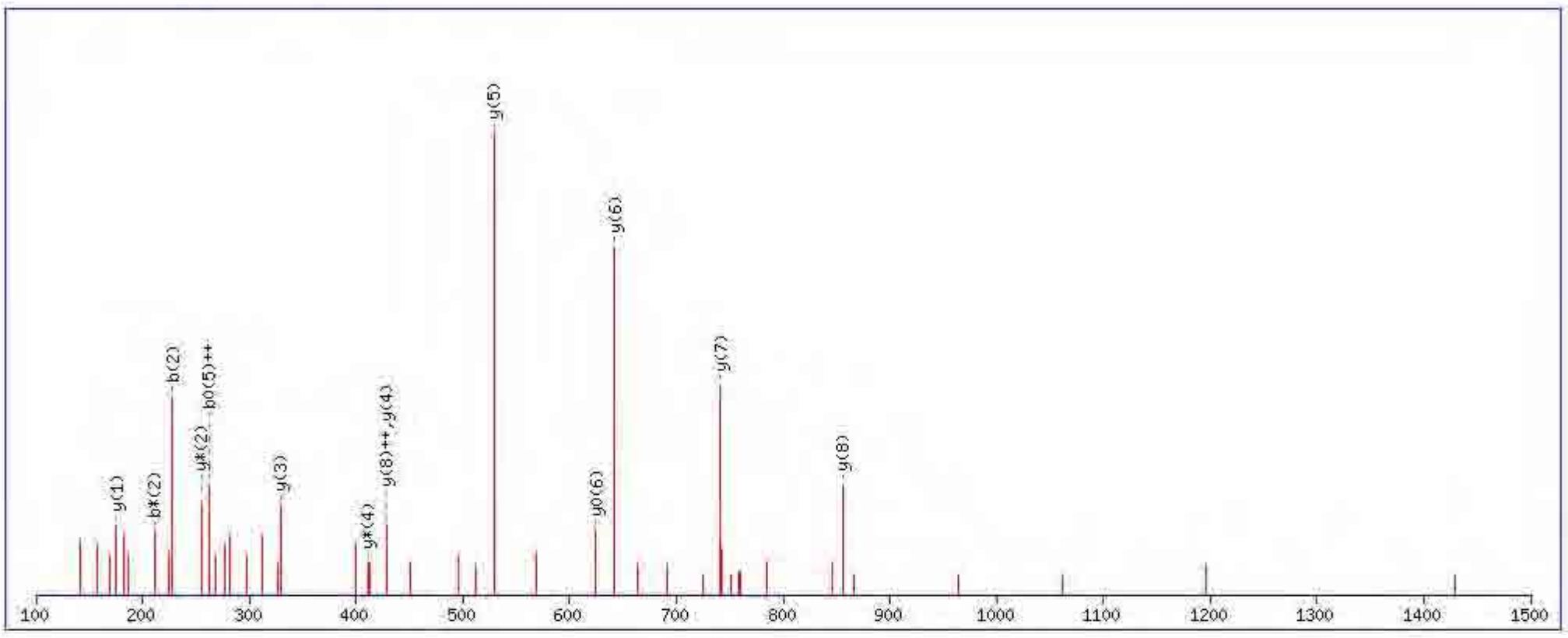
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNVITVGPR**
Found in **CATA_HUMAN**, Catalase OS=Homo sapiens GN=CAT PE=1 SV=3

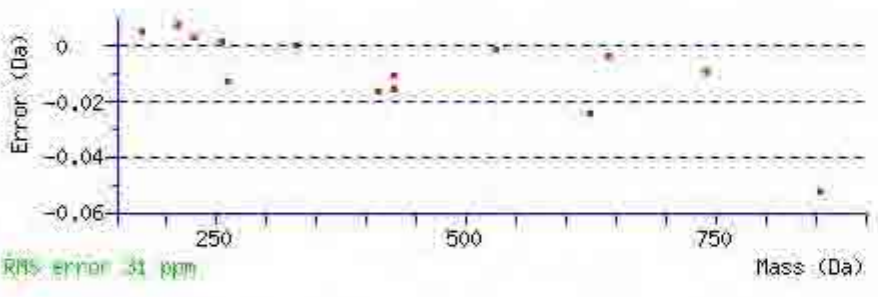
Match to Query 3663: 967.572088 from(484.793320,2+) rtinseconds(1351) index(6544)
Title: Locus:1.1.1.1530.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

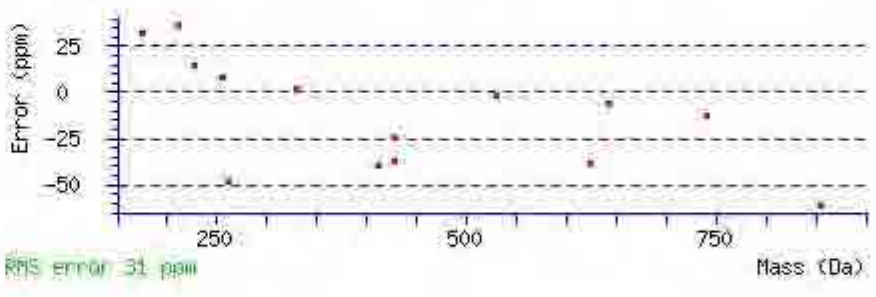
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 967.581467
Ions Score: 45 **Expect:** 0.0021
Matches : 14/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	228.134267	114.570771	211.107718	106.057497			N	*855.504678*	428.255977	838.478129	419.742703	837.494113	419.250695	8
3	327.202681	164.104978	310.176132	155.591704			V	*741.461751*	371.234514	724.435202	362.721239	723.451186	362.229231	7
4	440.286745	220.647010	423.260196	212.133736			I	*642.393337*	321.700307	625.366788	313.187032	624.382772	312.695024	6
5	541.334424	271.170850	524.307875	262.657576	523.323859	262.165568	T	*529.309273*	265.158275	512.282724	256.645000	511.298708	256.152992	5
6	640.402838	320.705057	623.376289	312.191782	622.392273	311.699774	V	*428.261594*	214.634435	411.235045	206.121161			4
7	697.424302	349.215789	680.397753	340.702515	679.413737	340.210507	G	*329.193180*	165.100228	312.166631	156.586954			3
8	794.477066	397.742171	777.450517	389.228897	776.466501	388.736889	P	272.171716	136.589496	255.145167	128.076222			2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LNVITVGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	967.581467	-0.009379	LNVITVGPR
18.1	967.581467	-0.009379	RAVTPVPTK
13.1	967.570206	0.001882	PNSIIPALK
12.6	967.581451	-0.009363	LNVAIVRPS
12.6	967.570221	0.001867	LNVVLEGPK
12.5	967.581482	-0.009394	KVVLGGPGGGK
12.1	967.581451	-0.009363	PLNVLKPR
12.1	967.581467	-0.009379	LLVGGQPLR
10.7	967.581436	-0.009348	LNPDLIRK
10.5	967.581467	-0.009379	LRGLPGQLV

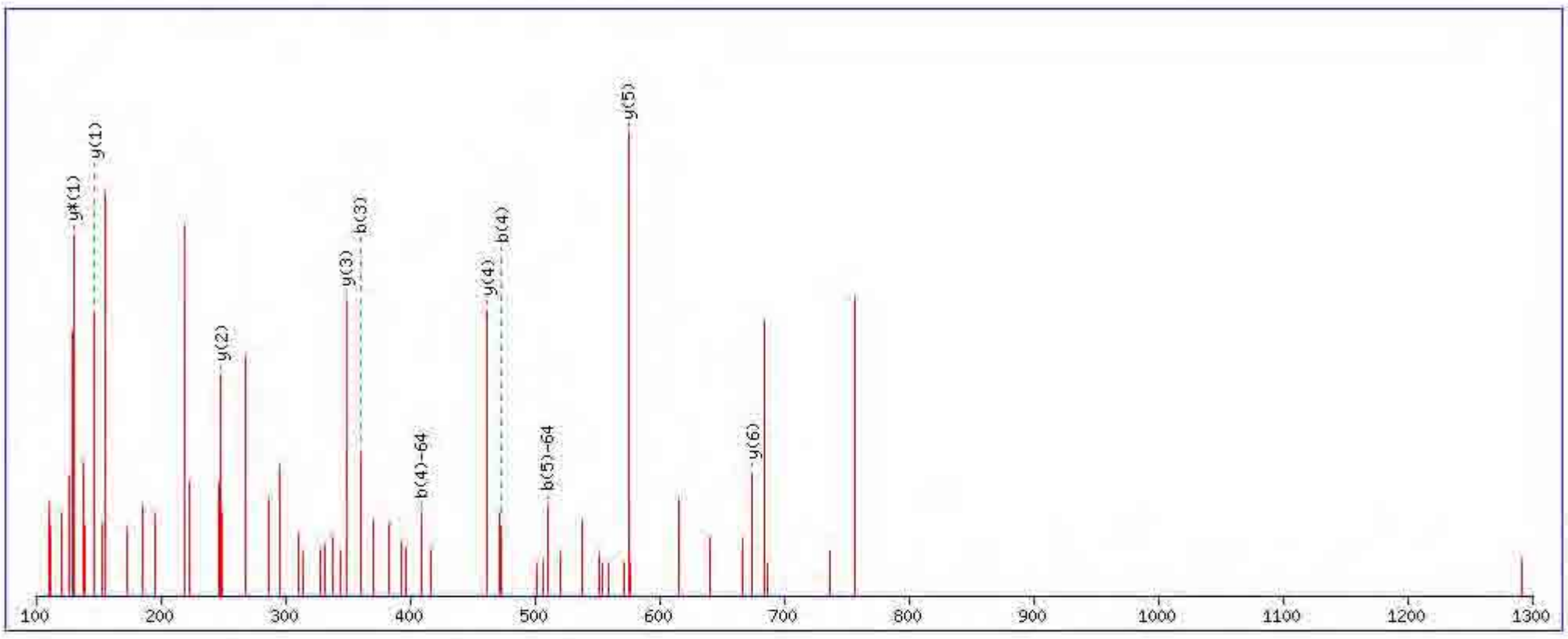
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVIITTK**
Found in **CXL14_HUMAN**, C-X-C motif chemokine 14 OS=Homo sapiens GN=CXCL14 PE=1 SV=2

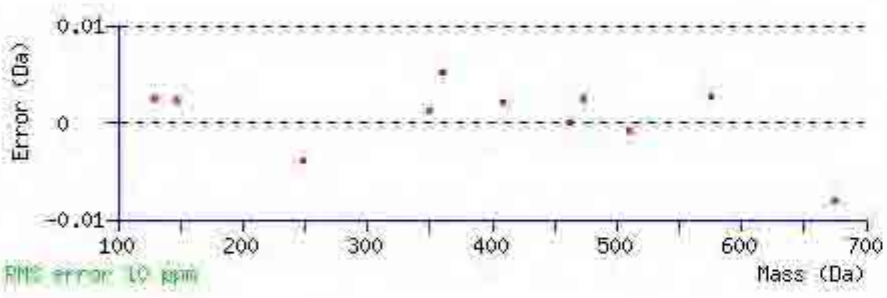
Match to Query 1014: 820.469908 from(411.242230,2+) rtinseconds(767) index(1624)
Title: Locus:1.1.1.1200.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

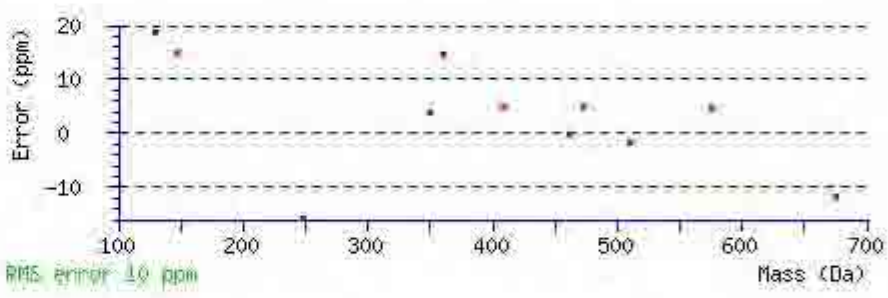
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 820.472824
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 44 **Expect:** 0.002
Matches : 11/66 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976			M							7
2	247.111090	124.059183			V	*674.444704*	337.725990	657.418155	329.212716	656.434139	328.720708	6
3	**360.195154**	180.601215			I	*575.376290*	288.191783	558.349741	279.678509	557.365725	279.186501	5
4	**473.279218**	237.143247			I	*462.292226*	231.649751	445.265677	223.136476	444.281661	222.644468	4
5	574.326897	287.667087	556.316332	278.661804	T	*349.208162*	175.107719	332.181613	166.594444	331.197597	166.102436	3
6	675.374576	338.190926	657.364011	329.185644	T	*248.160483*	124.583879	231.133934	116.070605	230.149918	115.578597	2
7					K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of MVIITTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.9	820.472824	-0.002916	MVIITTK
43.9	820.472824	-0.002916	MVLITTK
20.0	820.469467	0.000441	FVLDVTK
13.4	820.469467	0.000441	IFVPTTK
10.7	820.469467	0.000441	VFLISGVS
4.8	820.469452	0.000456	FVLKSEV
4.7	820.469437	0.000471	IKGYIVE
3.3	820.469467	0.000441	FVLKVTD
2.0	820.469437	0.000471	KLYGLLD
1.5	820.462921	0.006987	FVCALLR

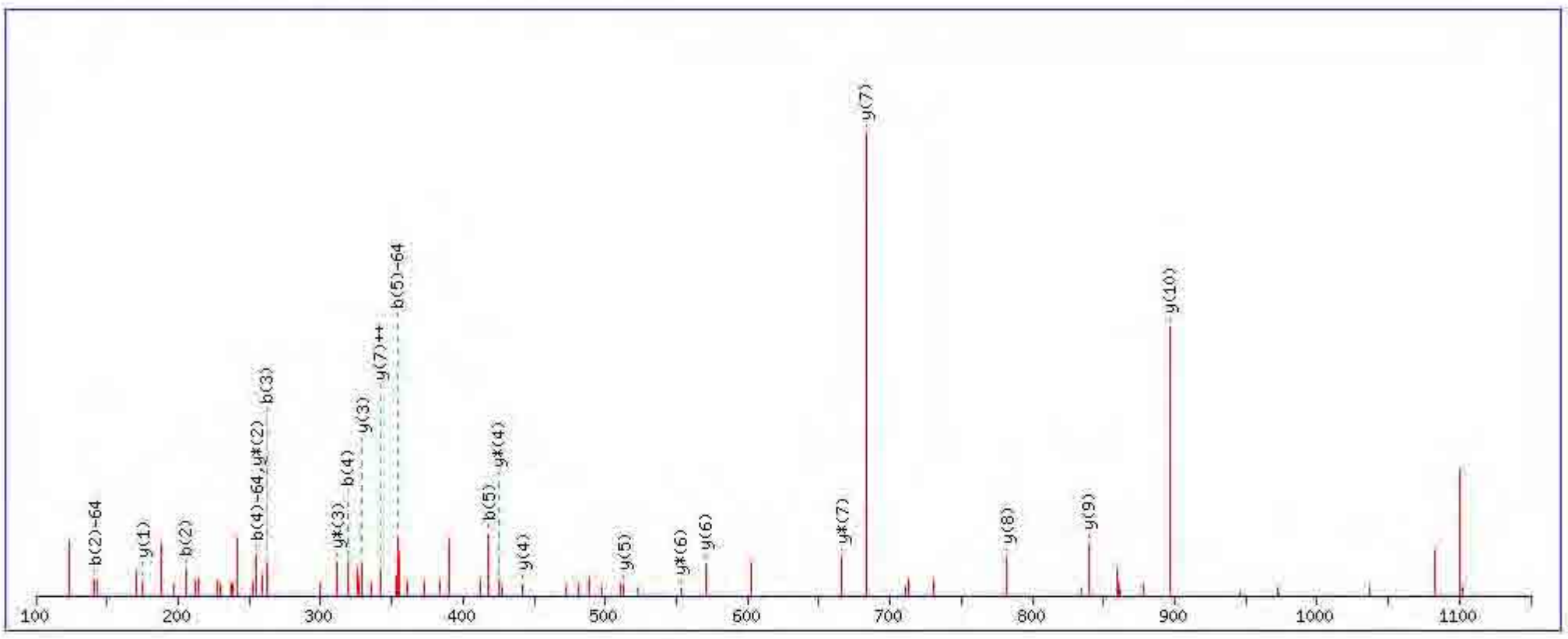
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMGGVPGALGPR**
Found in **CO8A1_HUMAN**, Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1 SV=2

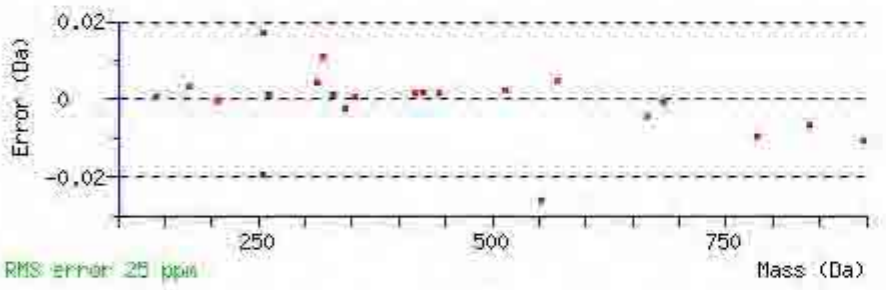
Match to Query 6039: 1099.544628 from(550.779590,2+) rtinseconds(850) index(2161)
Title: Locus:1.1.1.1246.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

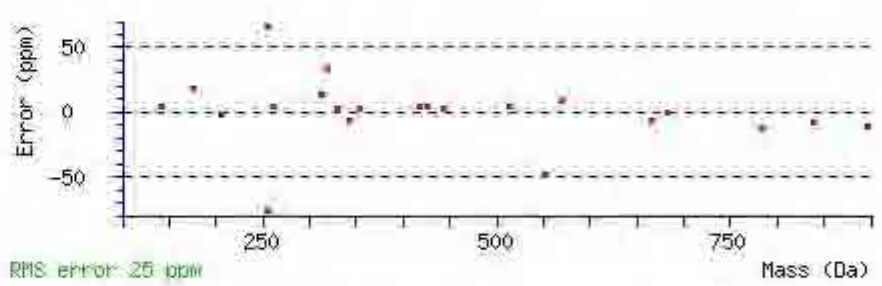
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1099.544449
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
P6 : Oxidation (P)
Ions Score: 45 Expect: 0.0091
Matches : 22/90 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008	G					12
2	**205.064140**	103.035708	M	1043.530243	522.268760	1026.503694	513.755485	11
3	**262.085604**	131.546440	G	***896.494843***	448.751060	879.468294	440.237785	10
4	**319.107068**	160.057172	G	***839.473379***	420.240328	822.446830	411.727053	9
5	**418.175482**	209.591379	V	***782.451915***	391.729596	765.425366	383.216321	8
6	531.223161	266.115219	P	***683.383501***	342.195389	666.356952	333.682114	7
7	588.244625	294.625951	G	***570.335822***	285.671549	553.309273	277.158275	6
8	659.281739	330.144508	A	***513.314358***	257.160817	496.287809	248.647543	5
9	772.365803	386.686540	L	***442.277244***	221.642260	425.250695	213.128986	4
10	829.387267	415.197272	G	***329.193180***	165.100228	312.166631	156.586953	3
11	926.440031	463.723654	P	272.171716	136.589496	255.145167	128.076221	2
12			R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of GMGGVPGALGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	1099.544449	0.000179	GMGGVPGALGPR
21.9	1099.548447	-0.003819	MGFFLARDK
14.4	1099.544449	0.000179	GMGGVPGALGPR
14.4	1099.550949	-0.006321	LAQEKPVGQD
11.9	1099.537033	0.007595	PQASGPPRSR
10.3	1099.548431	-0.003803	NMRALFGLY
10.3	1099.540588	0.004040	KCSVMFIGSL
8.6	1099.537018	0.007610	SSSRPSAGSHK
8.1	1099.544434	0.000194	TPLMHAVSGR
7.8	1099.537033	0.007595	GAPASGPPSRR

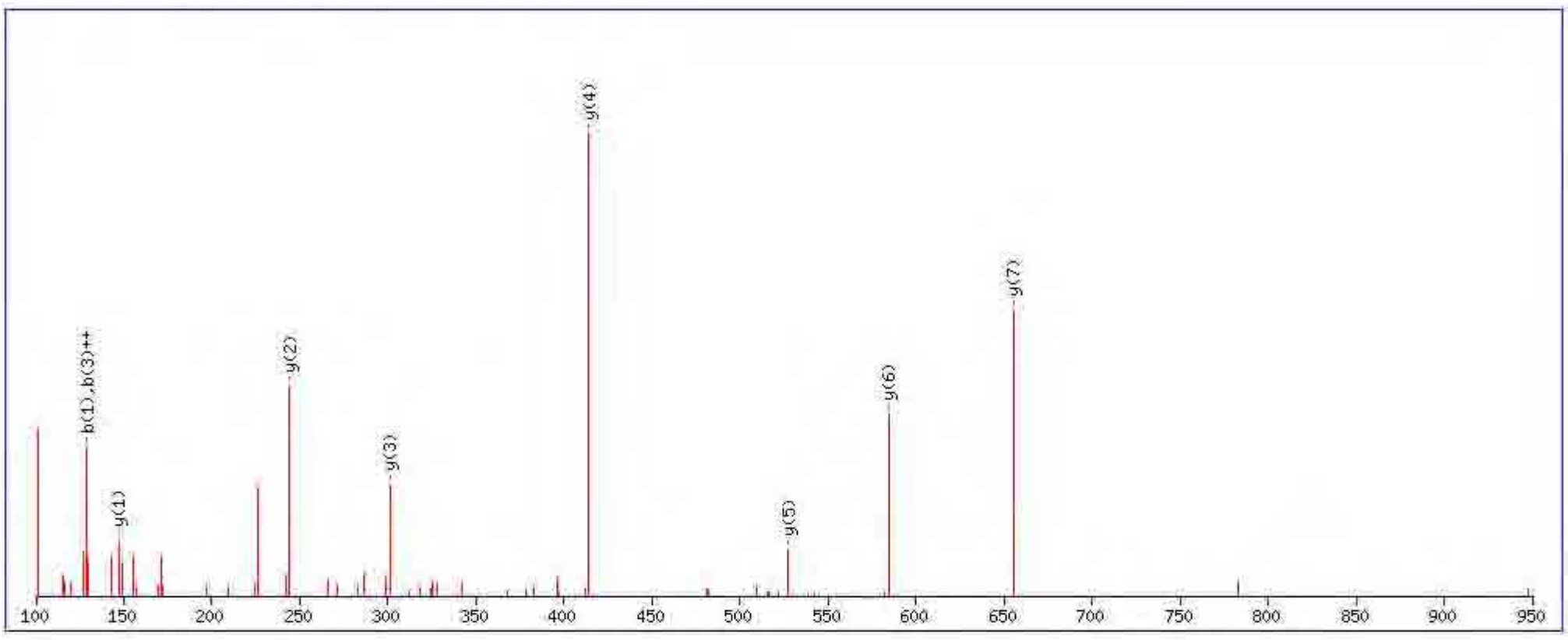
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAGPPGPK**
Found in **CO9A2_HUMAN**, Collagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2

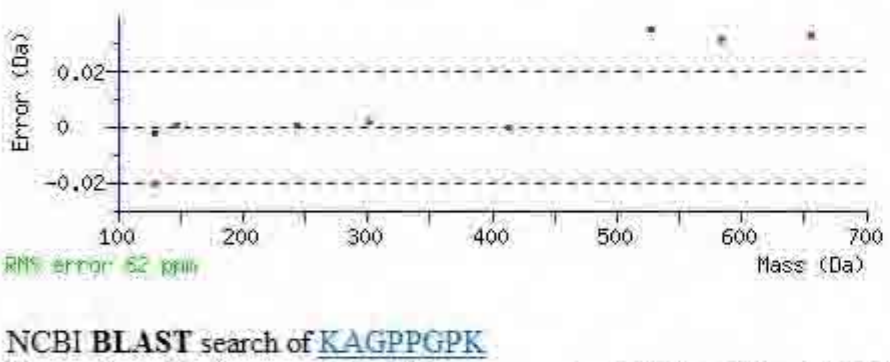
Match to Query 630: 782.426688 from(392.220620,2+) rtinseconds(562) index(755)
Title: Locus:1.1.1.1088.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

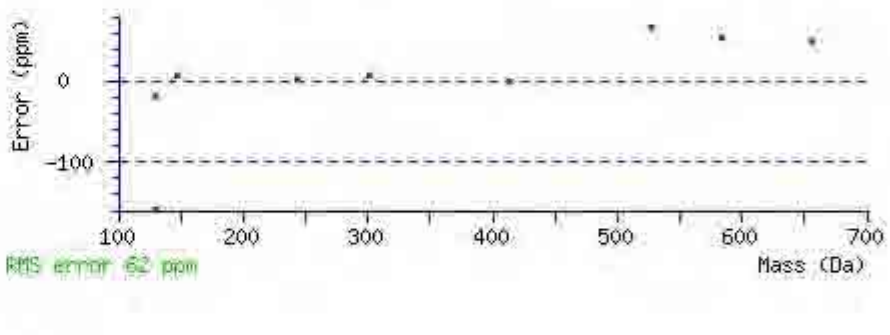
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 782.428650
Variable modifications:
P4 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 53 **Expect:** 0.00045
Matches : 9/56 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.102239	65.054757	112.075690	56.541483	K					8
2	200.139353	100.573315	183.112804	92.060040	A	*655.340968*	328.174122	638.314419	319.660848	7
3	257.160817	129.084047	240.134268	120.570772	G	*584.303854*	292.655565	567.277305	284.142291	6
4	370.208496	185.607886	353.181947	177.094612	P	*527.282390*	264.144833	510.255841	255.631559	5
5	483.256175	242.131726	466.229626	233.618451	P	*414.234711*	207.620994	397.208162	199.107719	4
6	540.277639	270.642458	523.251090	262.129183	G	*301.187032*	151.097154	284.160483	142.583880	3
7	637.330403	319.168840	620.303854	310.655565	P	*244.165568*	122.586422	227.139019	114.073148	2
8					K	*147.112804*	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of KAGPPGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	782.428650	-0.001962	KAGPPGPK
49.8	782.428650	-0.001962	GAAGLPGPK
37.3	782.428650	-0.001962	AKGPPGPK
30.8	782.428650	-0.001962	KPKPGPGA
24.8	782.428650	-0.001962	KAGPPGPK
24.2	782.428635	-0.001947	AANLPGPK
23.4	782.428650	-0.001962	GAAGLPGPK
16.9	782.428650	-0.001962	GPSGLAGPK
16.6	782.428665	-0.001977	GAPGVTGPK
15.3	782.428650	-0.001962	QPSVAPGK

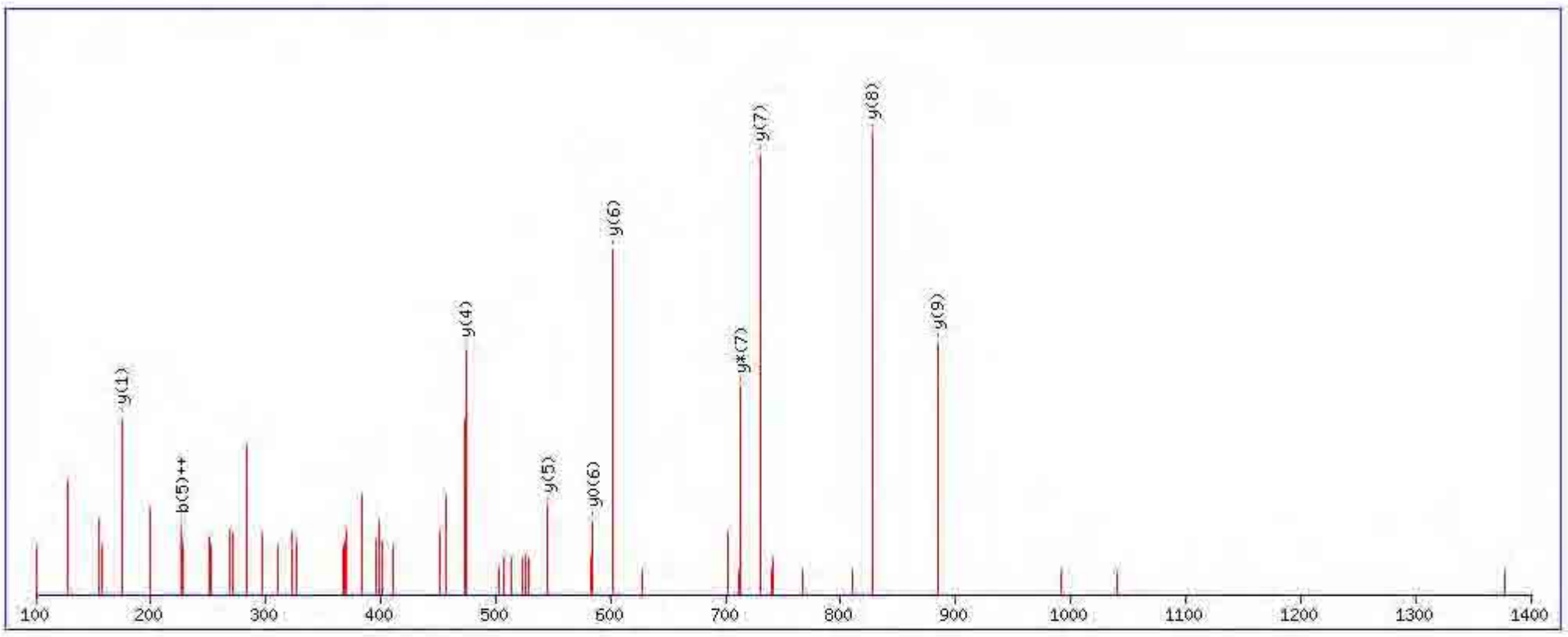
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPKGAPGER**
Found in **CO9A3_HUMAN**, Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2

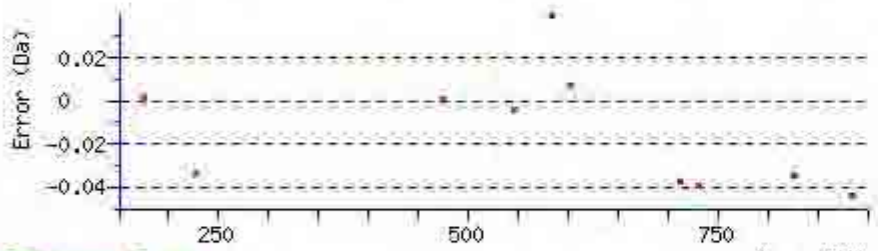
Match to Query 4160: 996.499688 from(499.257120,2+) rtinseconds(572) index(780)
Title: Locus:1.1.1.1093.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

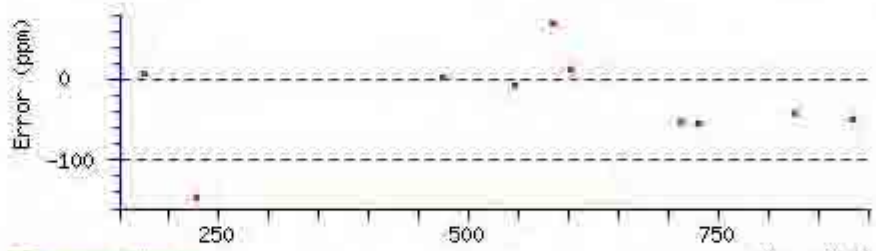
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 996.498856
Variable modifications:
P1 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 50 **Expect:** 0.0017
Matches : 10/84 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.054955	57.531116					P							10
2	171.076419	86.041847					G	*884.458457*	442.732867	867.431908	434.219592	866.447892	433.727584	9
3	268.129183	134.568229					P	*827.436993*	414.222135	810.410444	405.708860	809.426428	405.216852	8
4	396.224146	198.615711	379.197597	190.102436			K	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	7
5	453.245610	227.126443	436.219061	218.613168			G	*602.289266*	301.648271	585.262717	293.134997	584.278701	292.642989	6
6	524.282724	262.645000	507.256175	254.131726			A	*545.267802*	273.137539	528.241253	264.624265	527.257237	264.132257	5
7	637.330403	319.168840	620.303854	310.655565			P	*474.230688*	237.618982	457.204139	229.105708	456.220123	228.613700	4
8	694.351867	347.679572	677.325318	339.166297			G	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
9	823.394460	412.200868	806.367911	403.687594	805.383895	403.195586	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PGPKGAPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	996.498856	0.000832	PGPKGAPGER
31.4	996.498856	0.000832	PGPKGAPGER
24.1	996.498856	0.000832	PGPAGPKGER
23.3	996.498871	0.000817	LGPPQGGSPR
21.4	996.498871	0.000817	PGPSGPPGKR
20.7	996.498871	0.000817	PGQPGLPGSR
20.1	996.498856	0.000832	PGPQAGAGAGAK
18.4	996.498856	0.000832	GPPGGAPEKR
16.1	996.498871	0.000817	PGPSGPPGKR
16.1	996.498871	0.000817	PPGPAGKPGR

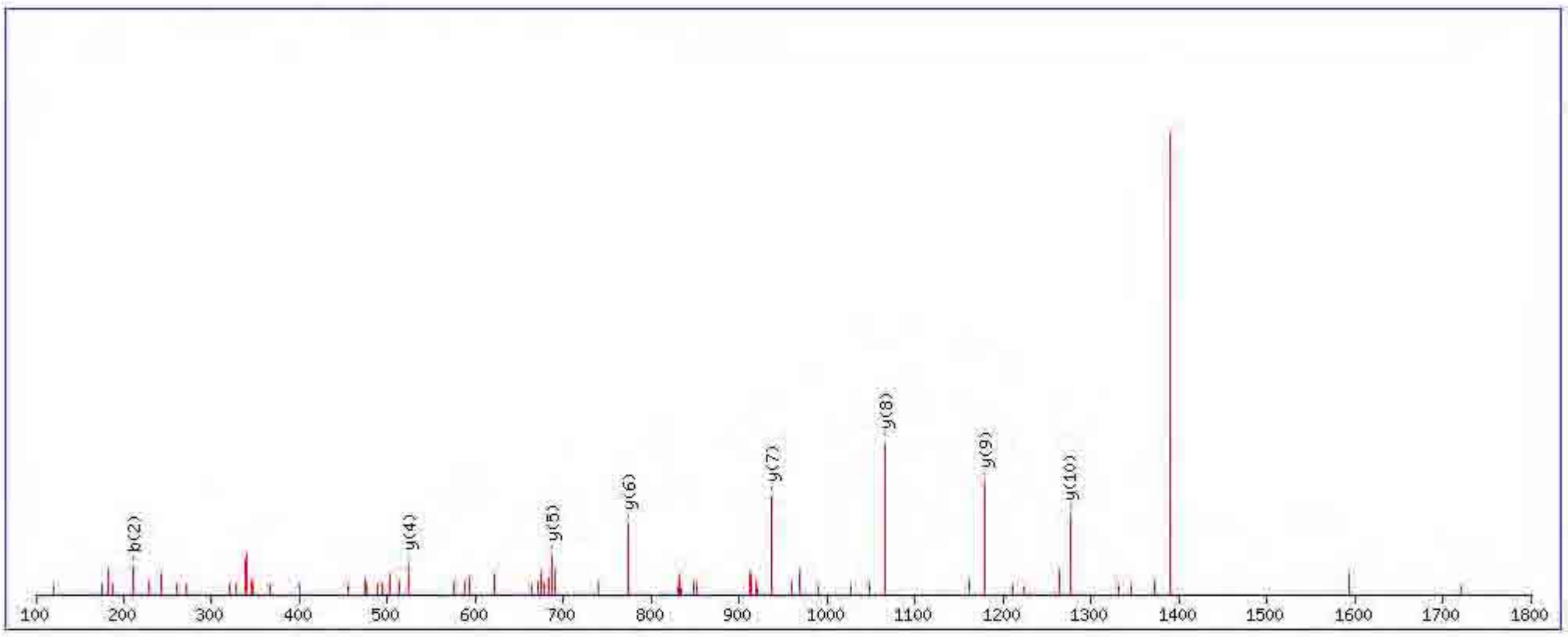
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

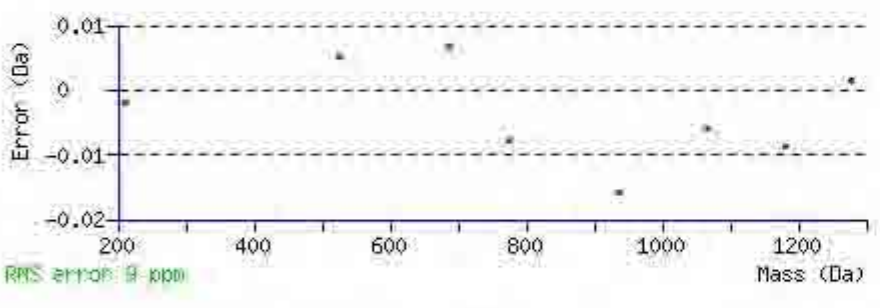
Match to Query 11608: 1388.662948 from(695.338750,2+) rtinseconds(1610) index(9440)
Title: Locus:1.1.1.1671.18
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

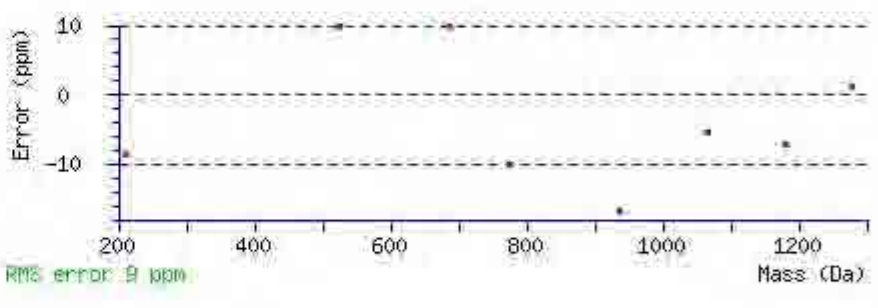
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 51 **Expect:** 0.00074
Matches : 8/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	*1276.584445*	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	*1179.531681*	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	*1066.447617*	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	*937.405024*	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	*774.341695*	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	*687.309667*	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	*524.246338*	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	1388.661194	0.001754	LPLEYSYGEYR
16.3	1388.667953	-0.005005	IPELLASGMVDNM
14.8	1388.667114	-0.004166	PPPELTDTATSTK
14.6	1388.657211	0.005737	LPEDQPPGPAALH
11.2	1388.658066	0.004882	IHLGGKPYLCGEC
8.7	1388.671082	-0.008134	IPELEEAELFAE
8.1	1388.667130	-0.004182	IPTPVEGSDSVSSV
5.8	1388.658051	0.004897	LPEHCIEYVRM
5.2	1388.667984	-0.005036	IPPMGLDCLSQVT
4.2	1388.664612	-0.001664	PPPPAPDMTFKK

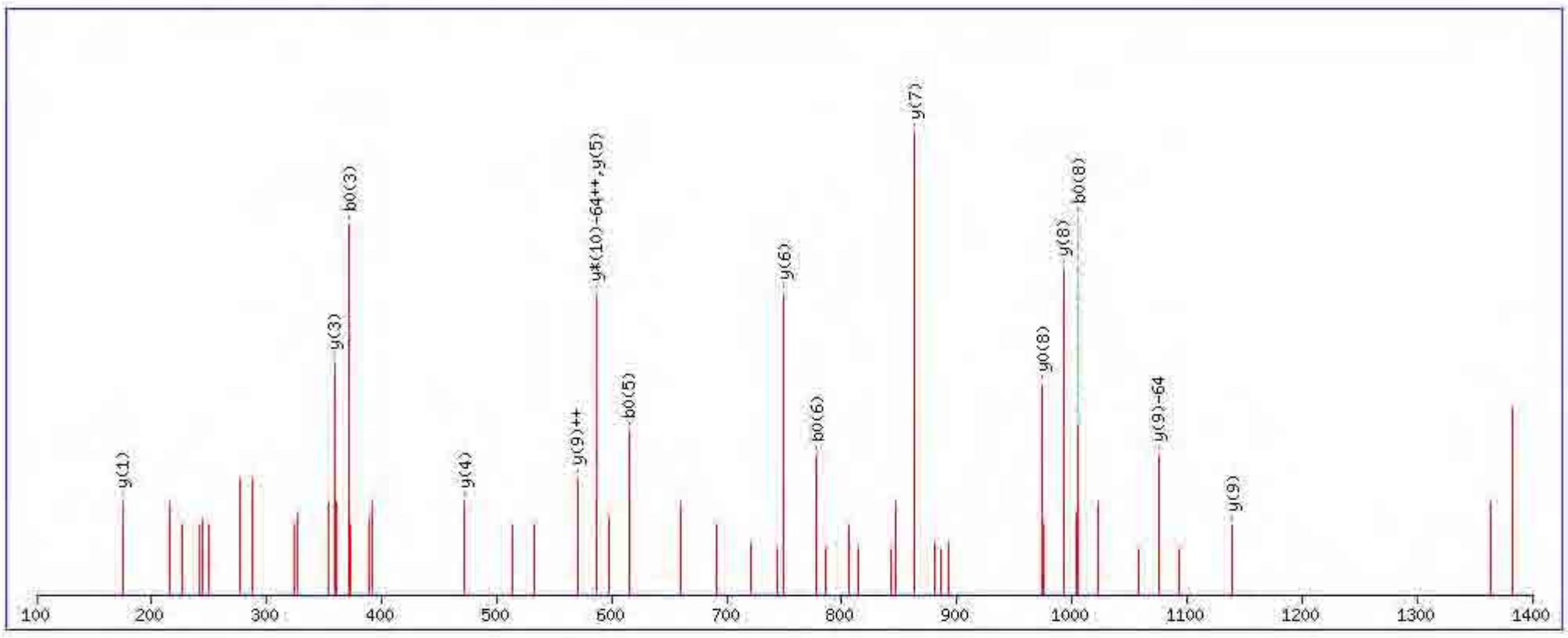
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

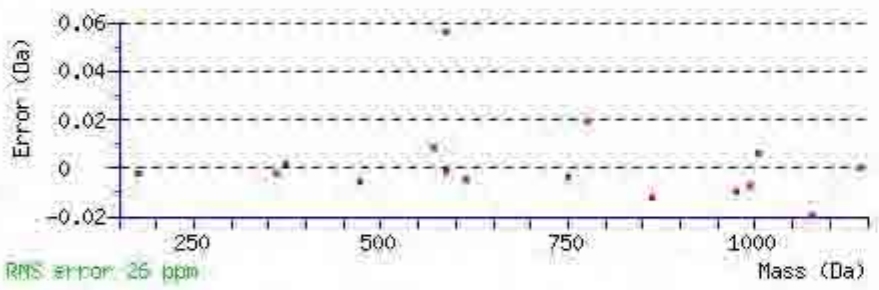
Match to Query 11482: 1380.666008 from(691.340280,2+) rtinseconds(1480) index(7965)
Title: Locus:1.1.1.1600.24
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

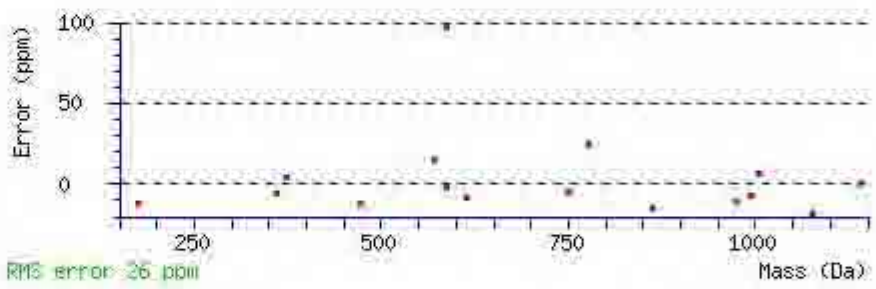
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 52 **Expect:** 0.00099
Matches : 16/154 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1252.635434	626.821355	1235.608885	618.308081	1234.624869	617.816073	10
3	390.169333	195.588304			372.158768	186.583022	M	*1139.551370*	570.279323	1122.524821	561.766049	1121.540805	561.274040	9
4	519.211926	260.109601			501.201361	251.104319	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	633.254853	317.131065	616.228304	308.617790	615.244288	308.125782	N	*863.473377*	432.240326	846.446828	423.727052			7
6	796.318182	398.662729	779.291633	390.149454	778.307617	389.657446	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	910.361109	455.684192	893.334560	447.170918	892.350544	446.678910	N	*586.367121*	293.687199	569.340572	285.173924			5
8	1023.445173	512.226224	1006.418624	503.712950	1005.434608	503.220942	I	*472.324194*	236.665735	455.297645	228.152460			4
9	1094.482287	547.744782	1077.455738	539.231507	1076.471722	538.739499	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1207.566351	604.286813	1190.539802	595.773539	1189.555786	595.281531	L	288.203016	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	1380.670700	-0.004692	EIMENYNIALR
18.9	1380.659500	0.006508	MELENYKQPVV
17.1	1380.663330	0.002678	LIYRSGGEDESR
8.1	1380.659485	0.006523	YIPEDEALMLR
8.0	1380.664215	0.001793	TVNMTWNKICR
6.5	1380.663361	0.002647	QPAQDTAPTPAPR
5.6	1380.674103	-0.008095	TLGSLMNIKNMSG
4.8	1380.670715	-0.004707	LEMKYALDPNR
4.5	1380.663361	0.002647	PVDNQPPEVTNR
4.5	1380.670731	-0.004723	IELYDCQQITR

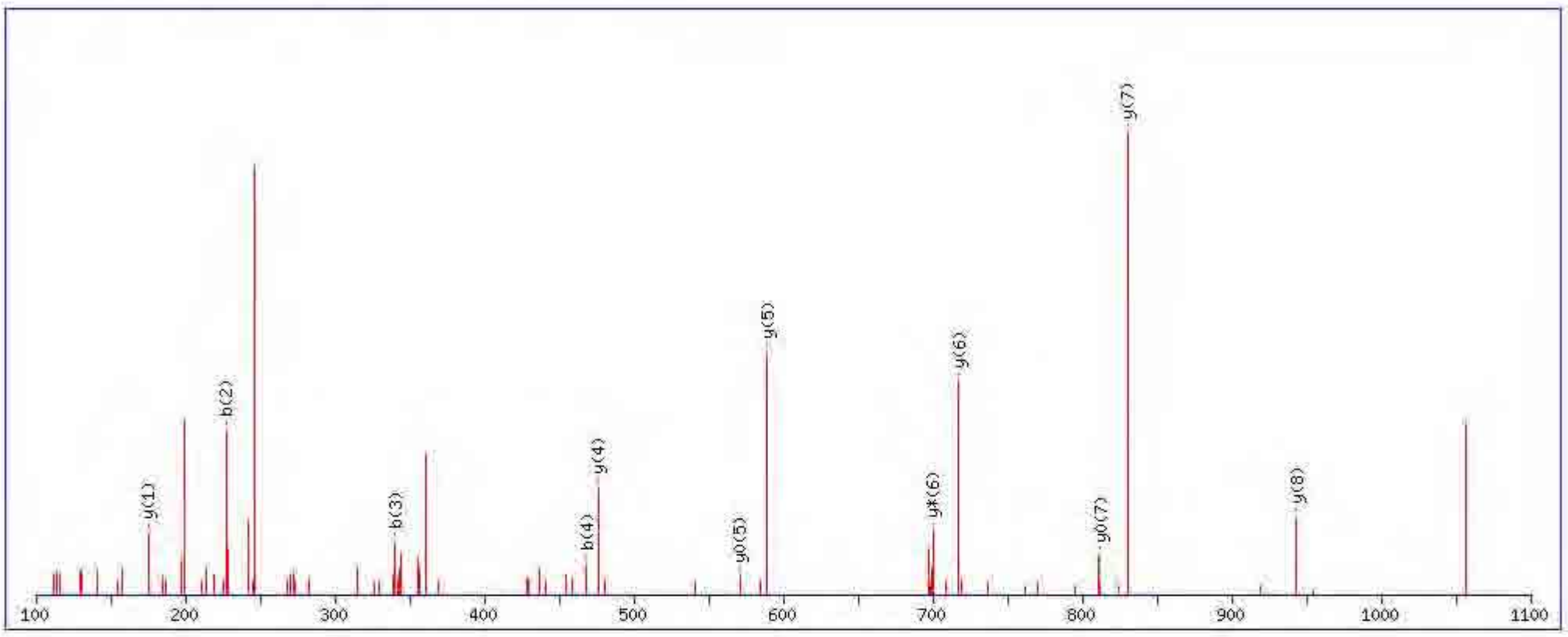
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPQLTSPR**
Found in **CAND1_HUMAN**, Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2

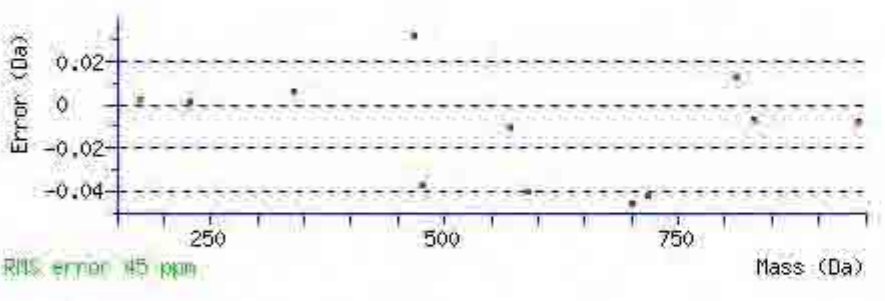
Match to Query 5181: 1055.596868 from(528.805710,2+) rtinseconds(1558) index(8809)
Title: Locus:1.1.1.1644.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

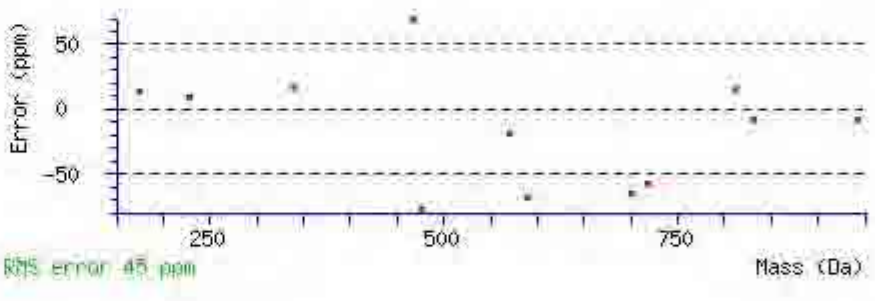
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597504
Variable modifications:
P3 : Oxidation (P)
P8 : Oxidation (P)
Ions Score: 44 **Expect:** 0.0038
Matches : 12/76 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*943.520723*	472.264000	926.494174	463.750725	925.510158	463.258717	8
3	340.223083	170.615179					P	*830.436659*	415.721968	813.410110	407.208693	812.426094	406.716685	7
4	468.281661	234.644468	451.255112	226.131194			Q	*717.388980*	359.198128	700.362431	350.684853	699.378415	350.192845	6
5	581.365725	291.186501	564.339176	282.673226			L	*589.330402*	295.168839	572.303853	286.655565	571.319837	286.163557	5
6	682.413404	341.710340	665.386855	333.197066	664.402839	332.705058	T	*476.246338*	238.626807	459.219789	230.113532	458.235773	229.621524	4
7	769.445432	385.226354	752.418883	376.713079	751.434867	376.221071	S	375.198659	188.102967	358.172110	179.589693	357.188094	179.097685	3
8	882.493111	441.750194	865.466562	433.236919	864.482546	432.744911	P	288.166631	144.586953	271.140082	136.073679			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLPQLTSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	1055.597488	-0.000620	PLIKVEEGR
44.1	1055.597504	-0.000636	LLPQLTSPR
28.7	1055.597488	-0.000620	LLKLDPADR
23.1	1055.601532	-0.004664	ILLGLWVQD
22.1	1055.604874	-0.008006	ILLIKNMDP
20.5	1055.597488	-0.000620	LGPLALETAR
17.3	1055.590302	0.006566	IIIFPPIPD
17.3	1055.590302	0.006566	IIIFPPIPD
16.2	1055.597473	-0.000605	ILLLADENR
16.2	1055.597504	-0.000636	IPLVSDPKR

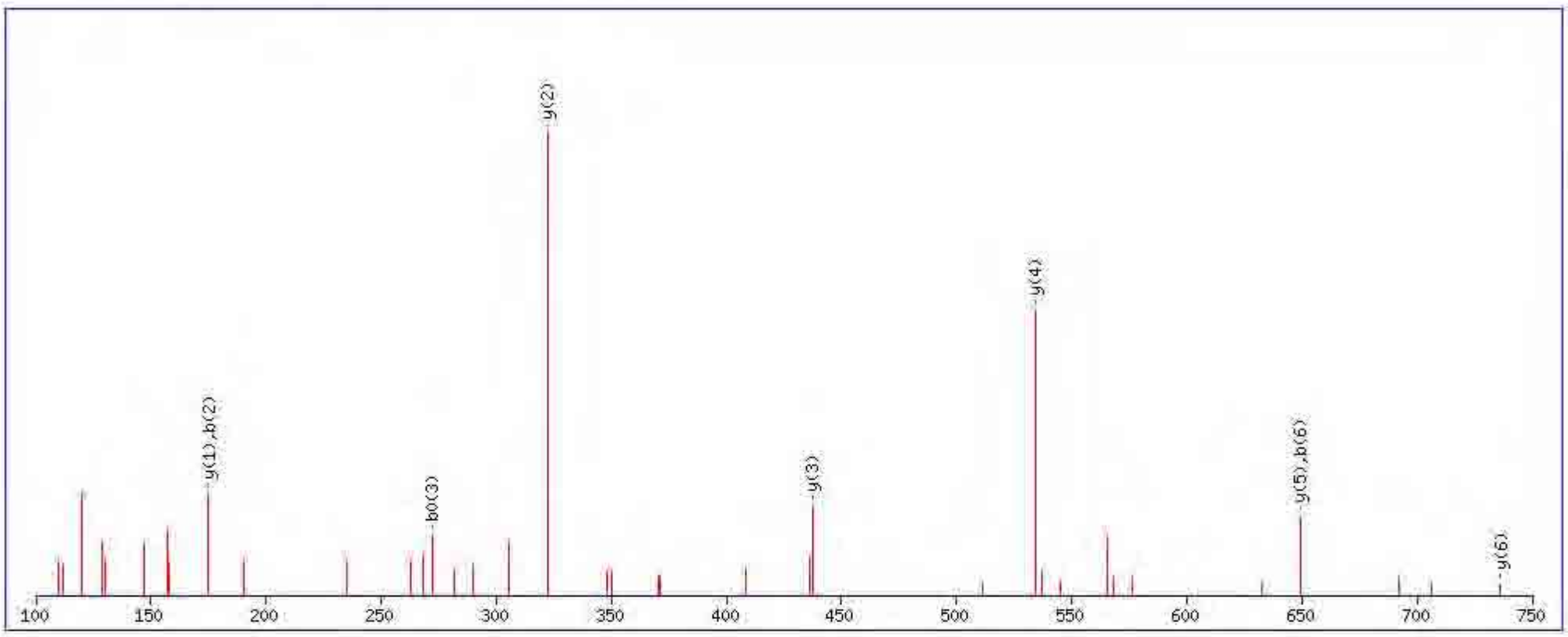
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSDPDFR**
Found in **DSC3_HUMAN**, Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3

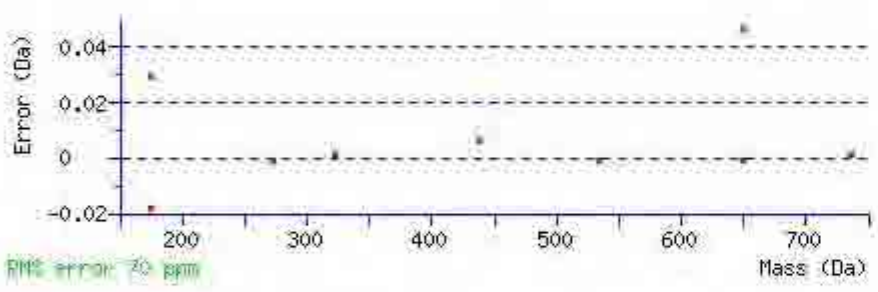
Match to Query 1030: 822.352548 from(412.183550,2+) rtinseconds(598) index(847)
Title: Locus:1.1.1.1108.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

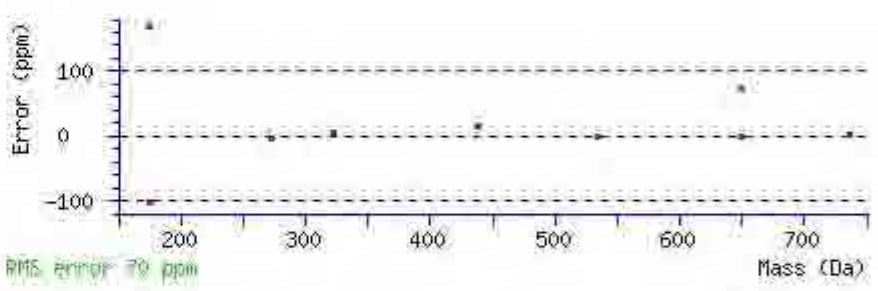
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 822.350800
Ions Score: 68 **Expect:** 1.3e-005
Matches : 9/56 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	175.071332	88.039304	157.060767	79.034021	S	736.326044	368.666660	719.299495	360.153386	718.315479	359.661378	6
3	290.098275	145.552776	272.087710	136.547493	D	649.294016	325.150646	632.267467	316.637372	631.283451	316.145364	5
4	387.151039	194.079158	369.140474	185.073875	P	534.267073	267.637175	517.240524	259.123900	516.256508	258.631892	4
5	502.177982	251.592629	484.167417	242.587347	D	437.214309	219.110793	420.187760	210.597518	419.203744	210.105510	3
6	649.246396	325.126836	631.235831	316.121554	F	322.187366	161.597321	305.160817	153.084047			2
7					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SSDPDFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	822.350800	0.001748	SSDPDFR
31.8	822.350800	0.001748	SAPDFDR
27.7	822.346771	0.005777	SSDAGSGSR
23.5	822.354156	-0.001608	SAVEMDR
20.7	822.354172	-0.001624	DSSPVMR
18.8	822.350769	0.001779	EEENFR
18.3	822.347626	0.004922	SQGNMMR
18.1	822.347641	0.004907	SCVGGMNR
18.1	822.350784	0.001764	SGEDYPR
16.8	822.350784	0.001764	AGEEDFR

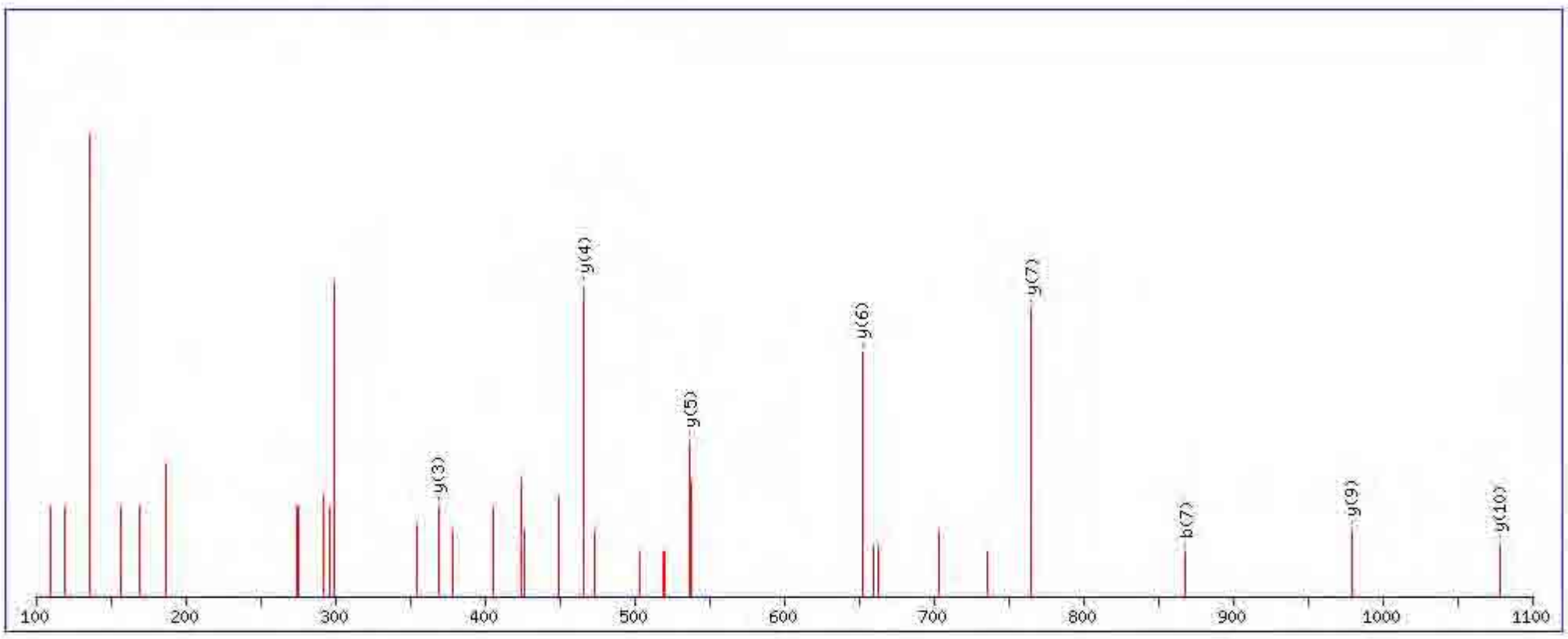
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYVTIIDAPGHR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

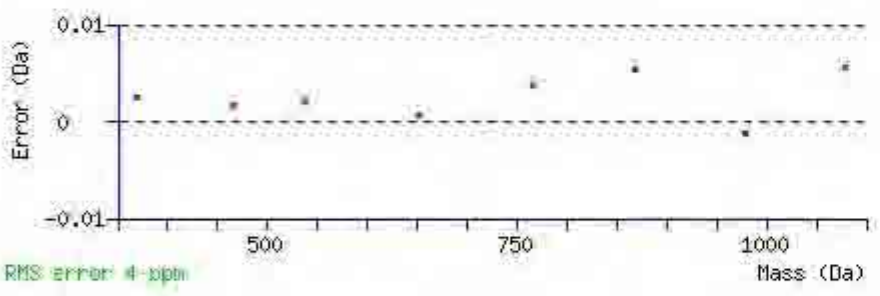
Match to Query 11772: 1403.716422 from(468.912750,3+) rtinseconds(1452) index(7638)
Title: Locus:1.1.1.1586.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

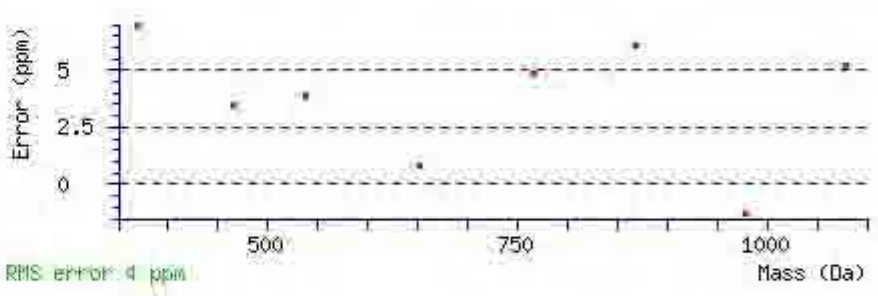
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1403.719742
Ions Score: 55 **Expect:** 2.9e-005
Matches : 8/94 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							12
2	327.133934	164.070605			Y	1241.663699	621.335487	1224.637150	612.822213	1223.653134	612.330205	11
3	426.202348	213.604812			V	*1078.600370*	539.803823	1061.573821	531.290549	1060.589805	530.798540	10
4	527.250027	264.128652	509.239462	255.123369	T	*979.531956*	490.269616	962.505407	481.756341	961.521391	481.264333	9
5	640.334091	320.670684	622.323526	311.665401	I	878.484277	439.745776	861.457728	431.232502	860.473712	430.740494	8
6	753.418155	377.212716	735.407590	368.207433	I	*765.400213*	383.203744	748.373664	374.690470	747.389648	374.198462	7
7	868.445098	434.726187	850.434533	425.720905	D	*652.316149*	326.661712	635.289600	318.148438	634.305584	317.656430	6
8	939.482212	470.244744	921.471647	461.239462	A	*537.289206*	269.148241	520.262657	260.634966			5
9	1036.534976	518.771126	1018.524411	509.765843	P	*466.252092*	233.629684	449.225543	225.116409			4
10	1093.556440	547.281858	1075.545875	538.276575	G	*369.199328*	185.103302	352.172779	176.590027			3
11	1230.615352	615.811314	1212.604787	606.806031	H	312.177864	156.592570	295.151315	148.079295			2
12					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YYVTIIDAPGHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.1	1403.719742	-0.003320	YYVTIIDAPGHR
6.3	1403.729630	-0.013208	KPEAPPPKVPEAP
3.5	1403.715714	0.000708	RGIPPEEPGAPPR
2.5	1403.715714	0.000708	RGIPPEEPGAPPR
2.0	1403.729630	-0.013208	KSIPDVDLNKPY
1.8	1403.723114	-0.006692	NPGLPPLPSMPPR
1.7	1403.726944	-0.010522	APPSPALSRSHPR
1.7	1403.726944	-0.010522	APPSPALSRSHPR
1.7	1403.715729	0.000693	RVPPAPPPEAPGR
1.7	1403.715729	0.000693	RVPPAPPPEAPGR

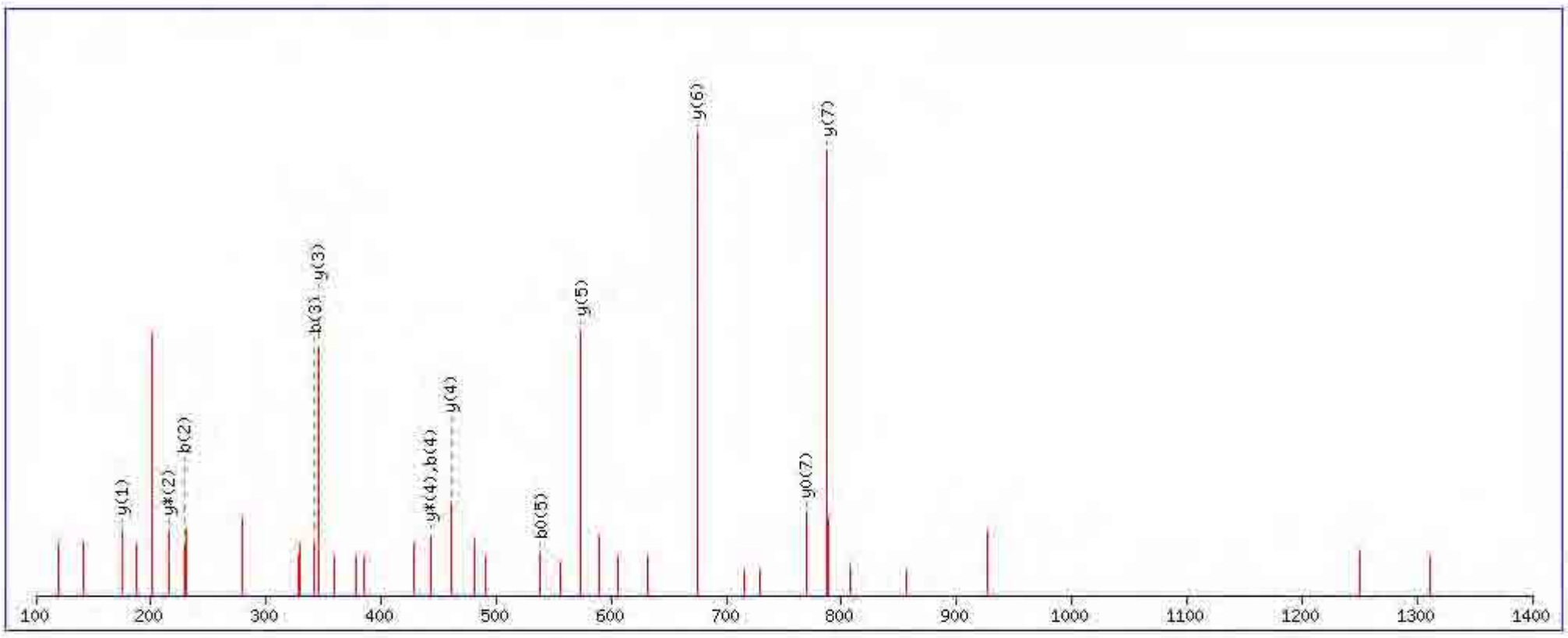
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILTIDIGR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

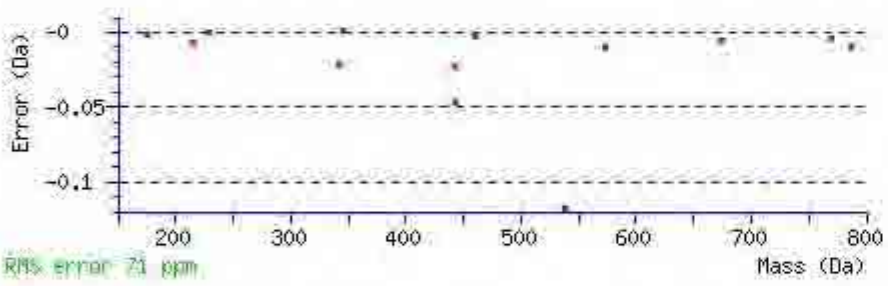
Match to Query 4463: 1014.571868 from(508.293210,2+) rtinseconds(1902) index(12918)
Title: Locus:1.1.1.1832.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

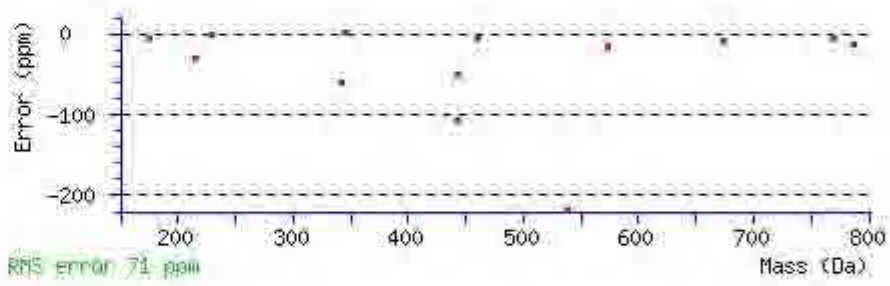
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1014.570953
Ions Score: 37 **Expect:** 0.0053
Matches : 13/74 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	D							9
2	**229.118283**	115.062779	211.107718	106.057497	I	900.551294	450.779285	883.524745	442.266011	882.540729	441.774003	8
3	**342.202347**	171.604811	324.191782	162.599529	L	***787.467230***	394.237253	770.440681	385.723979	769.456665	385.231971	7
4	**443.250026**	222.128651	425.239461	213.123369	T	***674.383166***	337.695221	657.356617	329.181947	656.372601	328.689939	6
5	556.334090	278.670683	538.323525	269.665401	I	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
6	671.361033	336.184155	653.350468	327.178872	D	***460.251423***	230.629350	443.224874	222.116075	442.240858	221.624067	4
7	784.445097	392.726187	766.434532	383.720904	I	***345.224480***	173.115878	328.197931	164.602604			3
8	841.466561	421.236919	823.455996	412.231636	G	232.140416	116.573846	215.113867	108.060572			2
9					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DILTIDIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1014.570953	0.000915	DILTIDIGR
12.0	1014.570953	0.000915	DILVDGKAGK
12.0	1014.564407	0.007461	PMLNKSVAR
10.4	1014.570938	0.000930	VELTKLQAN
9.9	1014.570953	0.000915	LDTTSIPLR
9.7	1014.578339	-0.006471	DLLLTPKCL
8.8	1014.570938	0.000930	NNTPLLSLK
8.7	1014.570969	0.000899	DVTTRITLP
8.0	1014.570938	0.000930	DLIESVLAR
7.7	1014.570953	0.000915	TLDLPALTR

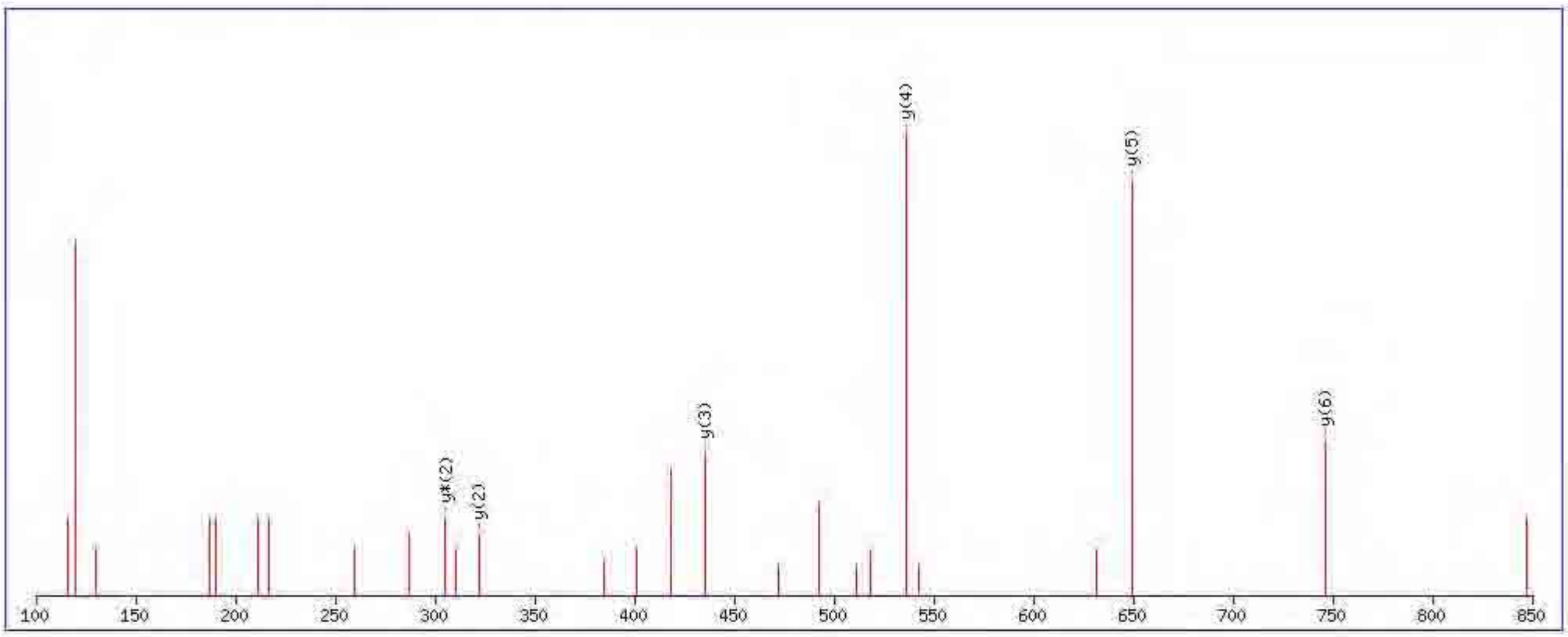
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPITLFR**
Found in **FBLN7_HUMAN**, Fibulin-7 OS=Homo sapiens GN=FBLN7 PE=2 SV=1

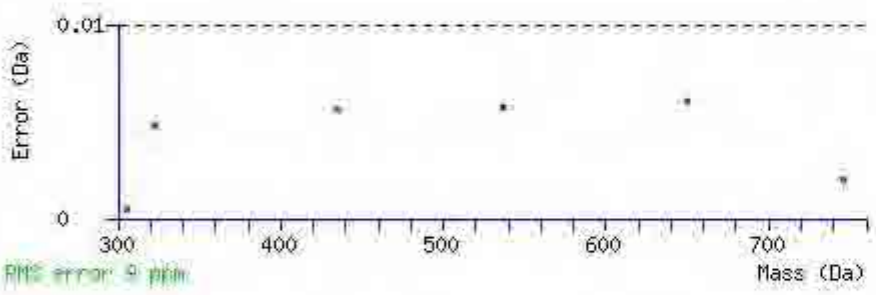
Match to Query 1568: 846.490168 from(424.252360,2+) rtinseconds(1571) index(8969)
Title: Locus:1.1.1.1651.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

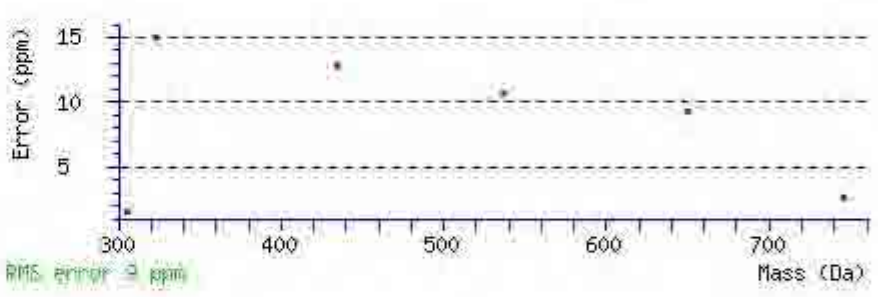
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 846.496338
Ions Score: 48 **Expect:** 0.0012
Matches : 6/54 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							7
2	199.107719	100.057497	181.097154	91.052215	P	*746.455937*	373.731607	729.429388	365.218332	728.445372	364.726324	6
3	312.191783	156.599529	294.181218	147.594247	I	*649.403173*	325.205224	632.376624	316.691950	631.392608	316.199942	5
4	413.239462	207.123369	395.228897	198.118087	T	*536.319109*	268.663193	519.292560	260.149918	518.308544	259.657910	4
5	526.323526	263.665401	508.312961	254.660119	L	*435.271430*	218.139353	418.244881	209.626078			3
6	673.391940	337.199608	655.381375	328.194325	F	*322.187366*	161.597321	305.160817	153.084046			2
7					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TPITLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	846.496338	-0.006170	TPITLFR
15.8	846.496338	-0.006170	TLPITFR
14.5	846.496338	-0.006170	TPIFTLR
14.5	846.496338	-0.006170	TPLFLTR
14.5	846.496338	-0.006170	TPLFTLR
14.5	846.485092	0.005076	TPLLPYK
14.0	846.485123	0.005045	TPFLLVGT
13.4	846.496353	-0.006185	TVIVPFR
7.8	846.496338	-0.006170	LVVRYTP
7.8	846.485123	0.005045	TPATLFVV

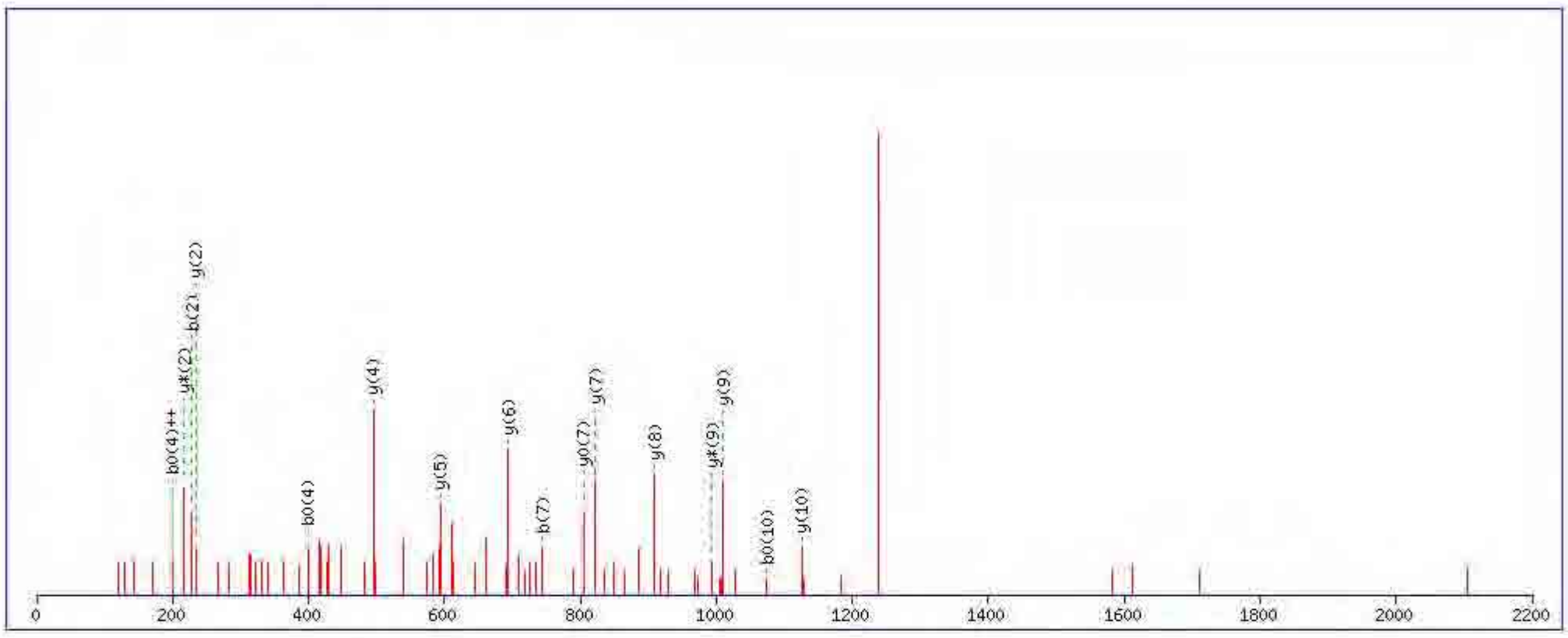
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTSEVVFNSK**
Found in **LEG7_HUMAN**, Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2

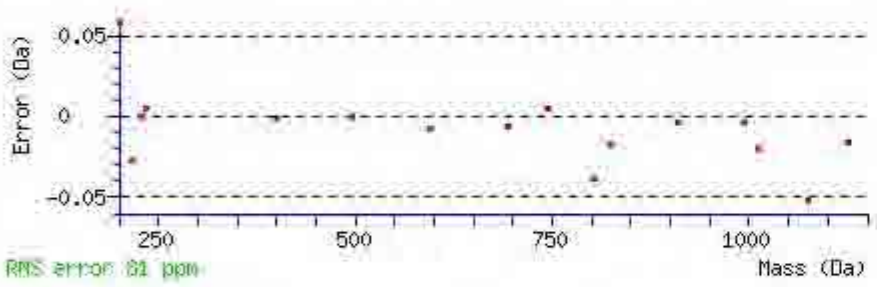
Match to Query 9200: 1237.609708 from(619.812130,2+) rtinseconds(1395) index(7060)
Title: Locus:1.1.1.1554.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

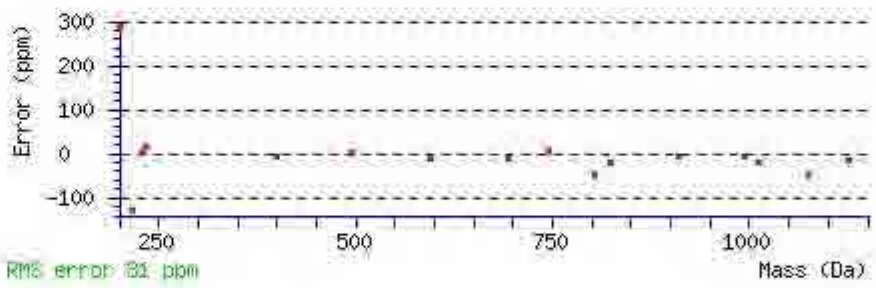
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1237.619034
Ions Score: 68 **Expect:** 6.2e-006
Matches : 16/100 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	**229.118283**	115.062779			211.107718	106.057497	D	*1125.542244*	563.274760	1108.515695	554.761486	1107.531679	554.269477	10
3	330.165962	165.586619			312.155397	156.581336	T	*1010.515301*	505.761288	993.488752	497.248014	992.504736	496.756006	9
4	417.197990	209.102633			399.187425	200.097350	S	*909.467622*	455.237449	892.441073	446.724174	891.457057	446.232166	8
5	546.240583	273.623930			528.230018	264.618647	E	*822.435594*	411.721435	805.409045	403.208160	804.425029	402.716152	7
6	645.308997	323.158137			627.298432	314.152854	V	*693.393001*	347.200138	676.366452	338.686864	675.382436	338.194856	6
7	**744.377411**	372.692343			726.366846	363.687061	V	*594.324587*	297.665932	577.298038	289.152657	576.314022	288.660649	5
8	891.445825	446.226550			873.435260	437.221268	F	*495.256173*	248.131724	478.229624	239.618450	477.245608	239.126442	4
9	1005.488752	503.248014	988.462203	494.734739	987.478187	494.242731	N	348.187759	174.597517	331.161210	166.084243	330.177194	165.592235	3
10	1092.520780	546.764028	1075.494231	538.250753	1074.510215	537.758745	S	*234.144832*	117.576054	217.118283	109.062779	216.134267	108.570771	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDTSEVVFNSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	1237.619034	-0.009326	LDTSEVVFNSK
11.7	1237.619049	-0.009341	IDVPPTANTPTP
11.7	1237.619049	-0.009341	IDVPPTANTPTP
10.3	1237.605118	0.004590	PDTSYGGTLRR
8.3	1237.619049	-0.009341	IDVPPTANTPTP
6.8	1237.605087	0.004621	LDREETPNHK
5.9	1237.601242	0.008466	LDLGYELMER
4.5	1237.619034	-0.009326	GAPTPASEPSVPL
4.4	1237.619049	-0.009341	IDVPPTANTPTP
3.2	1237.612488	-0.002780	MERIPSAQPPP

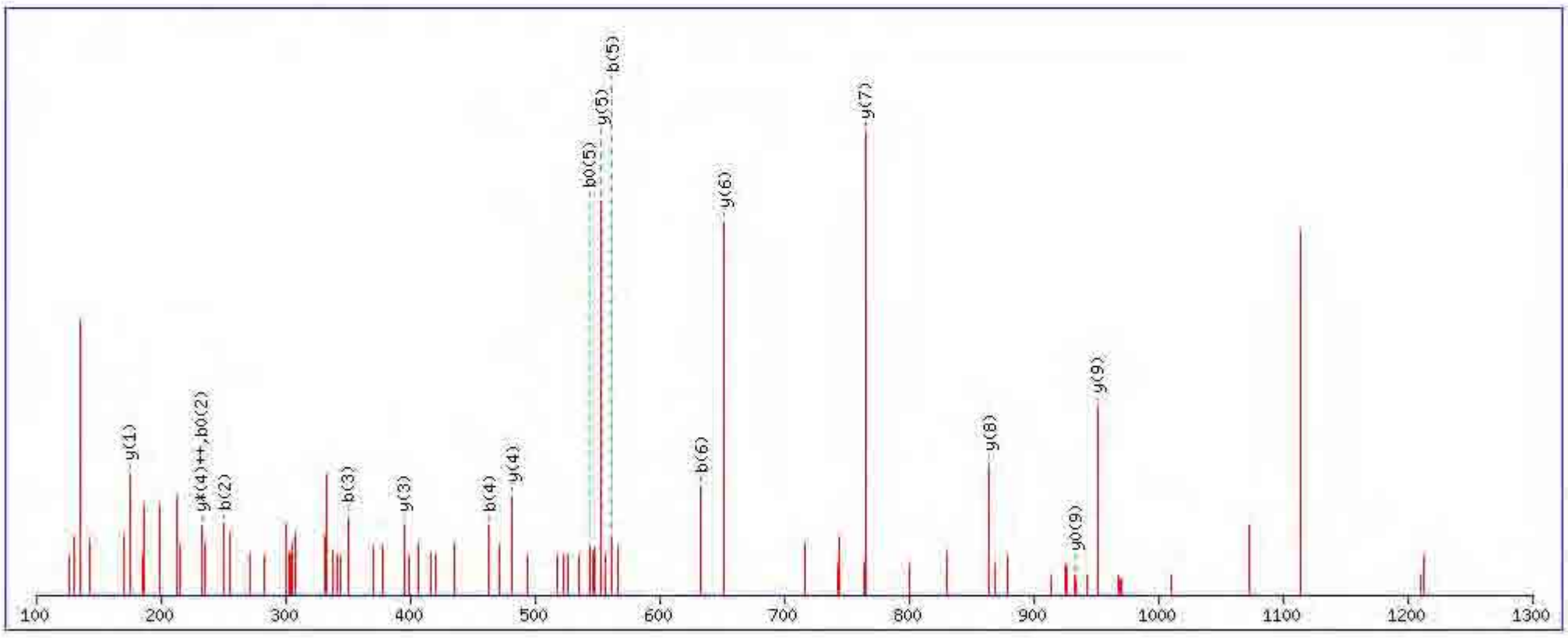
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSVLVASGYR**
Found in **GPHA2_HUMAN**, Glycoprotein hormone alpha-2 OS=Homo sapiens GN=GPHA2 PE=1 SV=1

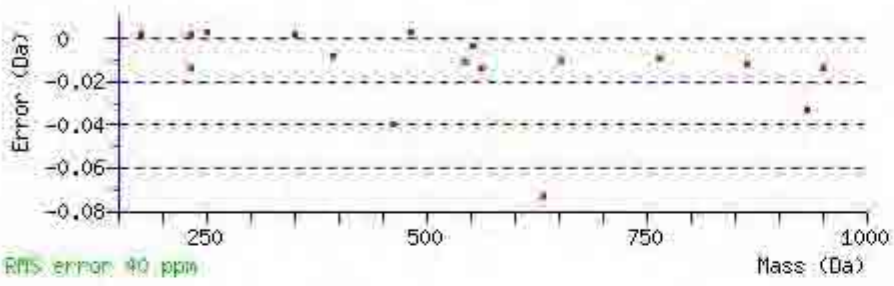
Match to Query 6353: 1113.584048 from(557.799300,2+) rtinseconds(1410) index(7187)
Title: Locus:1.1.1.1562.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

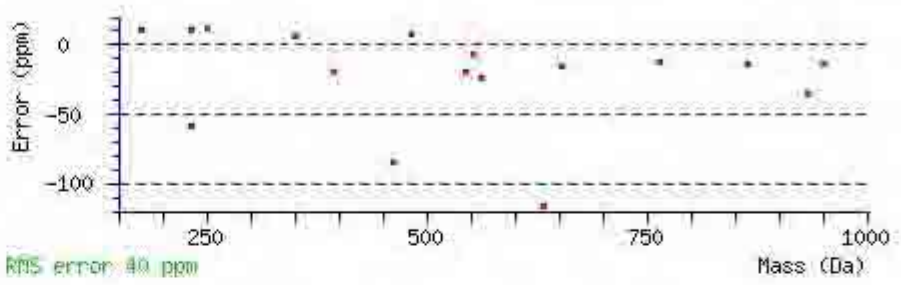
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1113.581848
Ions Score: 56 **Expect:** 0.0001
Matches : 17/82 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							10
2	251.102633	126.054954	233.092068	117.049672	S	951.525807	476.266542	934.499258	467.753267	933.515242	467.261259	9
3	350.171047	175.589161	332.160482	166.583879	V	864.493779	432.750528	847.467230	424.237253	846.483214	423.745245	8
4	463.255111	232.131193	445.244546	223.125911	L	765.425365	383.216321	748.398816	374.703046	747.414800	374.211038	7
5	562.323525	281.665401	544.312960	272.660118	V	652.341301	326.674289	635.314752	318.161014	634.330736	317.669006	6
6	633.360639	317.183958	615.350074	308.178675	A	553.272887	277.140082	536.246338	268.626807	535.262322	268.134799	5
7	720.392667	360.699972	702.382102	351.694689	S	482.235773	241.621524	465.209224	233.108250	464.225208	232.616242	4
8	777.414131	389.210704	759.403566	380.205421	G	395.203745	198.105511	378.177196	189.592236			3
9	940.477460	470.742368	922.466895	461.737086	Y	338.182281	169.594778	321.155732	161.081504			2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YSVLVASGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.0	1113.581848	0.002200	YSVLVASGYR
12.7	1113.578705	0.005343	MVCIVHLQR
12.0	1113.593094	-0.009046	LHVLESGGFR
6.2	1113.574005	0.010043	LPSMTGPLLPG
6.2	1113.574005	0.010043	TLALMGPPGLP
5.4	1113.589264	-0.005216	VSVFQFIMK
4.5	1113.593079	-0.009031	DPRLYHSVK
3.1	1113.574005	0.010043	TLALMGPPGLP
2.6	1113.577835	0.006213	GEKGAQGSPGVK
2.1	1113.585251	-0.001203	GITVTVHMPK

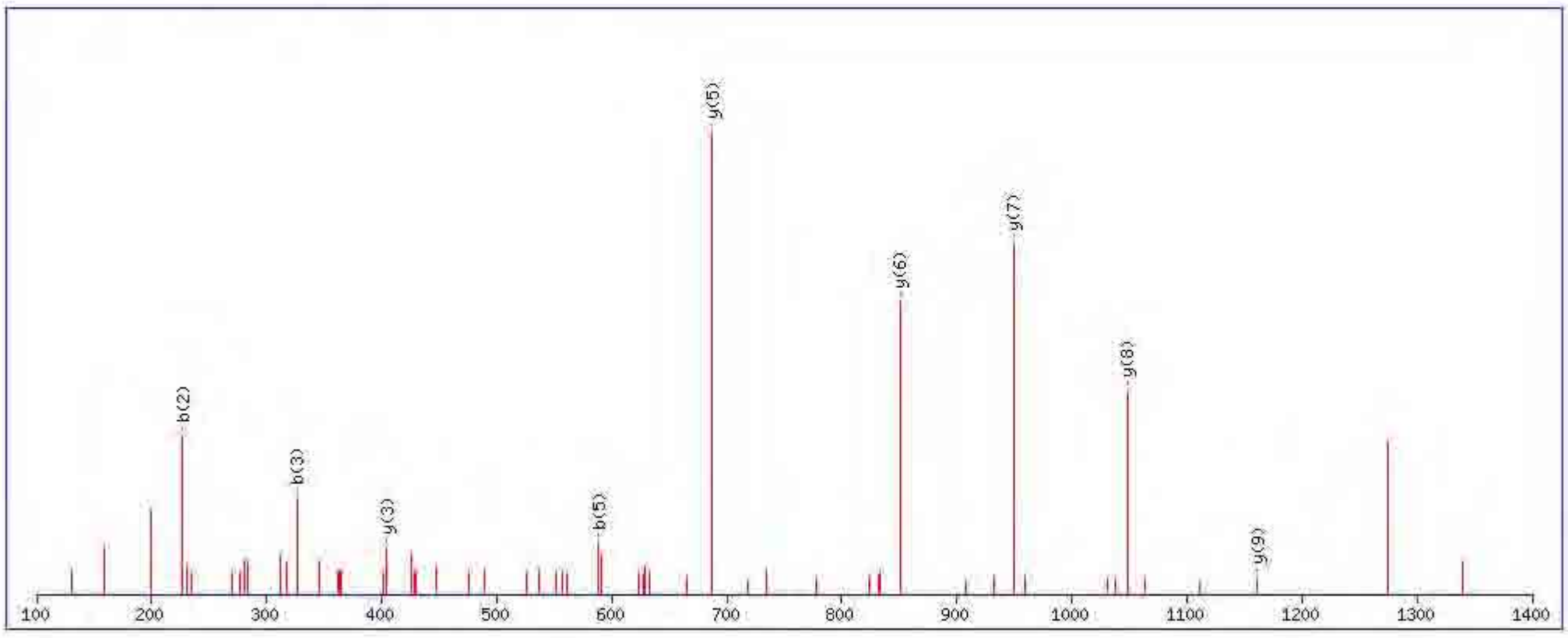
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLVVYPWTQR**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

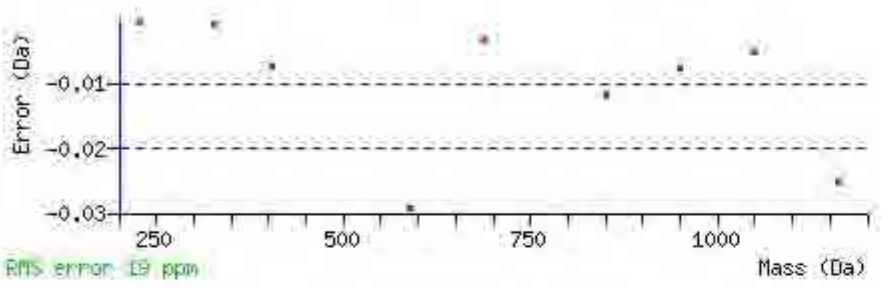
Match to Query 9786: 1273.715988 from(637.865270,2+) rtinseconds(2019) index(14259)
Title: Locus:1.1.1.1897.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

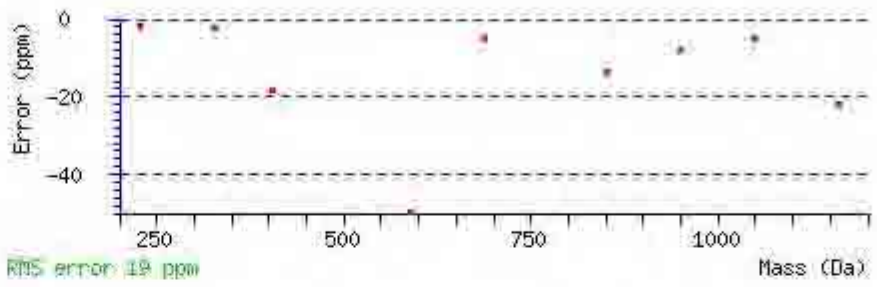
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1273.718292
Ions Score: 52 **Expect:** 0.00021
Matches : 9/74 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					L	*1161.641507*	581.324392	1144.614958	572.811117	1143.630942	572.319109	9
3	326.243818	163.625547					V	*1048.557443*	524.782360	1031.530894	516.269085	1030.546878	515.777077	8
4	425.312232	213.159754					V	*949.489029*	475.248153	932.462480	466.734878	931.478464	466.242870	7
5	588.375561	294.691419					Y	*850.420615*	425.713946	833.394066	417.200671	832.410050	416.708663	6
6	685.428325	343.217801					P	*687.357286*	344.182281	670.330737	335.669007	669.346721	335.176999	5
7	871.507638	436.257457					W	590.304522	295.655899	573.277973	287.142625	572.293957	286.650617	4
8	972.555317	486.781297			954.544752	477.776014	T	*404.225209*	202.616243	387.198660	194.102968	386.214644	193.610960	3
9	1100.613895	550.810586	1083.587346	542.297311	1082.603330	541.805303	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLVVYPWTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	1273.718292	-0.002304	LLVVYPWTQR
11.8	1273.710434	0.005554	LLVASWVMQIV
10.4	1273.706360	0.009628	LLQMANEKALK
10.0	1273.716949	-0.000961	IIVELVEFISP
10.0	1273.728180	-0.012192	ILVQYGADLLAV
10.0	1273.710434	0.005554	LIVNSLCPVIFG
10.0	1273.728195	-0.012207	LIVTQTPPYVK
10.0	1273.728195	-0.012207	LIVTQTPPYVK
10.0	1273.714249	0.001739	LLVESHHLQAK
8.3	1273.706406	0.009582	VLLTMIARVADG

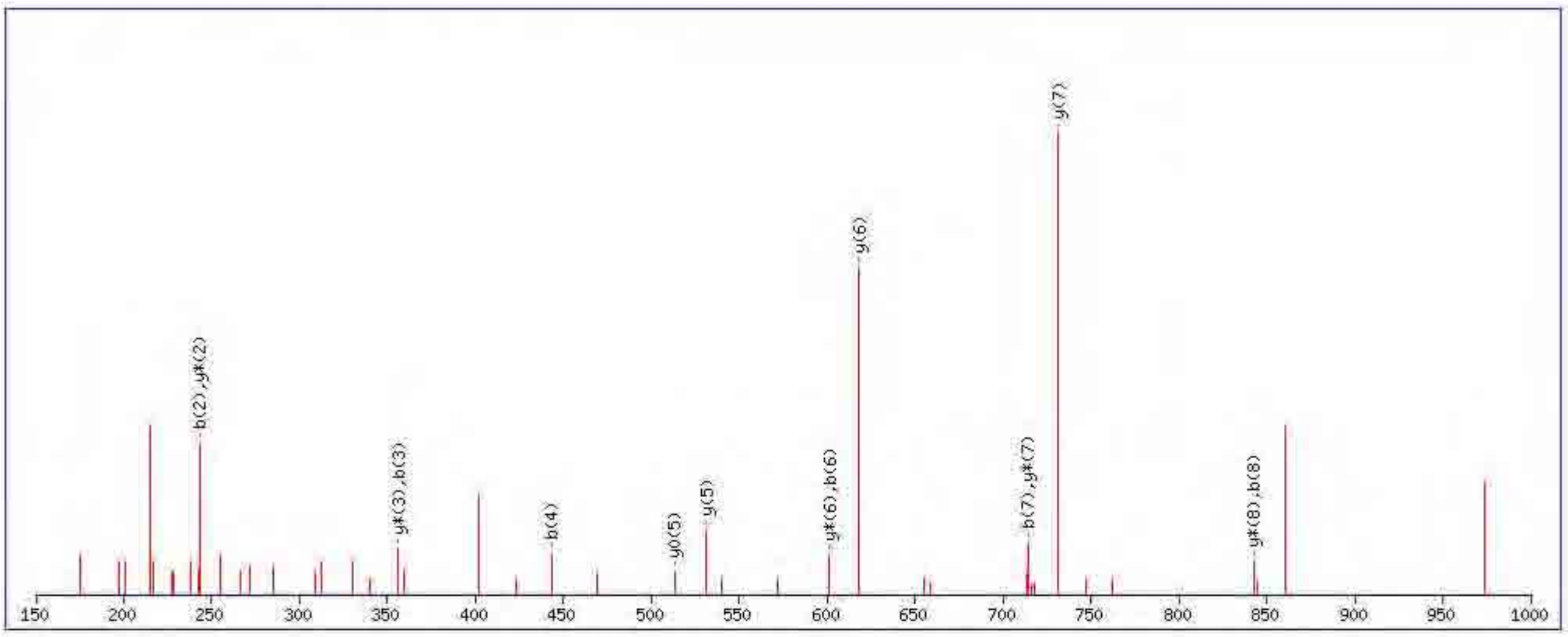
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQLSGTLQI**
Found in **COQ3_HUMAN**, Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial OS=Homo sapiens GN=COQ3 PE=1 SV=3

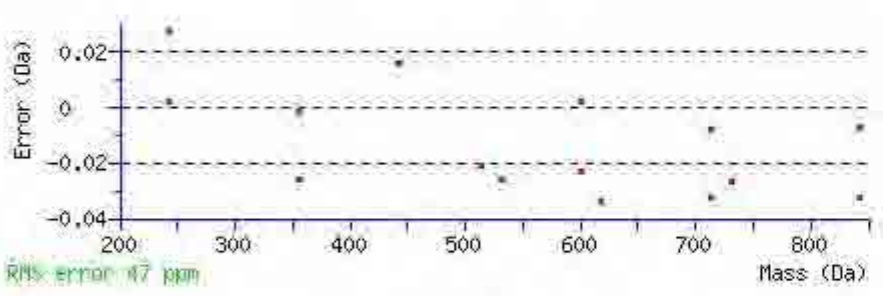
Match to Query 3743: 972.524028 from(487.269290,2+) rtinseconds(1248) index(5587)
Title: Locus:1.1.1.1472.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

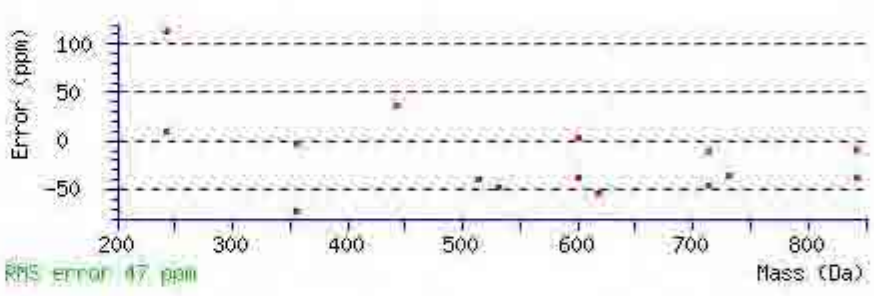
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 972.524002
Ions Score: 50 **Expect:** 0.0016
Matches : 15/82 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							9
2	*243.108781*	122.058029	226.082232	113.544754			Q	859.488360	430.247818	842.461811	421.734544	841.477795	421.242536	8
3	*356.192845*	178.600061	339.166296	170.086786			L	**731.429782**	366.218529	714.403233	357.705255	713.419217	357.213247	7
4	*443.224873*	222.116075	426.198324	213.602800	425.214308	213.110792	S	**618.345718**	309.676497	601.319169	301.163223	600.335153	300.671215	6
5	500.246337	250.626807	483.219788	242.113532	482.235772	241.621524	G	**531.313690**	266.160483	514.287141	257.647209	513.303125	257.155201	5
6	*601.294016*	301.150646	584.267467	292.637372	583.283451	292.145364	T	474.292226	237.649751	457.265677	229.136476	456.281661	228.644468	4
7	*714.378080*	357.692678	697.351531	349.179404	696.367515	348.687396	L	373.244547	187.125912	356.217998	178.612637			3
8	*842.436658*	421.721967	825.410109	413.208693	824.426093	412.716685	Q	260.160483	130.583879	243.133934	122.070605			2
9							I	132.101905	66.554590					1





NCBI **BLAST** search of NQLSGTLQI
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.4	972.524002	0.000026	NQLSGTLQI
47.5	972.523972	0.000056	LELSENRI
46.5	972.523972	0.000056	IEISELNR
39.0	972.523987	0.000041	EIISEVQR
30.5	972.523987	0.000041	LEISDIQR
27.4	972.523972	0.000056	ELSLEINR
26.6	972.523987	0.000041	PESLDRIK
26.1	972.523987	0.000041	ELPSAATLR
23.7	972.523987	0.000041	ILESVAEGR
23.6	972.523987	0.000041	QNSLKSPAL

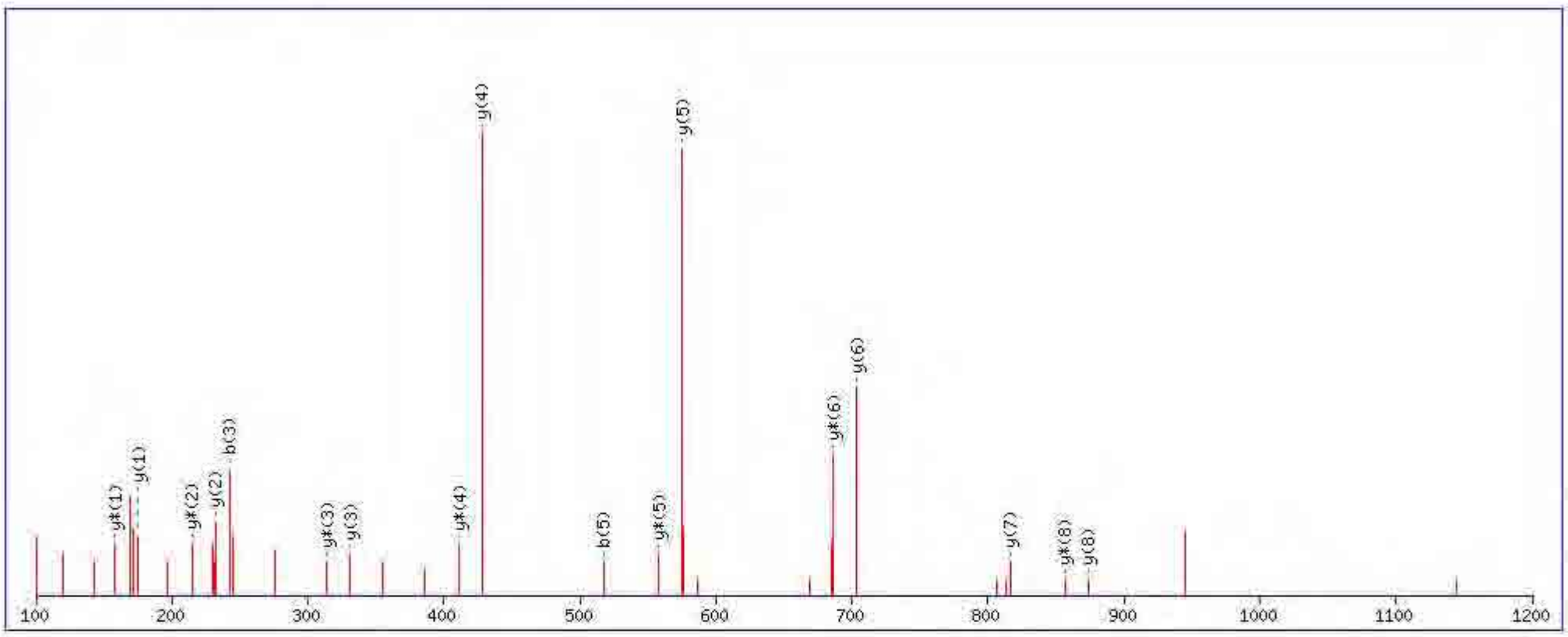
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

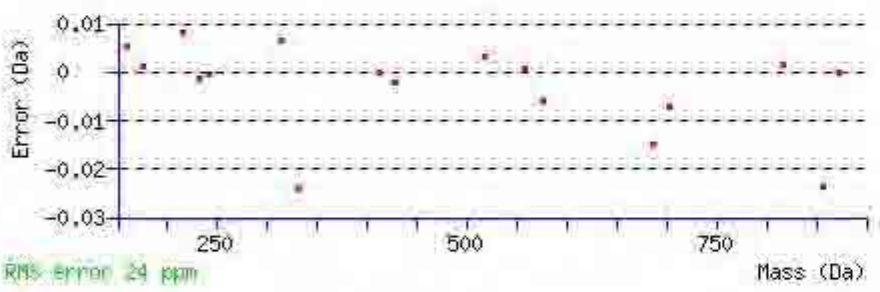
Match to Query 3299: 943.523428 from(472.768990,2+) rtinseconds(1497) index(8182)
Title: Locus:1.1.1.1610.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

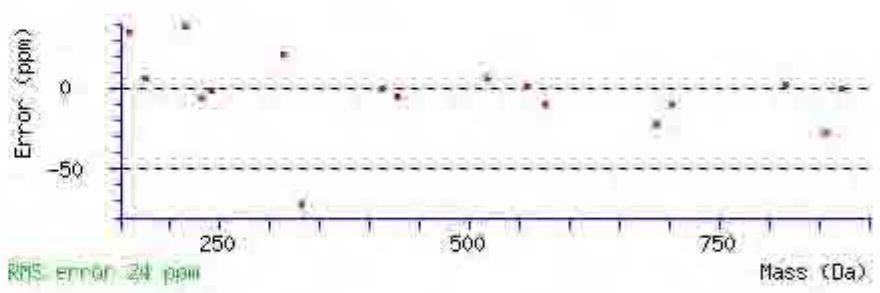
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Ions Score: 63 **Expect:** 6.5e-005
Matches : 17/58 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	*873.494114*	437.250695	856.467565	428.737421	8
3	**242.149918**	121.578597			L	*816.472650*	408.739963	799.446101	400.226689	7
4	370.208496	185.607886	353.181947	177.094612	Q	*703.388586*	352.197931	686.362037	343.684657	6
5	**517.276910**	259.142093	500.250361	250.628819	F	*575.330008*	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	*428.261594*	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	*331.208830*	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	*232.140416*	116.573846	215.113867	108.060571	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.6	943.523956	-0.000528	AGLQFPVGR
24.6	943.516068	0.007360	KLLQMQPA
18.7	943.519928	0.003500	QLDRTVGR
16.4	943.519913	0.003515	AAVLSRDGR
15.7	943.519897	0.003531	ATSKERPR
15.5	943.523956	-0.000528	AGSLVWGVR
14.8	943.516068	0.007360	KLLQMQPA
14.3	943.516068	0.007360	PSGKLMSPK
14.3	943.523926	-0.000498	KIQNQWK
14.3	943.527298	-0.003870	QIQACLLR

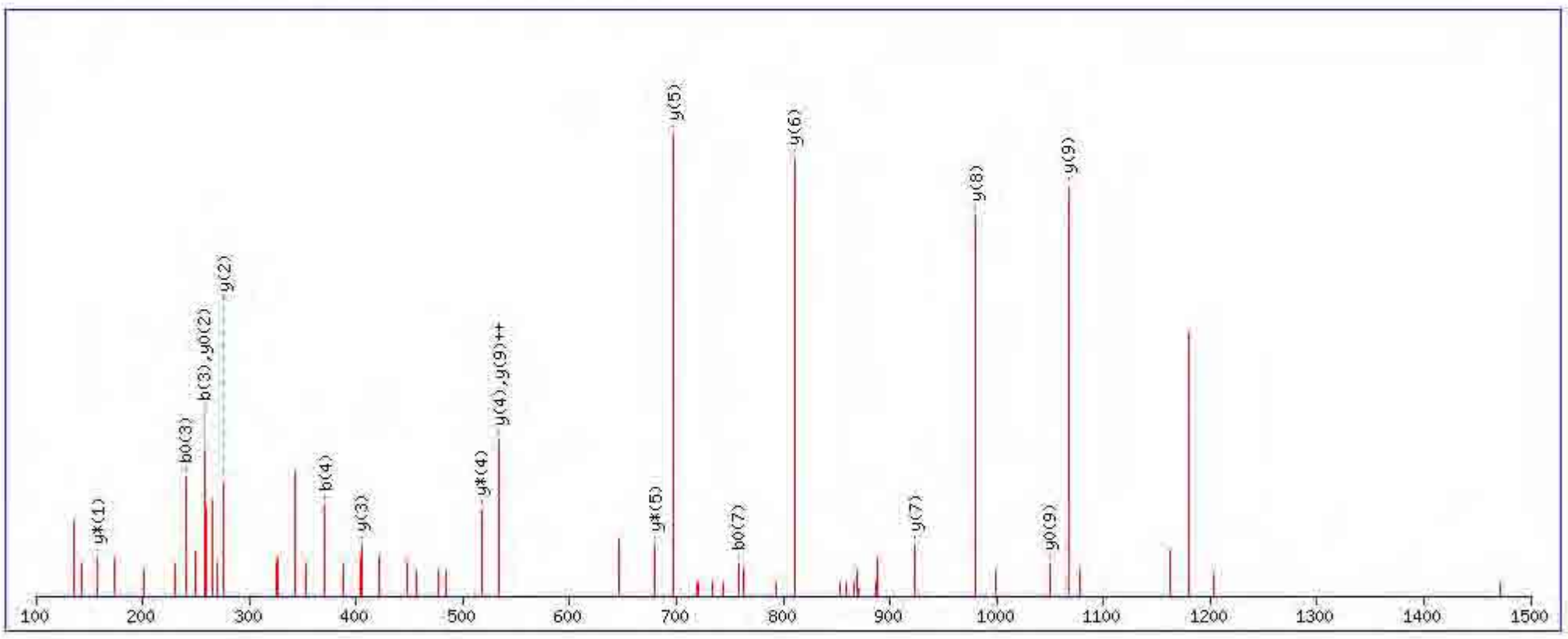
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISGLIYEETR**
Found in **H4_HUMAN**, Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

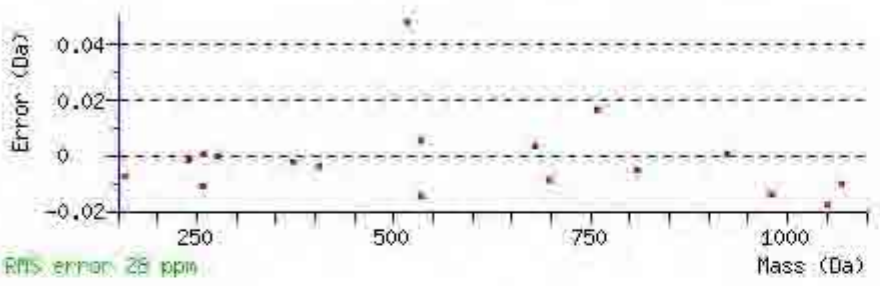
Match to Query 7939: 1179.607328 from(590.810940,2+) rtinseconds(1406) index(7154)
Title: Locus:1.1.1.1560.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

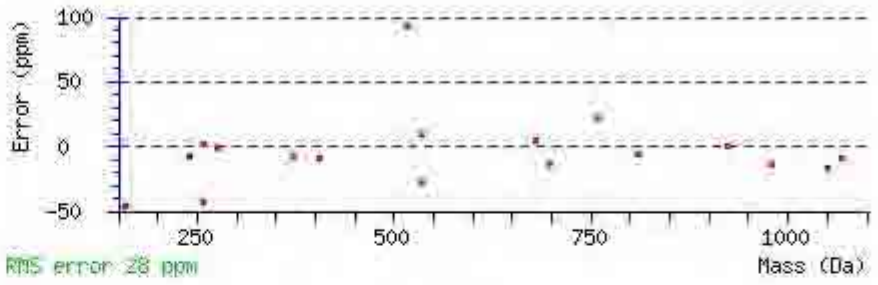
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1179.613525
Ions Score: 61 **Expect:** 0.00014
Matches : 18/86 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							10
2	201.123368	101.065322	183.112803	92.060039	S	*1067.536766*	534.272021	1050.510217	525.758747	1049.526201	525.266739	9
3	**258.144832**	129.576054	240.134267	120.570771	G	*980.504738*	490.756007	963.478189	482.242733	962.494173	481.750725	8
4	**371.228896**	186.118086	353.218331	177.112803	L	*923.483274*	462.245275	906.456725	453.732001	905.472709	453.239993	7
5	484.312960	242.660118	466.302395	233.654835	I	*810.399210*	405.703243	793.372661	397.189969	792.388645	396.697961	6
6	647.376289	324.191783	629.365724	315.186500	Y	*697.315146*	349.161211	680.288597	340.647937	679.304581	340.155929	5
7	776.418882	388.713079	758.408317	379.707797	E	*534.251817*	267.629547	517.225268	259.116272	516.241252	258.624264	4
8	905.461475	453.234376	887.450910	444.229093	E	*405.209224*	203.108250	388.182675	194.594975	387.198659	194.102967	3
9	1006.509154	503.758215	988.498589	494.752933	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ISGLIYEETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.4	1179.613525	-0.006197	ISGLIYEETR
21.1	1179.610855	-0.003527	PSGLHNQQKR
20.1	1179.613586	-0.006258	SPGPPPPVGVKT
15.8	1179.613525	-0.006197	LKAEPAAPPAAP
11.7	1179.610840	-0.003512	ISGHRPEAASR
11.1	1179.613525	-0.006197	LQEIQTAYSK
10.9	1179.613571	-0.006243	PGSPVLPPGAPK
10.5	1179.599823	0.007505	VTAVIPCFPYA
10.5	1179.613556	-0.006228	VTAVLKSQGYD
10.2	1179.616913	-0.009585	ISGVSVKSEMK

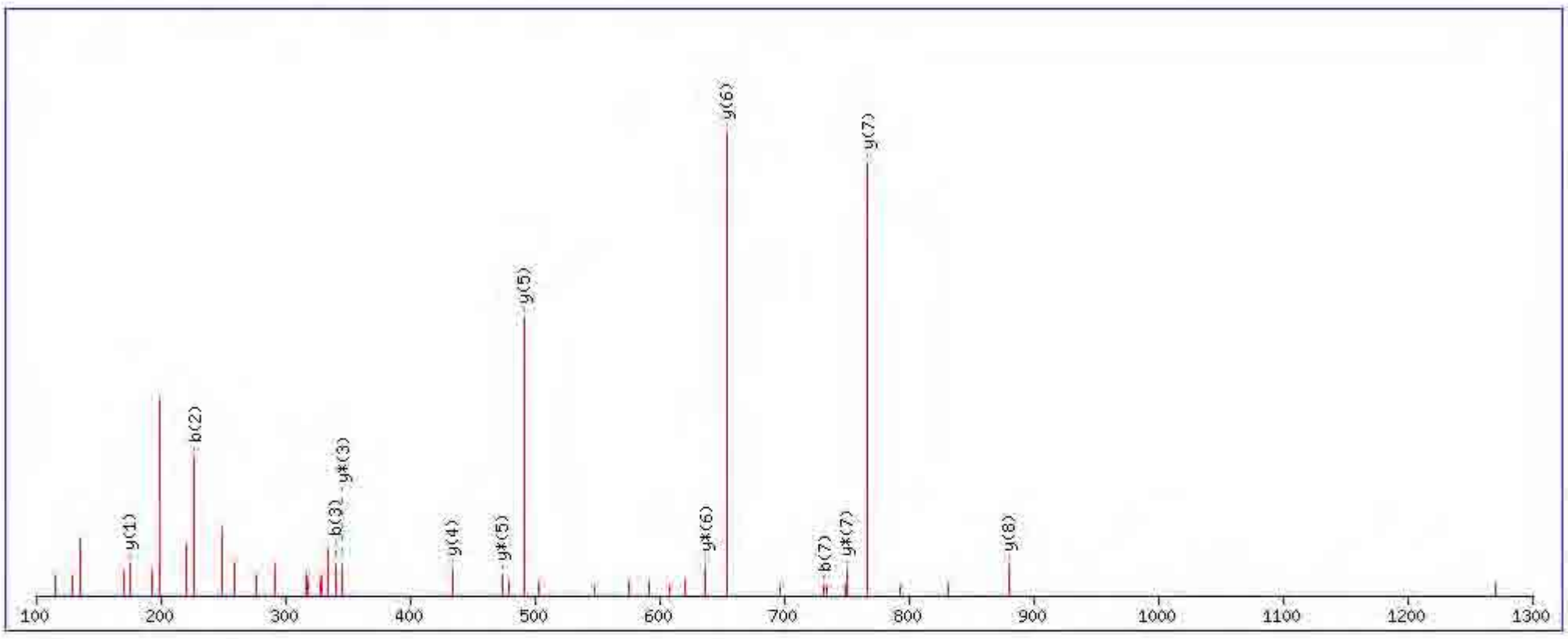
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGATSR**
Found in **KV303_HUMAN**, Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=1 SV=1

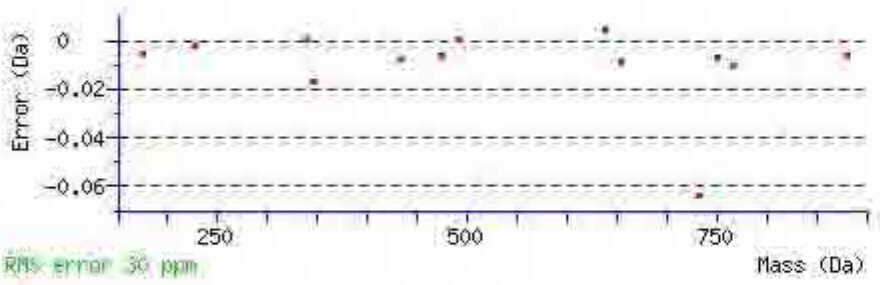
Match to Query 4099: 992.564088 from(497.289320,2+) rtinseconds(1321) index(6239)
Title: Locus:1.1.1.1513.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

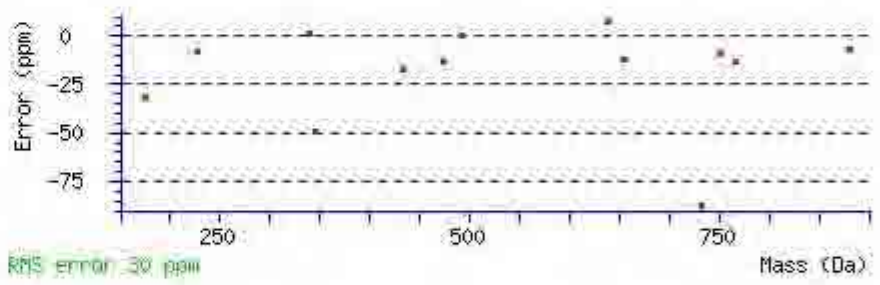
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 41 **Expect:** 0.0067
Matches : 13/66 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	880.488694	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	767.404630	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	654.320566	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	491.257237	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	434.235773	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	732.429054	366.718165	714.418489	357.712883	T	363.198659	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGATSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	992.565460	-0.001372	LLIYGATSR
39.3	992.565460	-0.001372	LLIYGASTR
20.5	992.554245	0.009843	ILPPLSPPQ
16.7	992.565475	-0.001387	PLLGPPDIR
15.6	992.554230	0.009858	LLLKSSEGF
15.4	992.554245	0.009843	ILPPLSPPQ
15.4	992.565475	-0.001387	ILPSVSHKP
15.4	992.565475	-0.001387	LLPHVSSPK
15.3	992.555588	0.008500	IPLGWHVR
14.9	992.554245	0.009843	ILPPLSPPQ

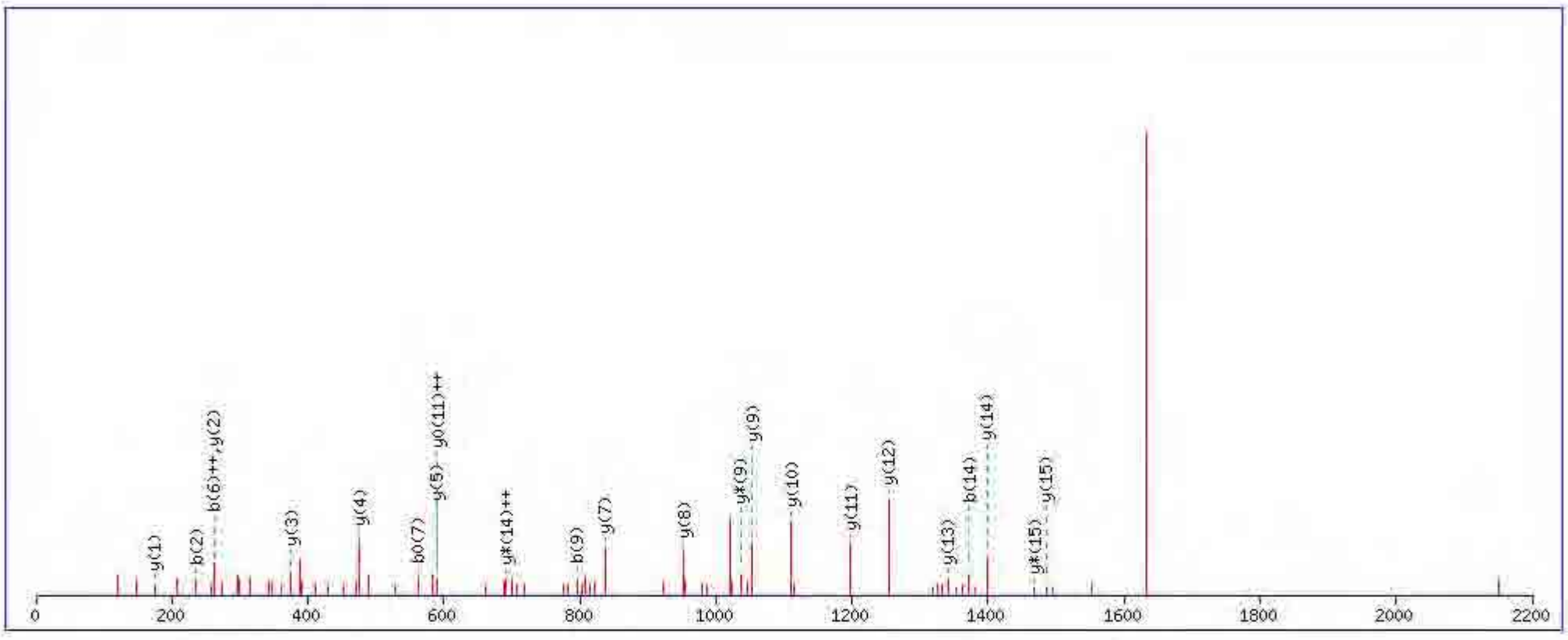
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSGSGTDFTLTISR**
Found in **KV302_HUMAN**, Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1

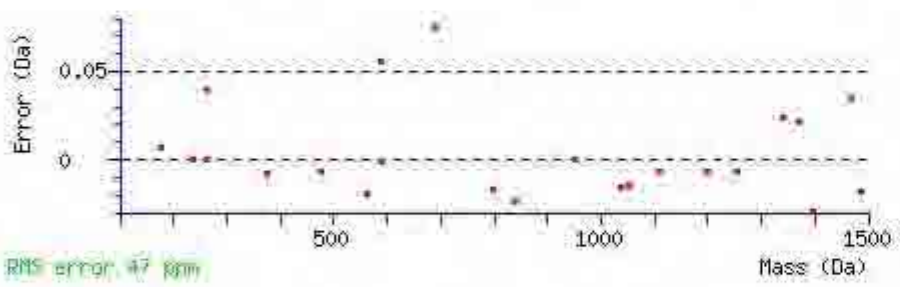
Match to Query 14692: 1631.795248 from(816.904900,2+) rtinseconds(1725) index(10811)
Title: Locus:1.1.1.1734.22
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

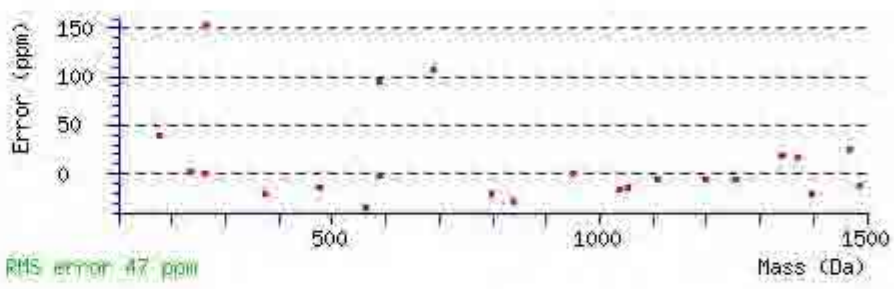
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1631.779144
Ions Score: 95 **Expect:** 6e-009
Matches : 23/146 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			F							16
2	235.107718	118.057497	217.097153	109.052214	S	*1485.717978*	743.362627	1468.691429	734.849352	1467.707413	734.357344	15
3	292.129182	146.568229	274.118617	137.562946	G	*1398.685950*	699.846613	1381.659401	691.333338	1380.675385	690.841330	14
4	379.161210	190.084243	361.150645	181.078960	S	*1341.664486*	671.335881	1324.637937	662.822607	1323.653921	662.330598	13
5	436.182674	218.594975	418.172109	209.589692	G	*1254.632458*	627.819867	1237.605909	619.306592	1236.621893	618.814584	12
6	523.214702	262.110989	505.204137	253.105707	S	*1197.610994*	599.309135	1180.584445	590.795861	1179.600429	590.303852	11
7	580.236166	290.621721	562.225601	281.616439	G	*1110.578966*	555.793121	1093.552417	547.279846	1092.568401	546.787838	10
8	681.283845	341.145561	663.273280	332.140278	T	*1053.557502*	527.282389	1036.530953	518.769115	1035.546937	518.277106	9
9	796.310788	398.659032	778.300223	389.653750	D	*952.509823*	476.758549	935.483274	468.245275	934.499258	467.753267	8
10	943.379202	472.193239	925.368637	463.187956	F	*837.482880*	419.245078	820.456331	410.731803	819.472315	410.239795	7
11	1044.426881	522.717078	1026.416316	513.711796	T	690.414466	345.710871	673.387917	337.197596	672.403901	336.705588	6
12	1157.510945	579.259110	1139.500380	570.253828	L	*589.366787*	295.187031	572.340238	286.673757	571.356222	286.181749	5
13	1258.558624	629.782950	1240.548059	620.777667	T	*476.282723*	238.644999	459.256174	230.131725	458.272158	229.639717	4
14	1371.642688	686.324982	1353.632123	677.319699	I	*375.235044*	188.121160	358.208495	179.607885	357.224479	179.115877	3
15	1458.674716	729.840996	1440.664151	720.835713	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
16					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FSGSGSGTDFTLTISR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
95.5	1631.779144	0.016104	FSGSGSGTDFTLTISR
7.3	1631.789856	0.005392	LKMIMEELHDVDK
5.9	1631.808960	-0.013712	SACIPPDNKGQFIAR
4.4	1631.782455	0.012793	EMAKNDPIELPTSR
4.4	1631.799088	-0.003840	SFRQHGPLICDGFR
3.9	1631.791183	0.004065	FNRALNCMNLPPDK
3.7	1631.808945	-0.013697	HMGRLAEAQTYLDK
3.3	1631.782471	0.012777	NMLTSTAVKHDLAES
2.6	1631.782471	0.012777	TPTEAPADCRALIDK
2.3	1631.790527	0.004721	FSKMFEIVFEDPK

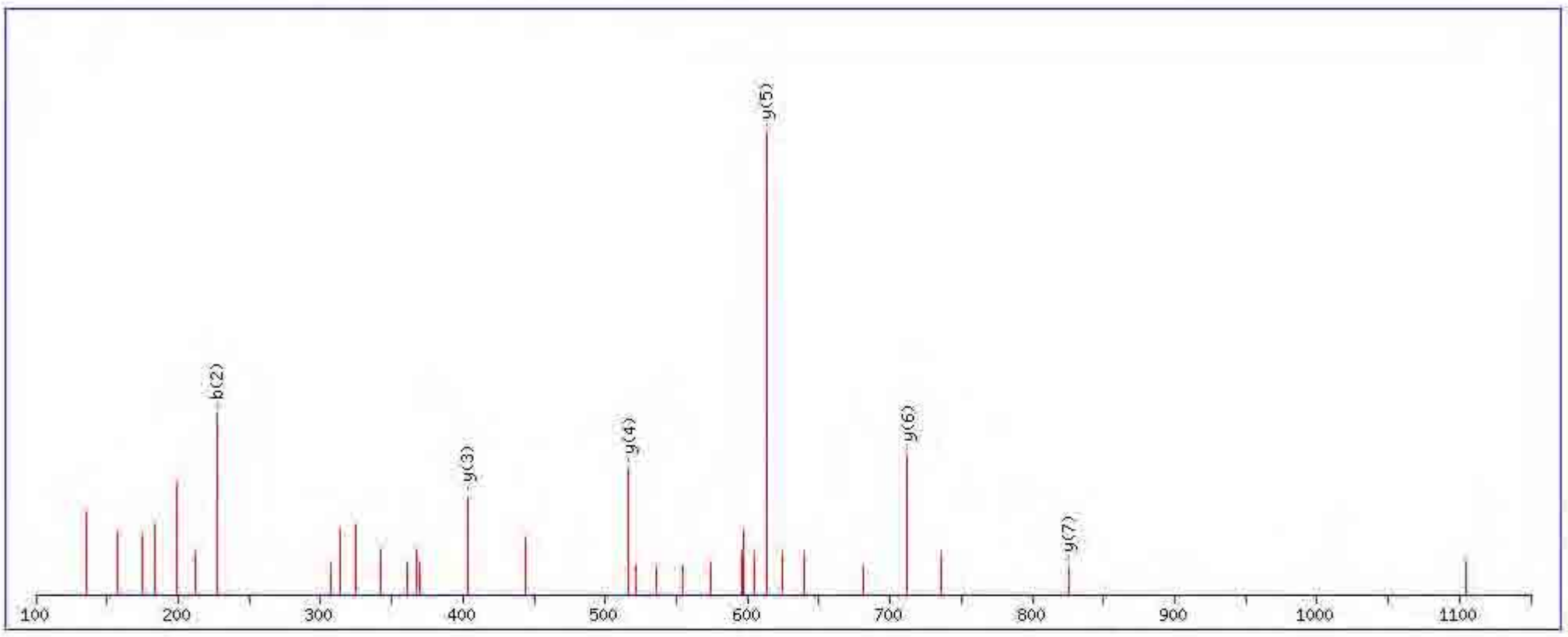
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIVPLNNR**
Found in **IGJ_HUMAN**, Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4

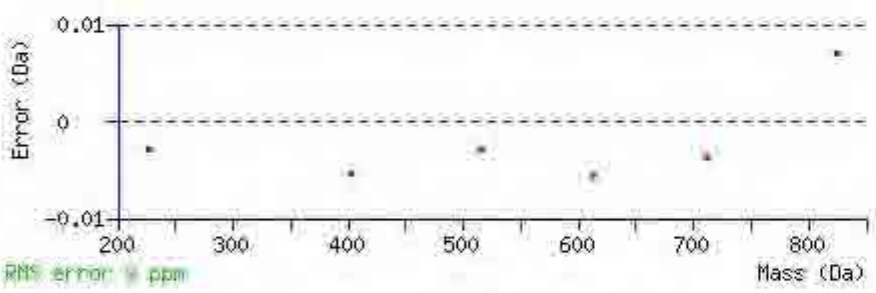
Match to Query 3204: 937.564748 from(469.789650,2+) rtinseconds(1255) index(5668)
Title: Locus:1.1.1.1476.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

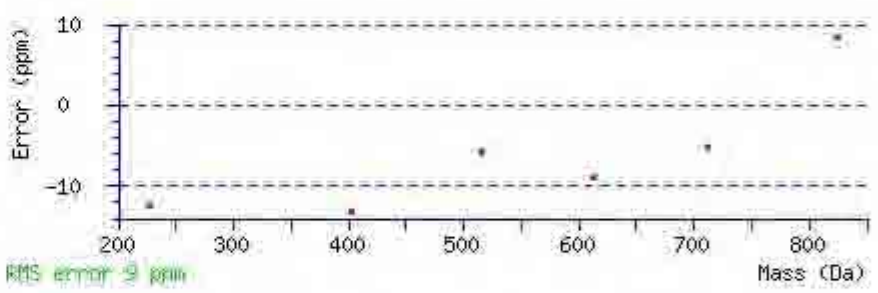
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 937.570877
Ions Score: 46 **Expect:** 0.00098
Matches : 6/46 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			I					8
2	227.175404	114.091340			I	825.494112	413.250694	808.467563	404.737419	7
3	326.243818	163.625547			V	712.410048	356.708662	695.383499	348.195387	6
4	423.296582	212.151929			P	613.341634	307.174455	596.315085	298.661181	5
5	536.380646	268.693961			L	516.288870	258.648073	499.262321	250.134798	4
6	650.423573	325.715425	633.397024	317.202150	N	403.204806	202.106041	386.178257	193.592766	3
7	764.466500	382.736888	747.439951	374.223614	N	289.161879	145.084577	272.135330	136.571303	2
8					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of IIVPLNNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	937.570877	-0.006129	IIVPLNNR
16.2	937.570892	-0.006144	LLVLTSHR
15.6	937.559677	0.005071	LLVGPPGTGK
14.2	937.563675	0.001073	LLISWIPP
13.6	937.559662	0.005086	IILVPRPD
13.6	937.559662	0.005086	PLIVPEVR
12.5	937.559647	0.005101	IPDPAGKLK
8.6	937.559662	0.005086	LVPLLDRP
5.8	937.559647	0.005101	LLDQPKPK
5.7	937.559662	0.005086	LPRTIPLP

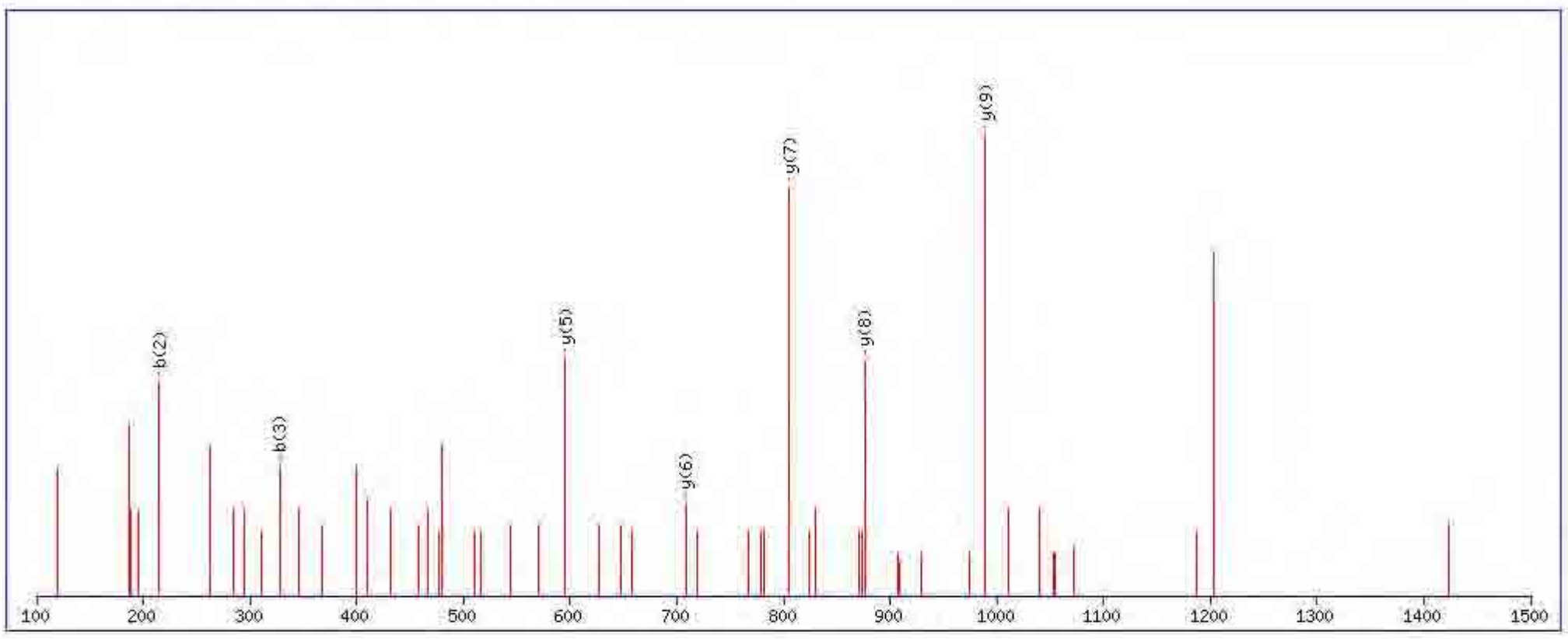
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLAPLSRGLY**
Found in **HSC20_HUMAN**, Iron-sulfur cluster co-chaperone protein HscB, mitochondrial OS=Homo sapiens GN=HSCB PE=1 SV=3

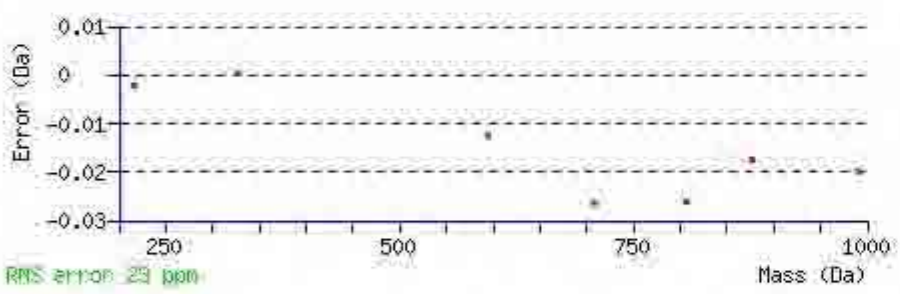
Match to Query 8487: 1202.695828 from(602.355190,2+) rtinseconds(2048) index(14619)
Title: Locus:1.1.1.1913.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

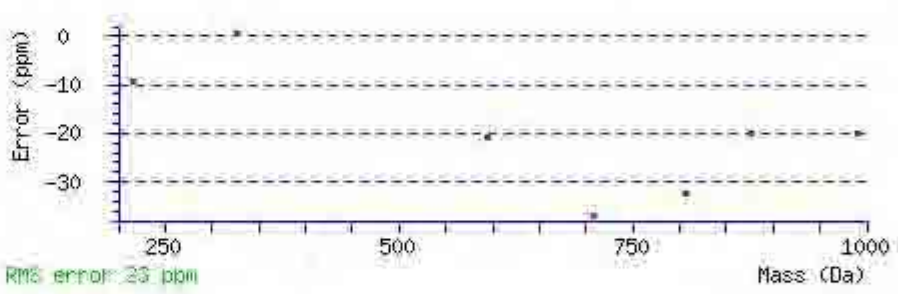
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1202.702286
Ions Score: 36 **Expect:** 0.01
Matches : 7/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	215.139019	108.073147			197.128454	99.067865	L	1102.661907	551.834592	1085.635358	543.321317	1084.651342	542.829309	10
3	328.223083	164.615179			310.212518	155.609897	L	*989.577843*	495.292560	972.551294	486.779285	971.567278	486.287277	9
4	399.260197	200.133737			381.249632	191.128454	A	*876.493779*	438.750528	859.467230	430.237253	858.483214	429.745245	8
5	496.312961	248.660119			478.302396	239.654836	P	*805.456665*	403.231971	788.430116	394.718696	787.446100	394.226688	7
6	609.397025	305.202151			591.386460	296.196868	L	*708.403901*	354.705589	691.377352	346.192314	690.393336	345.700306	6
7	696.429053	348.718165			678.418488	339.712882	S	*595.319837*	298.163557	578.293288	289.650282	577.309272	289.158274	5
8	852.530164	426.768720	835.503615	418.255446	834.519599	417.763438	R	508.287809	254.647543	491.261260	246.134268			4
9	909.551628	455.279452	892.525079	446.766178	891.541063	446.274170	G	352.186698	176.596987					3
10	1022.635692	511.821484	1005.609143	503.308210	1004.625127	502.816202	L	295.165234	148.086255					2
11							Y	182.081170	91.544223					1





NCBI **BLAST** search of TLLAPLSRGLY
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	1202.702286	-0.006458	TLLAPLSRGLY
13.9	1202.705643	-0.009815	TILALRIMEK
12.9	1202.698257	-0.002429	TLIAQSSKSLR
11.5	1202.691071	0.004757	TLPPLALFTSK
4.7	1202.691071	0.004757	LTLLAPLNSVF
4.3	1202.702286	-0.006458	LTALLLQRYP
4.3	1202.691055	0.004773	LTPSLVYALNL
3.8	1202.687073	0.008755	TILVSTTPVTR
2.9	1202.702316	-0.006488	LTIIRQTFPV
2.9	1202.705658	-0.009830	ITLMIKNVQK

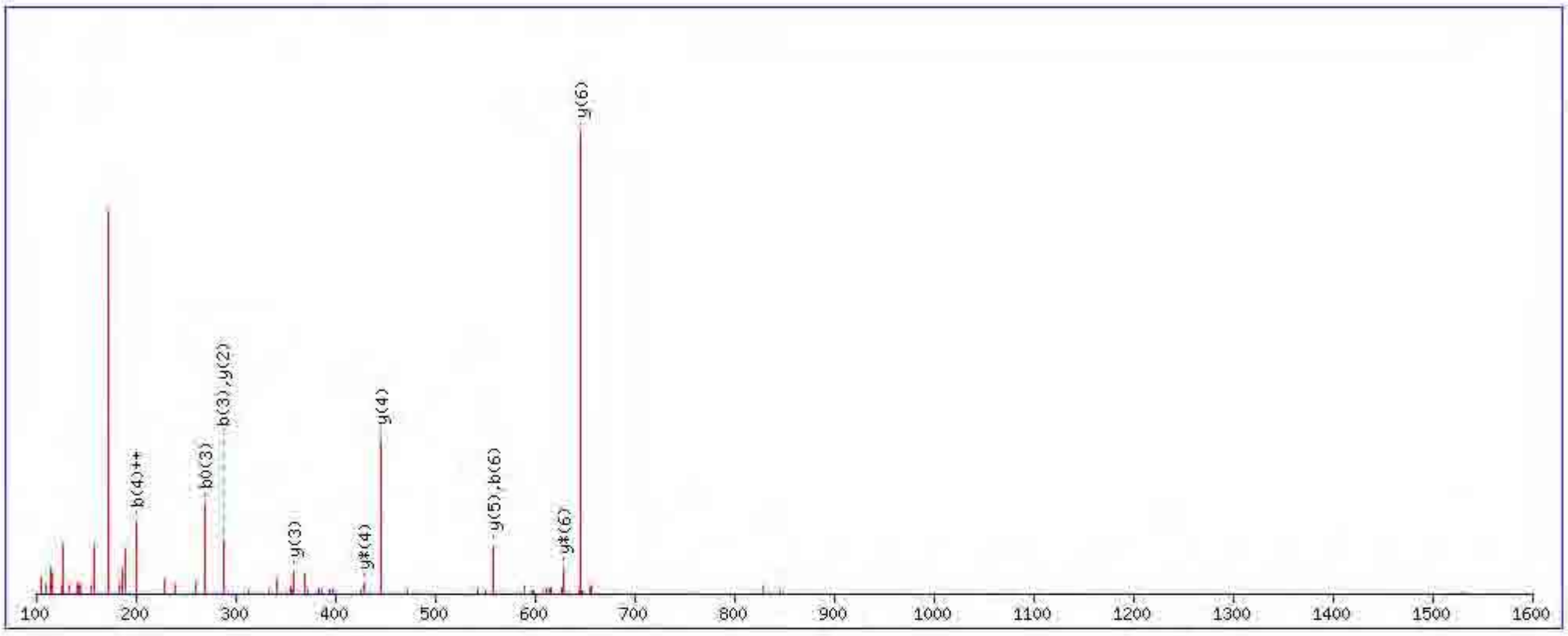
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSLSAIR**
Found in **LRC48_HUMAN**, Leucine-rich repeat-containing protein 48 OS=Homo sapiens GN=LRRC48 PE=2 SV=2

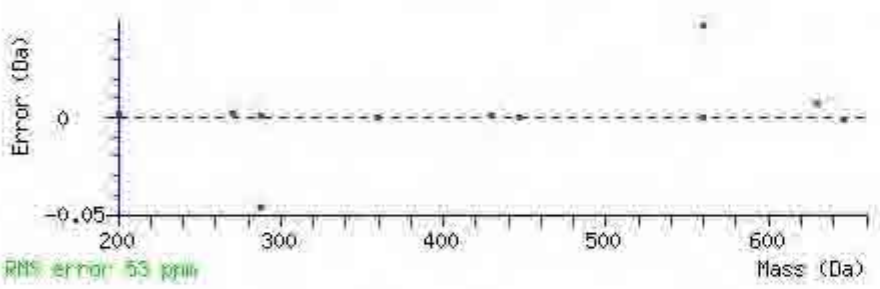
Match to Query 1544: 845.496668 from(423.755610,2+) rtinseconds(1183) index(4908)
Title: Locus:1.1.1.1436.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

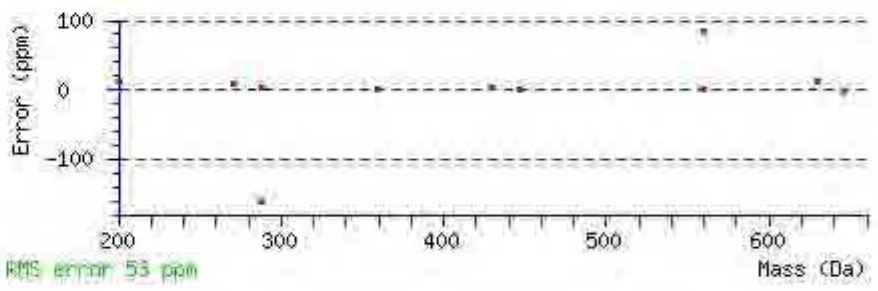
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 845.497040
Ions Score: 38 **Expect:** 0.011
Matches : 12/62 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	**201.123368**	101.065322	183.112803	92.060039	S	733.420278	367.213777	716.393729	358.700502	715.409713	358.208494	7
3	**288.155396**	144.581336	270.144831	135.576053	S	***646.388250***	323.697763	629.361701	315.184488	628.377685	314.692480	6
4	401.239460	201.123368	383.228895	192.118085	L	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	5
5	488.271488	244.639382	470.260923	235.634099	S	***446.272158***	223.639717	429.245609	215.126442	428.261593	214.634434	4
6	**559.308602**	280.157939	541.298037	271.152656	A	***359.240130***	180.123703	342.213581	171.610428			3
7	672.392666	336.699971	654.382101	327.694688	I	***288.203016***	144.605146	271.176467	136.091871			2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSLSAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.1	845.497040	-0.000372	LSSLSAIR
30.1	845.497055	-0.000387	TVSSLAIR
28.3	845.497040	-0.000372	SLSLLASR
24.5	845.497040	-0.000372	SLSALLSR
22.0	845.497055	-0.000387	VTSALLSR
19.6	845.497040	-0.000372	SSISLALR
17.1	845.497070	-0.000402	SLTVTLGR
15.6	845.497055	-0.000387	TASVLRSI
15.0	845.497040	-0.000372	SILSLSAR
15.0	845.497055	-0.000387	SILSLTGR

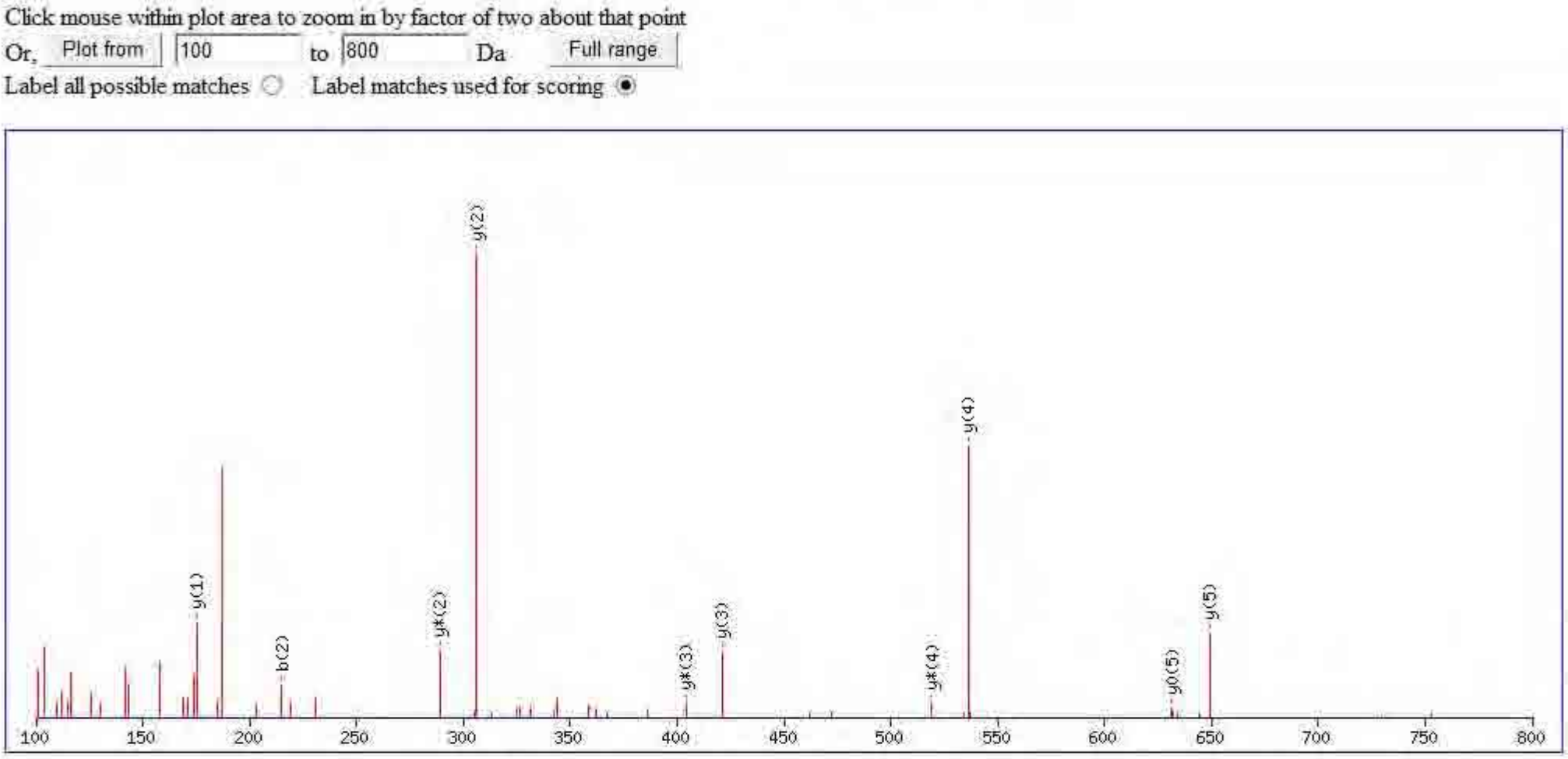
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLDDMR**
Found in **KDM5B_HUMAN**, Lysine-specific demethylase 5B OS=Homo sapiens GN=KDM5B PE=1 SV=3

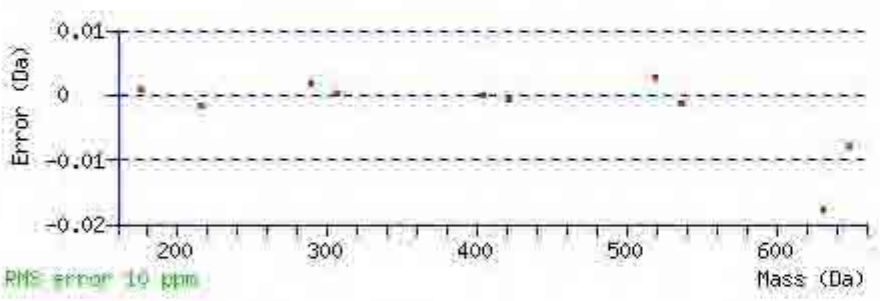
Match to Query 342: 749.335548 from(375.675050,2+) rtinseconds(688) index(1242)
Title: Locus:1.1.1.1157.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

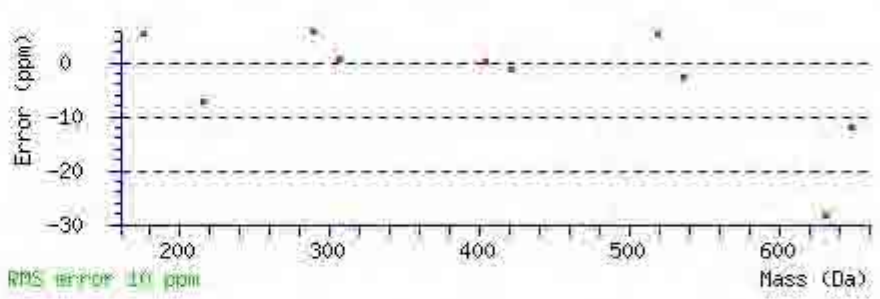
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 749.337784
Ions Score: 42 **Expect:** 0.0073
Matches : 10/46 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							6
2	215.139019	108.073147	197.128454	99.067865	L	*649.297387*	325.152332	632.270838	316.639057	631.286822	316.147049	5
3	330.165962	165.586619	312.155397	156.581336	D	*536.213323*	268.610300	519.186774	260.097025	518.202758	259.605017	4
4	445.192905	223.100090	427.182340	214.094808	D	*421.186380*	211.096828	404.159831	202.583553	403.175815	202.091546	3
5	576.233390	288.620333	558.222825	279.615051	M	*306.159437*	153.583356	289.132888	145.070082			2
6					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TLDDMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	749.337784	-0.002236	TLDDMR
33.0	749.337784	-0.002236	TLDDRM
24.7	749.337784	-0.002236	TEVDMR
23.3	749.337799	-0.002251	TPDMVR
19.0	749.342484	-0.006936	CQGRMR
17.7	749.337784	-0.002236	TVEDRM
17.3	749.337784	-0.002236	DVETMR
14.6	749.337769	-0.002221	TLEECR
11.8	749.337784	-0.002236	TEDVMR
11.7	749.337784	-0.002236	DITDMR

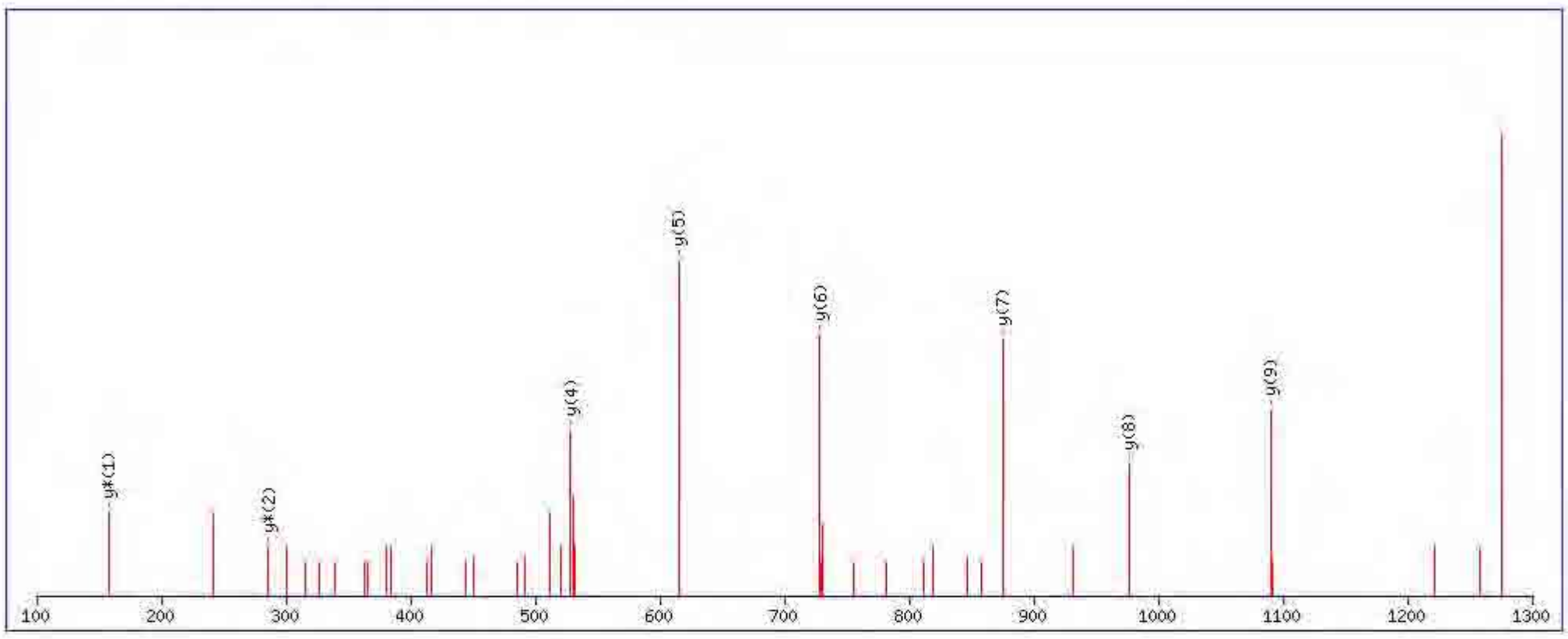
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NANTFISPQQR**
Found in **MGP_HUMAN**, Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2

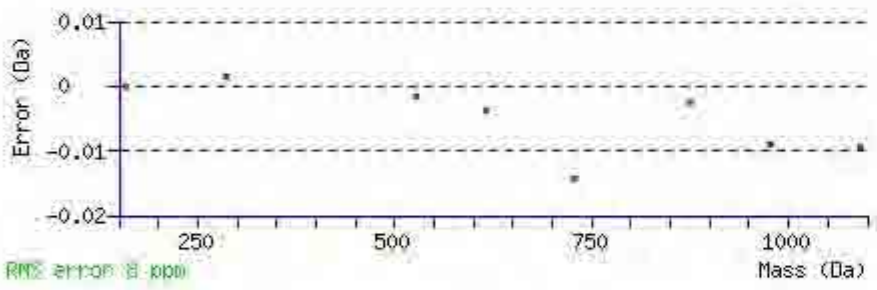
Match to Query 9793: 1274.641888 from(638.328220,2+) rtinseconds(992) index(3486)
Title: Locus:1.1.1.1326.26
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

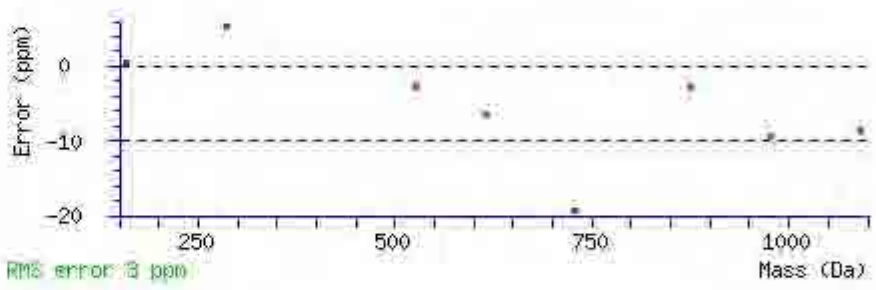
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1274.636734
Ions Score: 48 **Expect:** 0.0011
Matches : 8/106 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	186.087317	93.547296	169.060768	85.034022			A	1161.601098	581.304187	1144.574549	572.790913	1143.590533	572.298905	10
3	300.130244	150.568760	283.103695	142.055486			N	*1090.563984*	545.785630	1073.537435	537.272356	1072.553419	536.780348	9
4	401.177923	201.092600	384.151374	192.579325	383.167358	192.087317	T	*976.521057*	488.764167	959.494508	480.250892	958.510492	479.758884	8
5	548.246337	274.626807	531.219788	266.113532	530.235772	265.621524	F	*875.473378*	438.240327	858.446829	429.727053	857.462813	429.235045	7
6	661.330401	331.168839	644.303852	322.655564	643.319836	322.163556	I	*728.404964*	364.706120	711.378415	356.192846	710.394399	355.700838	6
7	748.362429	374.684853	731.335880	366.171578	730.351864	365.679570	S	*615.320900*	308.164088	598.294351	299.650814	597.310335	299.158806	5
8	845.415193	423.211235	828.388644	414.697960	827.404628	414.205952	P	*528.288872*	264.648074	511.262323	256.134800			4
9	973.473771	487.240524	956.447222	478.727249	955.463206	478.235241	Q	431.236108	216.121692	414.209559	207.608417			3
10	1101.532349	551.269813	1084.505800	542.756538	1083.521784	542.264530	Q	303.177530	152.092403	286.150981	143.579128			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NANTFISPQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	1274.636734	0.005154	NANTFISPQQR
14.9	1274.639465	0.002423	SVPTFTVIPEGP
14.9	1274.639465	0.002423	SVPTFTVIPEGP
7.3	1274.650650	-0.008762	REFDLSDPLAL
7.0	1274.646622	-0.004734	KGQDTSEELLR
5.7	1274.642792	-0.000904	EVADLSMGDLLL
4.2	1274.642792	-0.000904	TPSDMPLLELK
4.0	1274.650665	-0.008777	EGTLFPERTLP
4.0	1274.629532	0.012356	WGEPEPFLRL
3.5	1274.632904	0.008984	YVAPPSLRMPP

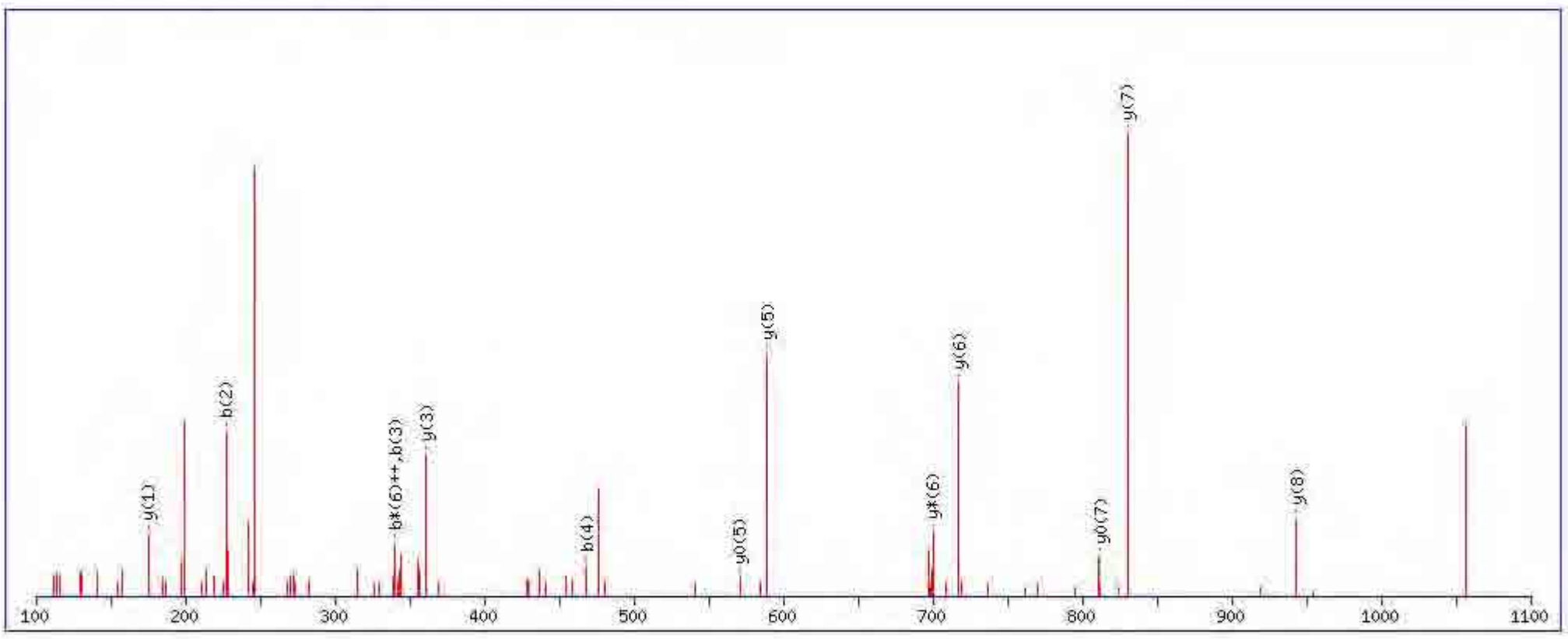
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLIKVEEGR**
Found in **NR4A3_HUMAN**, Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=2 SV=3

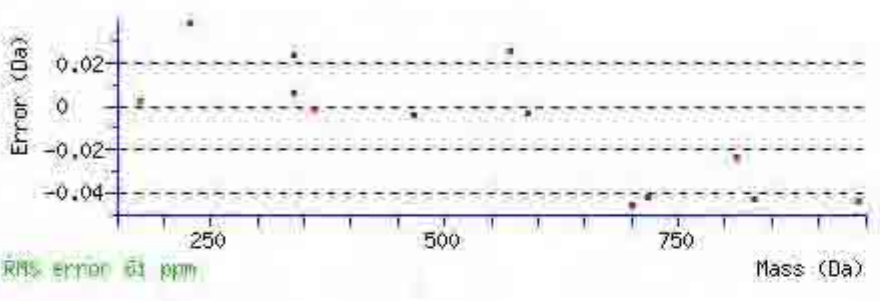
Match to Query 5181: 1055.596868 from(528.805710,2+) rtinseconds(1558) index(8809)
Title: Locus:1.1.1.1644.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

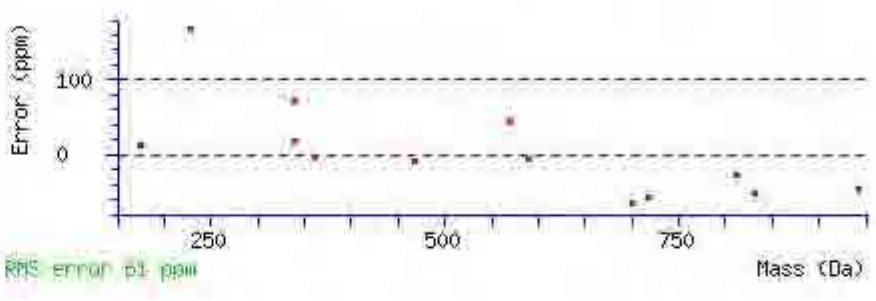
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597488
Variable modifications:
P1 : Oxidation (P)
Ions Score: 44 **Expect:** 0.0037
Matches : 13/76 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116					P							9
2	227.139019	114.073147					L	*943.557107*	472.282192	926.530558	463.768917	925.546542	463.276909	8
3	340.223083	170.615179					I	*830.473043*	415.740160	813.446494	407.226885	812.462478	406.734877	7
4	468.318046	234.662661	451.291497	226.149386			K	*717.388979*	359.198128	700.362430	350.684853	699.378414	350.192845	6
5	567.386460	284.196868	550.359911	275.683594			V	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	E	490.225602	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	825.471646	413.239461	808.445097	404.726187	807.461081	404.234179	E	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	882.493110	441.750193	865.466561	433.236919	864.482545	432.744911	G	232.140416	116.573846	215.113867	108.060571			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PLIKVEEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.2	1055.597488	-0.000620	PLIKVEEGR
44.1	1055.597504	-0.000636	LLPQLTSPR
28.7	1055.597488	-0.000620	LLKLDPADR
23.1	1055.601532	-0.004664	ILLGLWVQD
22.1	1055.604874	-0.008006	ILLIKNMDP
20.5	1055.597488	-0.000620	LGPLALETAR
17.3	1055.590302	0.006566	IIIFPPIPD
17.3	1055.590302	0.006566	IIIFPPIPD
16.2	1055.597473	-0.000605	ILLLADENR
16.2	1055.597504	-0.000636	IPLVSDPKR

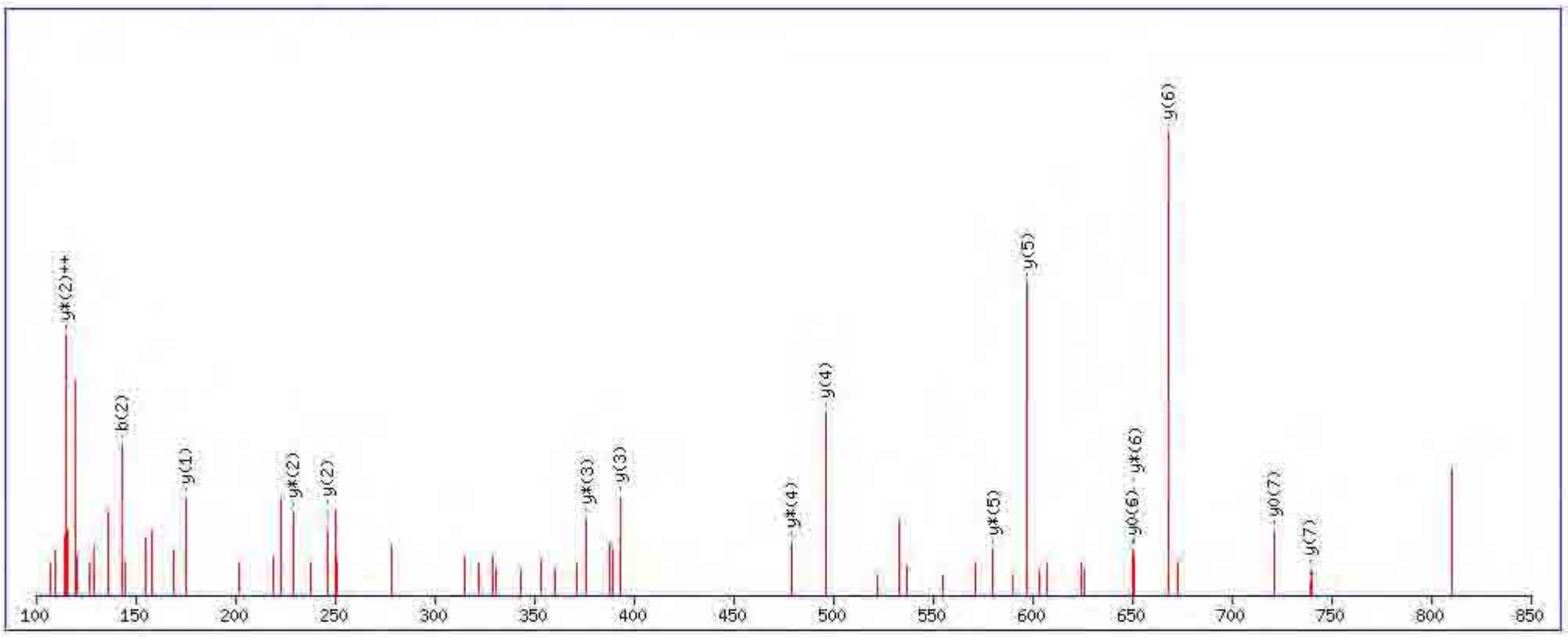
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAATCFAR**
Found in **PA2GA_HUMAN**, Phospholipase A2, membrane associated OS=Homo sapiens GN=PLA2G2A PE=1 SV=2

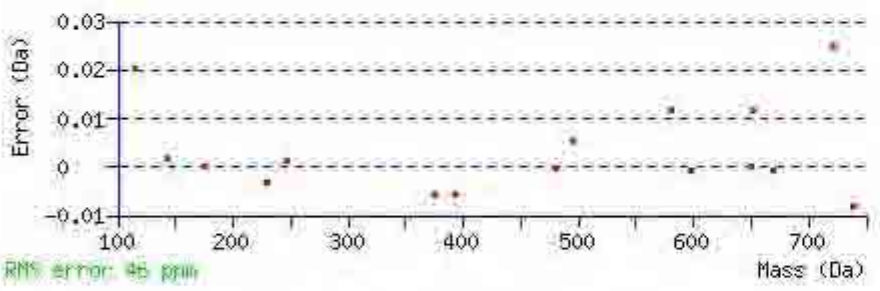
Match to Query 905: 809.388308 from(405.701430,2+) rtinseconds(756) index(1572)
Title: Locus:1.1.1.1194.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

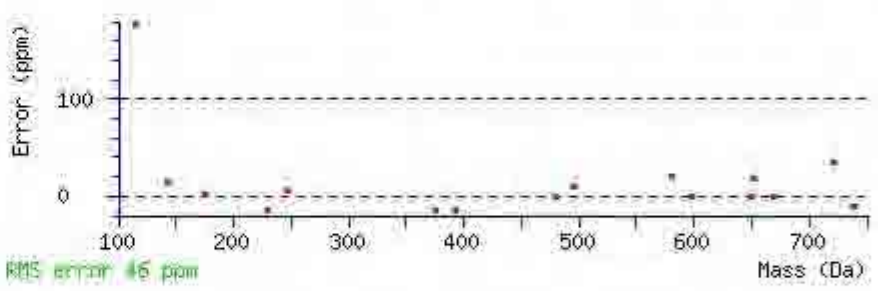
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 809.385391
Ions Score: 56 **Expect:** 0.00018
Matches : 16/56 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							8
2	143.081504	72.044390			A	*739.355572*	370.181424	722.329023	361.668150	721.345007	361.176142	7
3	214.118618	107.562947			A	*668.318458*	334.662867	651.291909	326.149593	650.307893	325.657585	6
4	315.166297	158.086786	297.155732	149.081504	T	*597.281344*	299.144310	580.254795	290.631036	579.270779	290.139028	5
5	418.175482	209.591379	400.164917	200.586097	C	*496.233665*	248.620471	479.207116	240.107196			4
6	565.243896	283.125586	547.233331	274.120304	F	*393.224480*	197.115878	376.197931	188.602604			3
7	636.281010	318.644143	618.270445	309.638861	A	*246.156066*	123.581671	229.129517	115.068397			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AAATCFAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.0	809.385391	0.002917	AAATCFAR
15.0	809.388779	-0.000471	GRTCMVK
10.6	809.385391	0.002917	CGKEFAR
9.0	809.391922	-0.003614	APAAPAAPP
5.9	809.391922	-0.003614	APAPASAPP
5.4	809.385391	0.002917	AARFDCK
5.0	809.382034	0.006274	WSGFSAR
4.7	809.391937	-0.003629	DLPGPQAP
4.7	809.391937	-0.003629	DLPGPQAP
4.4	809.391922	-0.003614	DPPGEKPA

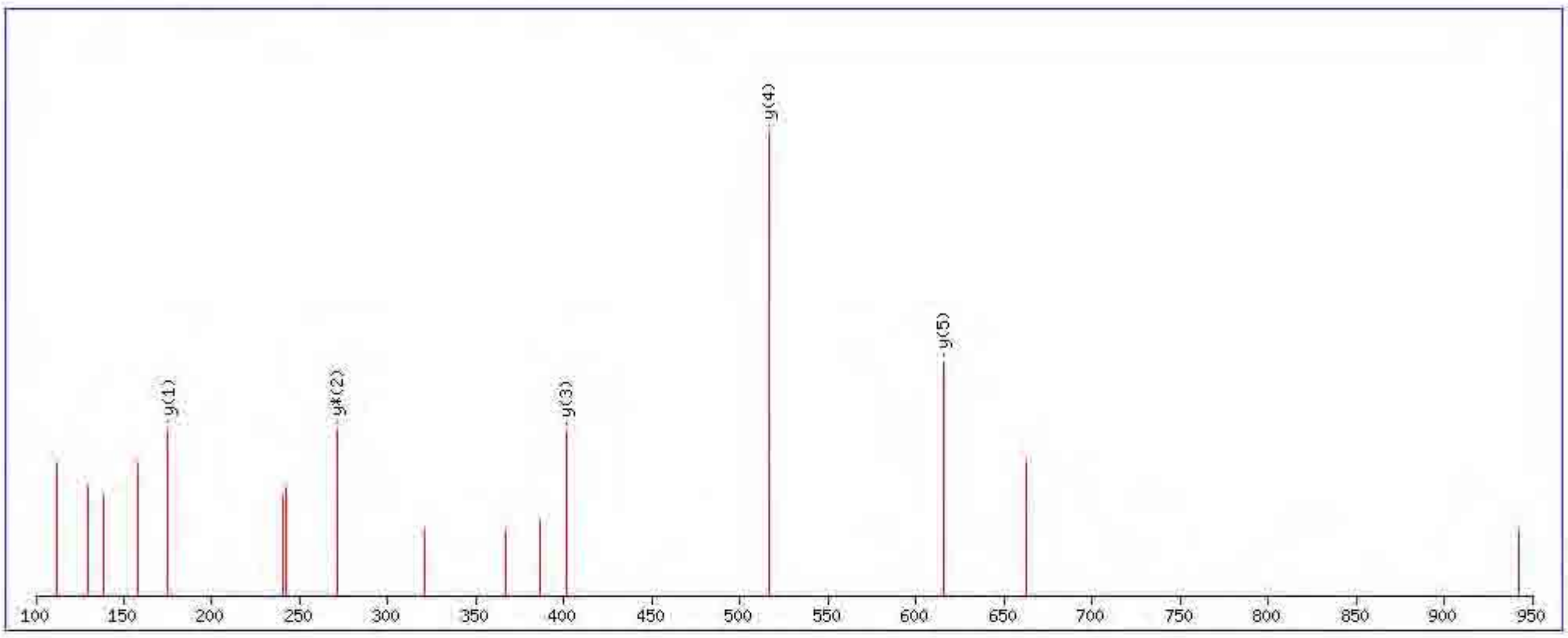
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVDILR**
Found in **CLVS2_HUMAN**, Clavesin-2 OS=Homo sapiens GN=CLVS2 PE=2 SV=1

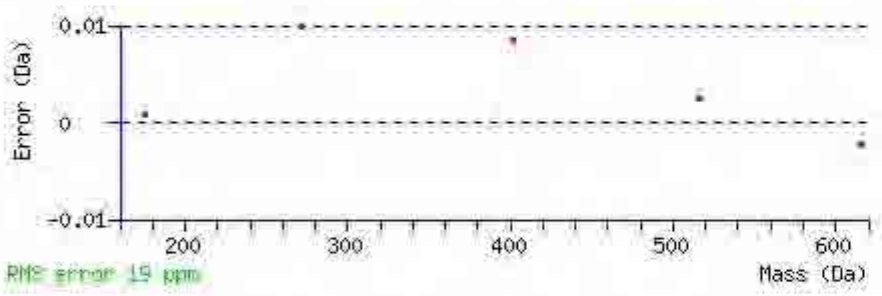
Match to Query 194: 727.461848 from(364.738200,2+) rtinseconds(1475) index(7894)
Title: Locus:1.1.1.1598.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

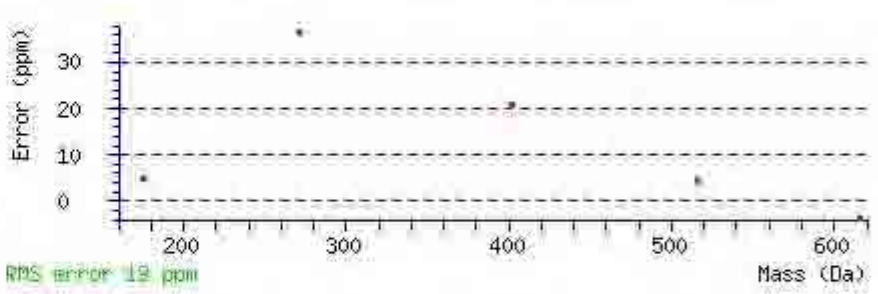
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 727.459213
Ions Score: 42 **Expect:** 0.005
Matches : 5/40 fragment ions using 5 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							6
2	213.159754	107.083515			V	*615.382437*	308.194857	598.355888	299.681582	597.371872	299.189574	5
3	328.186697	164.596986	310.176132	155.591704	D	*516.314023*	258.660650	499.287474	250.147375	498.303458	249.655367	4
4	441.270761	221.139018	423.260196	212.133736	I	*401.287080*	201.147178	384.260531	192.633904			3
5	554.354825	277.681051	536.344260	268.675768	L	288.203016	144.605146	271.176467	136.091872			2
6					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LVDILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	727.459213	0.002635	LVDILR
41.8	727.459213	0.002635	LVDLIR
41.8	727.459213	0.002635	LVDLLR
24.1	727.459213	0.002635	IVEVLR
24.1	727.459213	0.002635	IVLDLR
24.1	727.459213	0.002635	LVEVIR
24.1	727.459213	0.002635	LVEVLR
24.1	727.459213	0.002635	LVIDIR
24.1	727.459213	0.002635	LVIDLR
24.1	727.459213	0.002635	LVLDLR

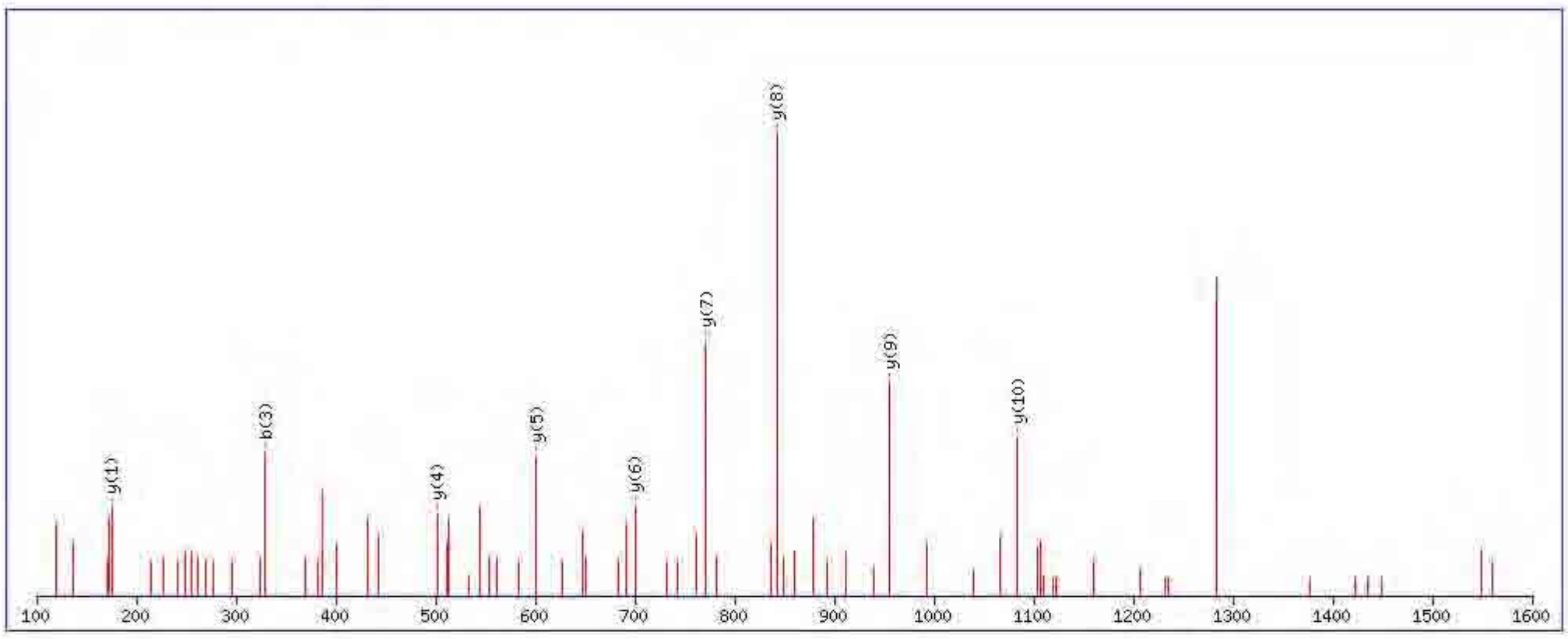
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVQIAAVVDVIR**
Found in **PIP_HUMAN**, Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1

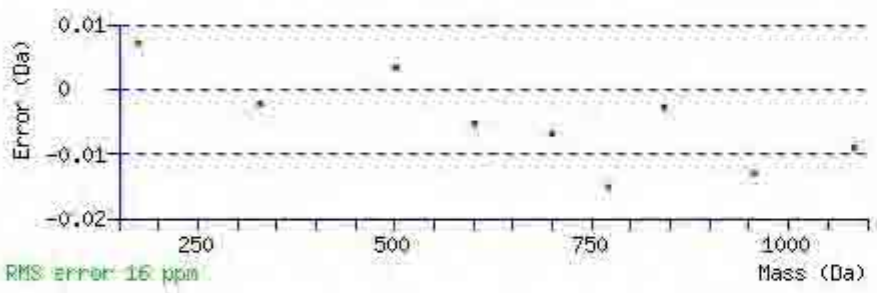
Match to Query 9982: 1282.760628 from(642.387590,2+) rtinseconds(2027) index(14362)
Title: Locus:1.1.1.1901.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

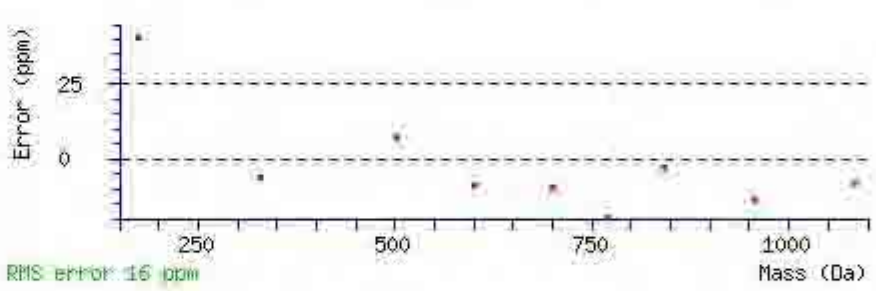
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1282.760895
Ions Score: 67 **Expect:** 1e-005
Matches : 9/122 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	201.123369	101.065322			183.112804	92.060040	V	1182.720485	591.863880	1165.693936	583.350606	1164.709920	582.858598	11
3	329.181947	165.094611	312.155398	156.581337	311.171382	156.089329	Q	*1083.652071*	542.329673	1066.625522	533.816399	1065.641506	533.324391	10
4	442.266011	221.636643	425.239462	213.123369	424.255446	212.631361	I	*955.593493*	478.300384	938.566944	469.787110	937.582928	469.295102	9
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	A	*842.509429*	421.758352	825.482880	413.245078	824.498864	412.753070	8
6	584.340239	292.673758	567.313690	284.160483	566.329674	283.668475	A	*771.472315*	386.239795	754.445766	377.726521	753.461750	377.234513	7
7	683.408653	342.207965	666.382104	333.694690	665.398088	333.202682	V	*700.435201*	350.721238	683.408652	342.207964	682.424636	341.715956	6
8	782.477067	391.742171	765.450518	383.228897	764.466502	382.736889	V	*601.366787*	301.187031	584.340238	292.673757	583.356222	292.181749	5
9	897.504010	449.255643	880.477461	440.742368	879.493445	440.250360	D	*502.298373*	251.652824	485.271824	243.139550	484.287808	242.647542	4
10	996.572424	498.789850	979.545875	490.276575	978.561859	489.784567	V	387.271430	194.139353	370.244881	185.626078			3
11	1109.656488	555.331882	1092.629939	546.818607	1091.645923	546.326599	I	288.203016	144.605146	271.176467	136.091871			2
12							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TVQIAAVVDVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.7	1282.760895	-0.000267	TVQIAAVVDVIR
23.6	1282.760864	-0.000236	VTKPKIPEAIR
13.3	1282.772095	-0.011467	SLKPGLARGQIK
13.3	1282.749649	0.010979	TVKPKLDLPPK
12.2	1282.749634	0.010994	LSKALADIVIPQ
9.2	1282.750992	0.009636	TVIPKFRPGPR
4.5	1282.760849	-0.000221	LSKPIALALDSR
4.5	1282.772110	-0.011482	SIQPITRTVLR
3.1	1282.750961	0.009667	GRLDALWALLR
3.0	1282.760849	-0.000221	NLTLPKNLLNK

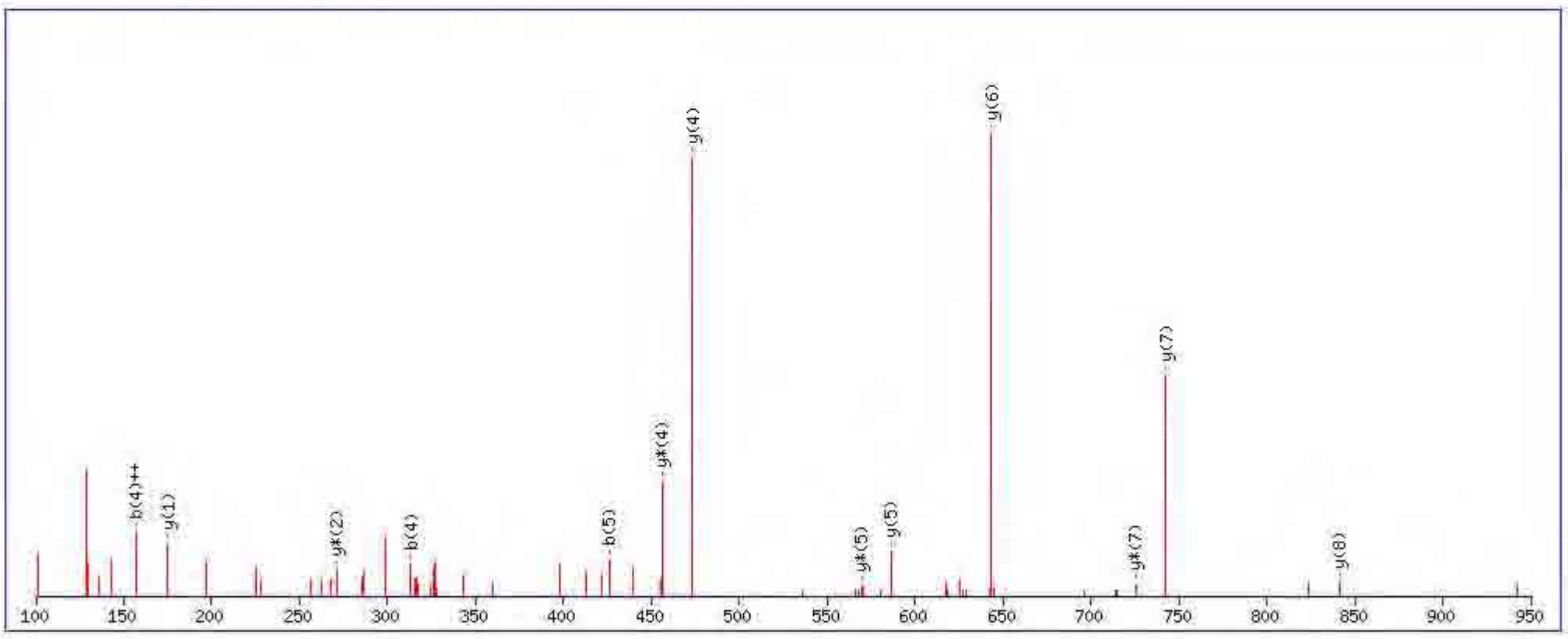
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVVGPQGLR**
Found in **F178B_HUMAN**, Protein FAM178B OS=Homo sapiens GN=FAM178B PE=2 SV=2

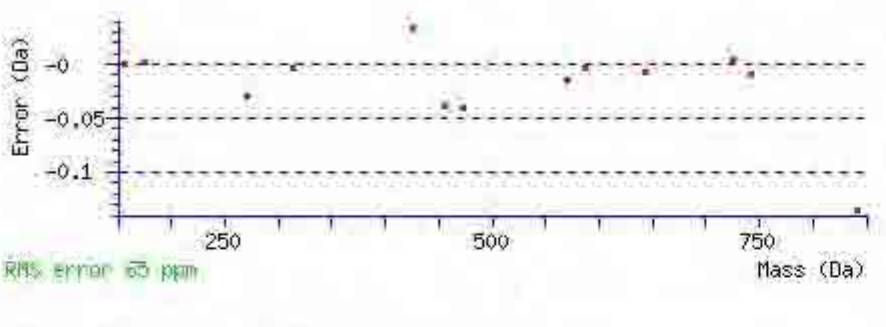
Match to Query 2546: 897.501608 from(449.758080,2+) rtinseconds(911) index(2630)
Title: Locus:1.1.1.1281.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

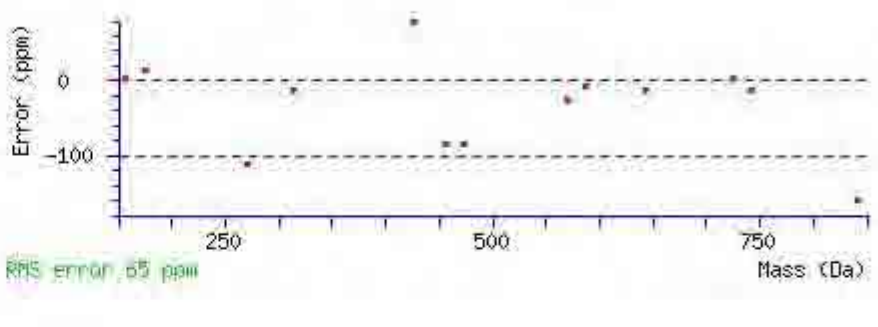
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 897.503235
Variable modifications:
P5 : Oxidation (P)
Ions Score: 41 **Expect:** 0.0073
Matches : 14/54 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008			G					9
2	157.097154	79.052215			V	*841.489029*	421.248153	824.462480	412.734878	8
3	256.165568	128.586422			V	*742.420615*	371.713946	725.394066	363.200671	7
4	313.187032	157.097154			G	*643.352201*	322.179739	626.325652	313.666464	6
5	426.234711	213.620994			P	*586.330737*	293.669007	569.304188	285.155732	5
6	554.293289	277.650283	537.266740	269.137008	Q	*473.283058*	237.145167	456.256509	228.631893	4
7	611.314753	306.161015	594.288204	297.647740	G	345.224480	173.115878	328.197931	164.602604	3
8	724.398817	362.703047	707.372268	354.189772	L	288.203016	144.605146	271.176467	136.091872	2
9					R	*175.118952*	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of GVVGPQGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.0	897.503235	-0.001627	GVVGPQGLR
39.1	897.503235	-0.001627	GVVGLPGQR
20.5	897.503235	-0.001627	GVVLGPRGAG
12.1	897.503204	-0.001596	AAPGLRLGAG
11.3	897.495987	0.005621	KALLSGYF
11.2	897.503204	-0.001596	RRPLLPD
10.1	897.503204	-0.001596	SPQPGKLR
9.0	897.503220	-0.001612	GVVPTAQRA
9.0	897.503204	-0.001596	PAGALKPGR
8.8	897.503235	-0.001627	GVPGKPGRV

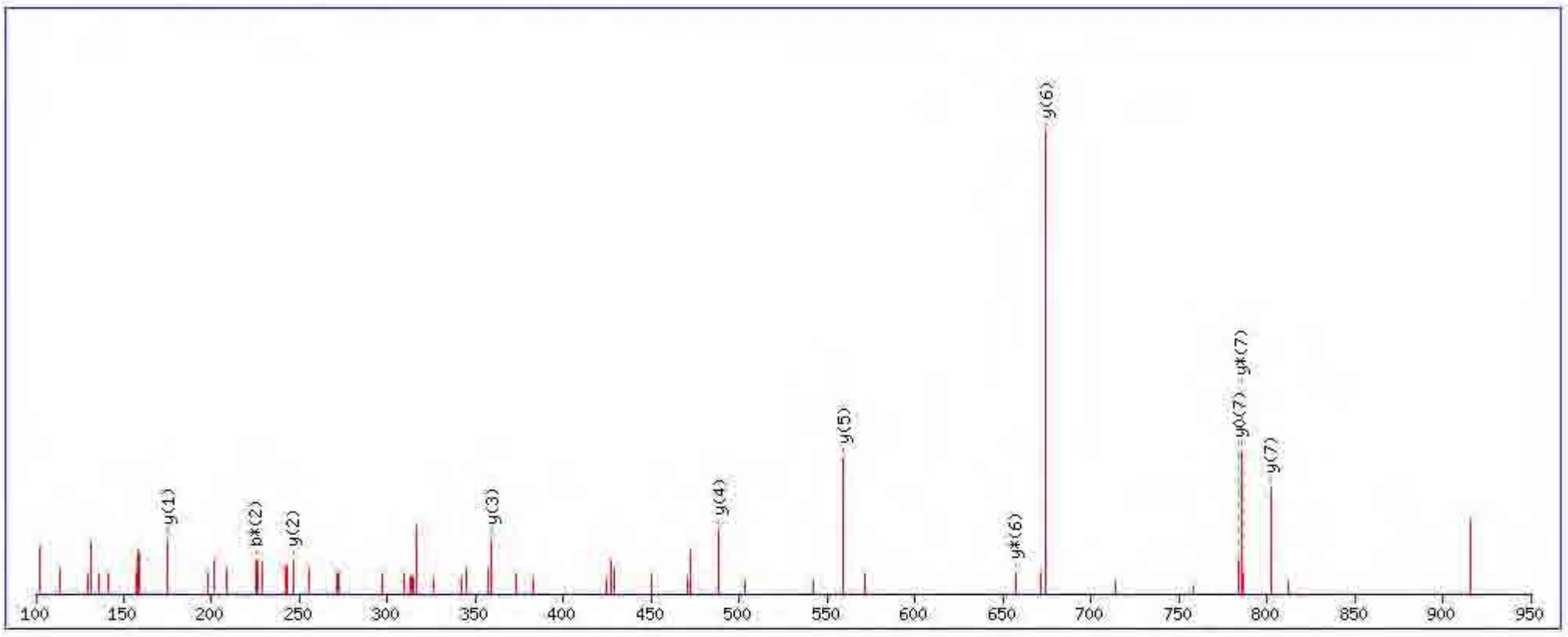
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQDAEIAR**
Found in **S10A6_HUMAN**, Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1

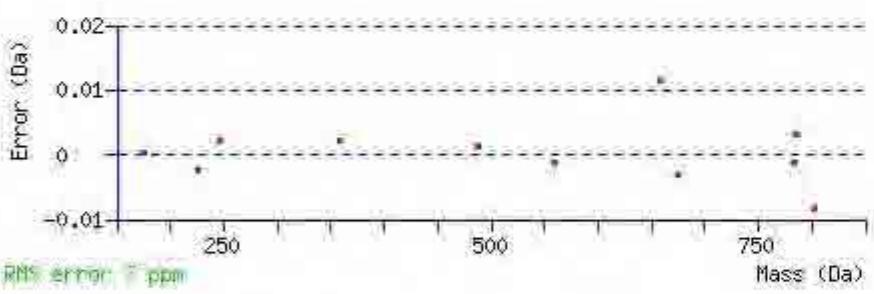
Match to Query 2841: 914.478528 from(458.246540,2+) rtinseconds(765) index(1618)
Title: Locus:1.1.1.1199.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

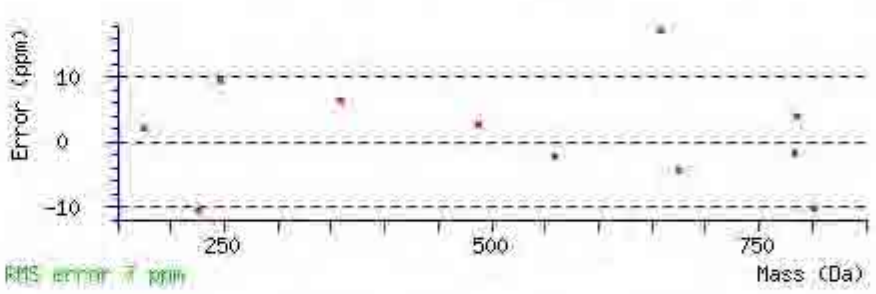
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 914.482117
Ions Score: 45 **Expect:** 0.008
Matches : 11/72 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							8
2	242.149918	121.578597	225.123369	113.065323			Q	*802.405358*	401.706317	785.378809	393.193043	784.394793	392.701035	7
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	D	*674.346780*	337.677028	657.320231	329.163754	656.336215	328.671746	6
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	A	*559.319837*	280.163557	542.293288	271.650282	541.309272	271.158274	5
5	557.256568	279.131922	540.230019	270.618648	539.246003	270.126640	E	*488.282723*	244.644999	471.256174	236.131725	470.272158	235.639717	4
6	670.340632	335.673954	653.314083	327.160680	652.330067	326.668672	I	*359.240130*	180.123703	342.213581	171.610428			3
7	741.377746	371.192511	724.351197	362.679237	723.367181	362.187229	A	*246.156066*	123.581671	229.129517	115.068396			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LQDAEIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	914.482117	-0.003589	LQDAEIAR
42.1	914.482132	-0.003604	PKDAPSLR
29.9	914.482132	-0.003604	LQDLSSPR
27.2	914.482147	-0.003619	IKDPGPTR
27.2	914.482147	-0.003619	IKDVPGDR
26.8	914.482117	-0.003589	LQGEIEAR
26.8	914.482147	-0.003619	PQGEVITR
21.3	914.482117	-0.003589	LQAEEVAR
18.5	914.482132	-0.003604	IKPSDSPR
18.5	914.482132	-0.003604	IQLDSSPR

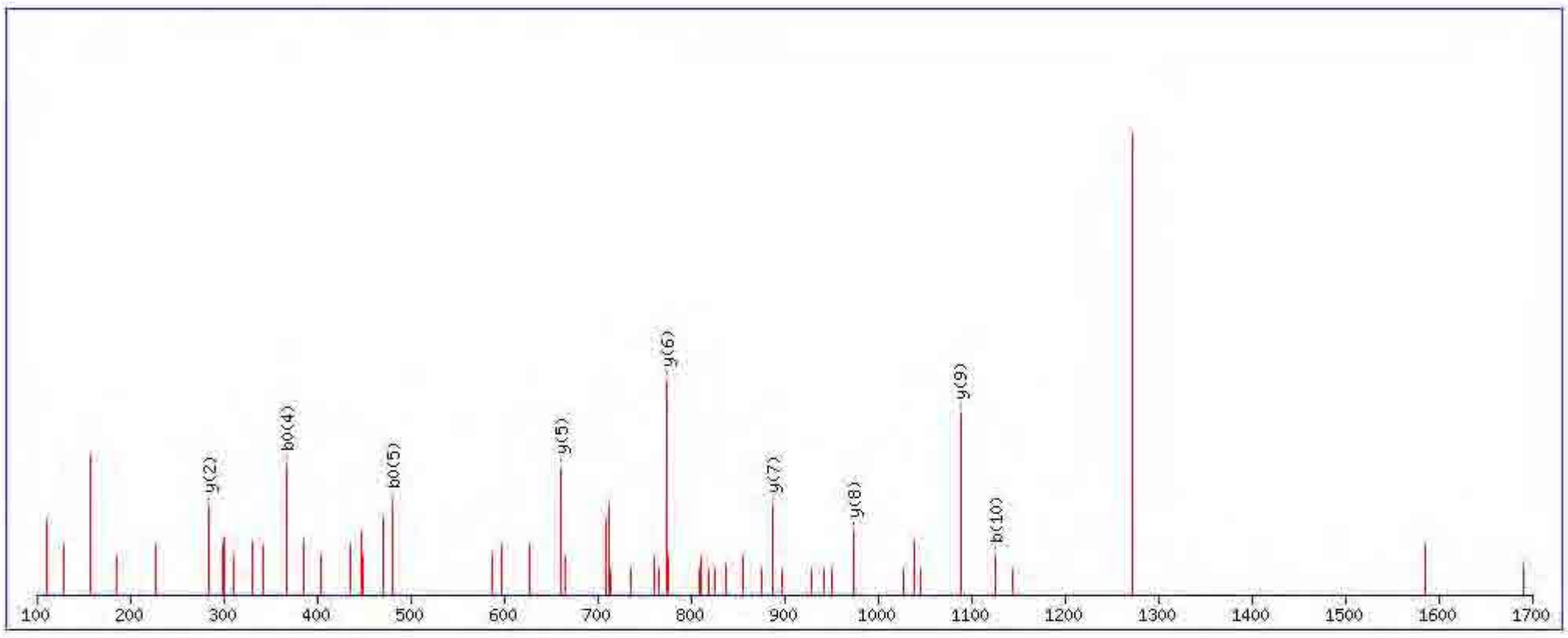
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALNSIIDVYHK**
Found in **S10A8_HUMAN**, Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1

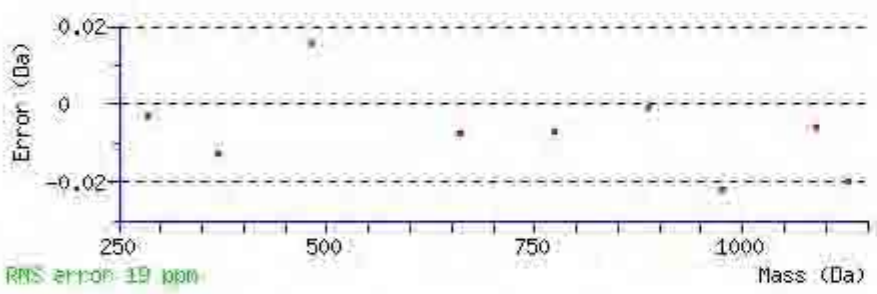
Match to Query 9762: 1271.682188 from(636.848370,2+) rtinseconds(1520) index(8404)
Title: Locus:1.1.1.1623.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

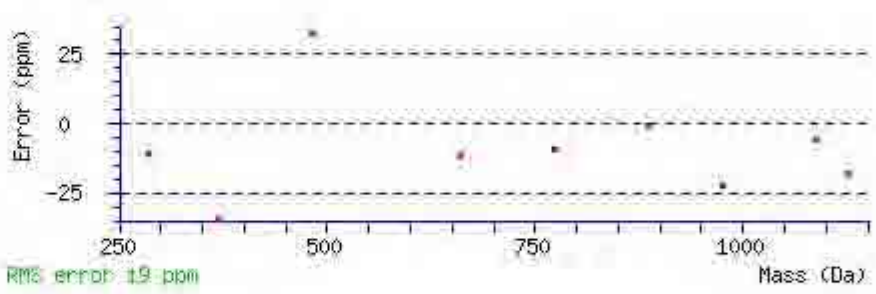
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1271.687363
Ions Score: 39 **Expect:** 0.0038
Matches : 9/102 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	185.128454	93.067865					L	1201.657549	601.332413	1184.631000	592.819138	1183.646984	592.327130	10
3	299.171381	150.089328	282.144832	141.576054			N	*1088.573485*	544.790381	1071.546936	536.277106	1070.562920	535.785098	9
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	S	*974.530558*	487.768917	957.504009	479.255642	956.519993	478.763634	8
5	499.287473	250.147375	482.260924	241.634100	481.276908	241.142092	I	*887.498530*	444.252903	870.471981	435.739628	869.487965	435.247620	7
6	612.371537	306.689407	595.344988	298.176132	594.360972	297.684124	I	*774.414466*	387.710871	757.387917	379.197596	756.403901	378.705588	6
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	D	*661.330402*	331.168839	644.303853	322.655564	643.319837	322.163556	5
8	826.466894	413.737085	809.440345	405.223811	808.456329	404.731803	V	546.303459	273.655368	529.276910	265.142093			4
9	989.530223	495.268750	972.503674	486.755475	971.519658	486.263467	Y	447.235045	224.121160	430.208496	215.607886			3
10	1126.589135	563.798205	1109.562586	555.284931	1108.578570	554.792923	H	*284.171716*	142.589496	267.145167	134.076221			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ALNSIIDVYHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	1271.687363	-0.005175	ALNSIIDVYHK
12.3	1271.687363	-0.005175	FEIRDLLPAAQ
12.1	1271.672104	0.010084	QVASASIKLENP
11.7	1271.672104	0.010084	LNASIADLQSQL
8.8	1271.683334	-0.001146	RTQLEEIQQK
7.8	1271.683380	-0.001192	QVTGNPKGTSVGK
7.5	1271.672089	0.010099	QQELLEKEQK
7.5	1271.676804	0.005384	QQELLRQAMR
7.0	1271.670273	0.011915	QAWKFLLGYF
5.6	1271.676147	0.006041	AIFPTPDPAALK

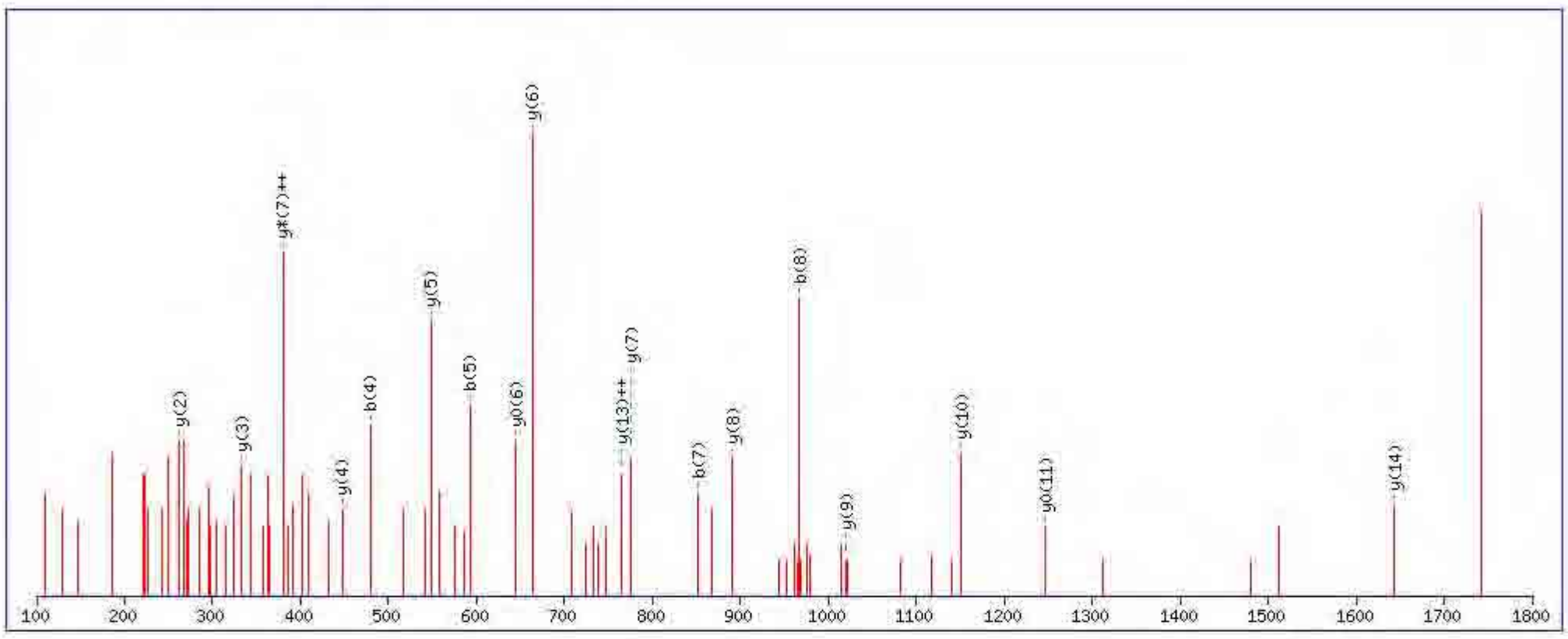
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIEHIMEDLDTNADK**
Found in **S10A9_HUMAN**, Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1

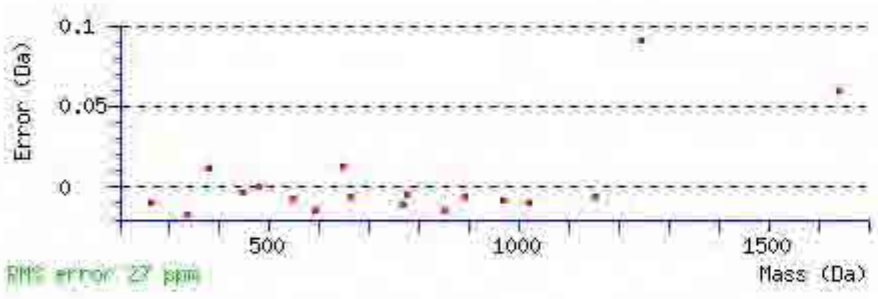
Match to Query 15510: 1741.818672 from(581.613500,3+) rtinseconds(1555) index(8775)
Title: Locus:1.1.1.1642.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

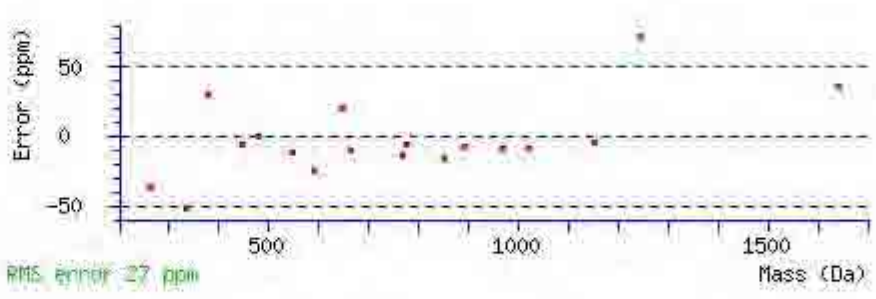
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1741.819244
Ions Score: 70 **Expect:** 3.1e-006
Matches : 18/140 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							15
2	213.159754	107.083515					I	*1643.758128*	822.382702	1626.731579	813.869428	1625.747563	813.377419	14
3	342.202347	171.604811			324.191782	162.599529	E	1530.674064	765.840670	1513.647515	757.327396	1512.663499	756.835388	13
4	**479.261259**	240.134267			461.250694	231.128985	H	1401.631471	701.319373	1384.604922	692.806099	1383.620906	692.314091	12
5	**592.345323**	296.676300			574.334758	287.671017	I	1264.572559	632.789918	1247.546010	624.276643	1246.561994	623.784635	11
6	723.385808	362.196542			705.375243	353.191260	M	*1151.488495*	576.247886	1134.461946	567.734611	1133.477930	567.242603	10
7	**852.428401**	426.717839			834.417836	417.712556	E	*1020.448010*	510.727643	1003.421461	502.214369	1002.437445	501.722361	9
8	**967.455344**	484.231310			949.444779	475.226027	D	*891.405417*	446.206347	874.378868	437.693072	873.394852	437.201064	8
9	1080.539408	540.773342			1062.528843	531.768059	L	*776.378474*	388.692875	759.351925	380.179601	758.367909	379.687593	7
10	1195.566351	598.286813			1177.555786	589.281531	D	*663.294410*	332.150843	646.267861	323.637569	645.283845	323.145561	6
11	1296.614030	648.810653			1278.603465	639.805370	T	*548.267467*	274.637372	531.240918	266.124097	530.256902	265.632089	5
12	1410.656957	705.832116	1393.630408	697.318842	1392.646392	696.826834	N	*447.219788*	224.113532	430.193239	215.600258	429.209223	215.108250	4
13	1481.694071	741.350673	1464.667522	732.837399	1463.683506	732.345391	A	*333.176861*	167.092069	316.150312	158.578794	315.166296	158.086786	3
14	1596.721014	798.864145	1579.694465	790.350871	1578.710449	789.858862	D	*262.139747*	131.573512	245.113198	123.060237	244.129182	122.568229	2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VIEHIMEDLDTNADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.3	1741.819244	-0.000572	VIEHIMEDLDTNADK
10.8	1741.834518	-0.015846	NMGILGSYDPQQIFK
5.1	1741.811859	0.006813	ETESRGSESGIFTNTK
4.6	1741.801514	0.017158	DFALTQGSMITPSCQK
4.5	1741.801483	0.017189	EKSSCQIIQFMEGDK
0.9	1741.801514	0.017158	LAEDMTVCVADFGLSR
0.4	1741.827118	-0.008446	TNQFGDLSPKEHQEL
0.2	1741.824142	-0.005470	MIWEWKSCSIVMLT
0.0	1741.814072	0.004600	LAHGGARPHPCPDCPKA

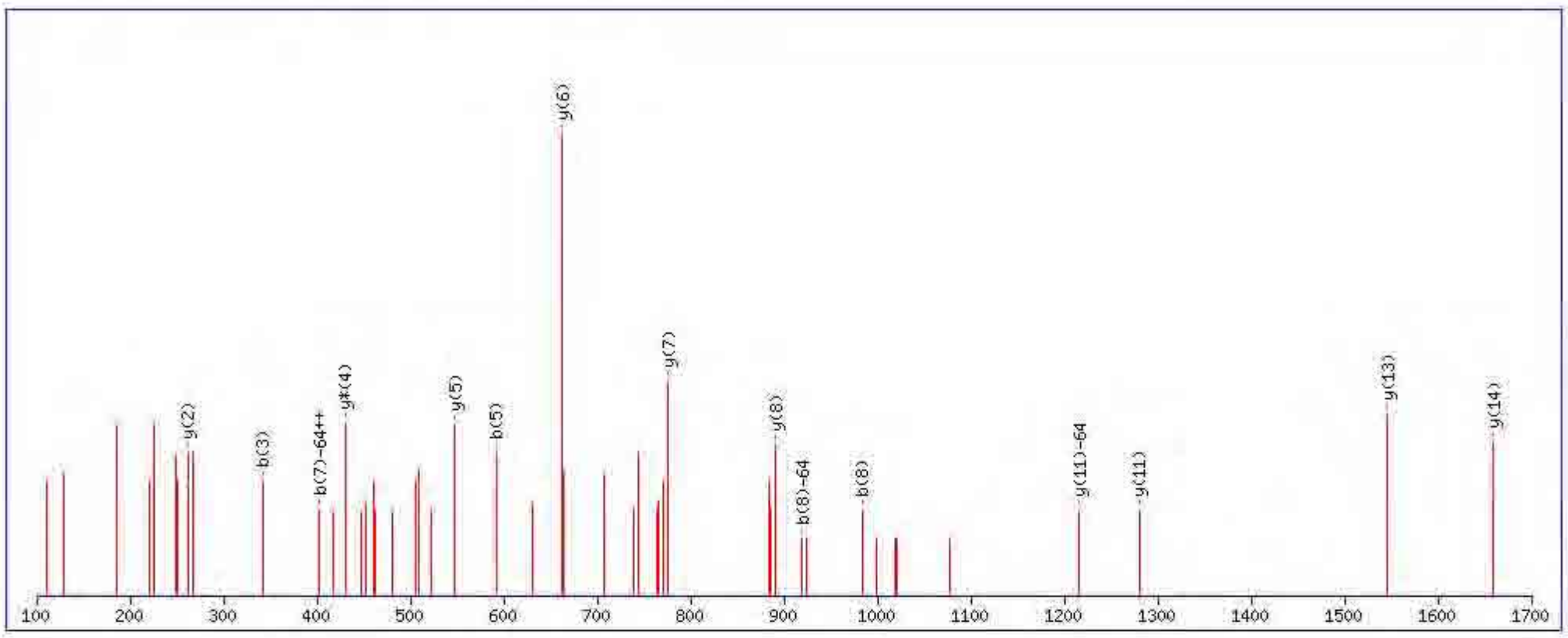
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIEHIMEDLDTNADK**
Found in **S10A9_HUMAN**, Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1

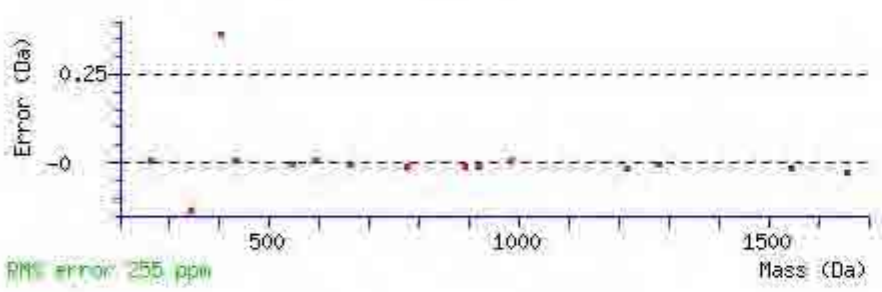
Match to Query 15591: 1757.805732 from(586.942520,3+) rtinseconds(1205) index(5065)
Title: Locus:1.1.1.1448.19
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

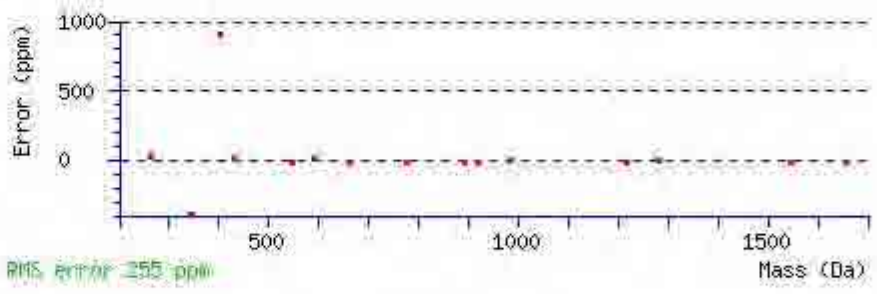
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1757.814163
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 52 **Expect:** 7e-005
Matches : 15/212 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							15
2	213.159754	107.083515					I	*1659.753043*	830.380159	1642.726494	821.866885	1641.742478	821.374877	14
3	**342.202347**	171.604811			324.191782	162.599529	E	*1546.668979*	773.838128	1529.642430	765.324853	1528.658414	764.832845	13
4	479.261259	240.134267			461.250694	231.128985	H	1417.626386	709.316831	1400.599837	700.803557	1399.615821	700.311549	12
5	**592.345323**	296.676300			574.334758	287.671017	I	*1280.567474*	640.787375	1263.540925	632.274101	1262.556909	631.782093	11
6	739.380723	370.194000			721.370158	361.188717	M	1167.483410	584.245343	1150.456861	575.732069	1149.472845	575.240061	10
7	868.423316	434.715296			850.412751	425.710014	E	1020.448010	510.727643	1003.421461	502.214369	1002.437445	501.722361	9
8	**983.450259**	492.228768			965.439694	483.223485	D	*891.405417*	446.206347	874.378868	437.693072	873.394852	437.201064	8
9	1096.534323	548.770799			1078.523758	539.765517	L	*776.378474*	388.692875	759.351925	380.179601	758.367909	379.687593	7
10	1211.561266	606.284271			1193.550701	597.278988	D	*663.294410*	332.150843	646.267861	323.637569	645.283845	323.145561	6
11	1312.608945	656.808111			1294.598380	647.802828	T	*548.267467*	274.637372	531.240918	266.124097	530.256902	265.632089	5
12	1426.651872	713.829574	1409.625323	705.316300	1408.641307	704.824291	N	447.219788	224.113532	430.193239	215.600258	429.209223	215.108250	4
13	1497.688986	749.348131	1480.662437	740.834857	1479.678421	740.342848	A	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
14	1612.715929	806.861603	1595.689380	798.348328	1594.705364	797.856320	D	*262.139747*	131.573512	245.113198	123.060237	244.129182	122.568229	2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VIEHIMEDLDTNADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	1757.814163	-0.008431	VIEHIMEDLDTNADK
7.0	1757.818222	-0.012490	TMWSPPGIPLDSPTEV
4.2	1757.793030	0.012702	NMAILDPPDADHLYSA
4.2	1757.793030	0.012702	NMAILDPPDADHLYSA
2.8	1757.811676	-0.005944	SLFCPLDMGRLNPTY
2.8	1757.821579	-0.015847	KCIYVGMATDLVLDDS
1.3	1757.822037	-0.016305	TNQFGDLSPKEHQEL
1.3	1757.822037	-0.016305	QQTRSPSPTLSYYSSG
0.5	1757.806778	-0.001046	KVPPSGSGGSELSNGEAGE
0.5	1757.818222	-0.012490	TMWSPPGIPLDSPTEV

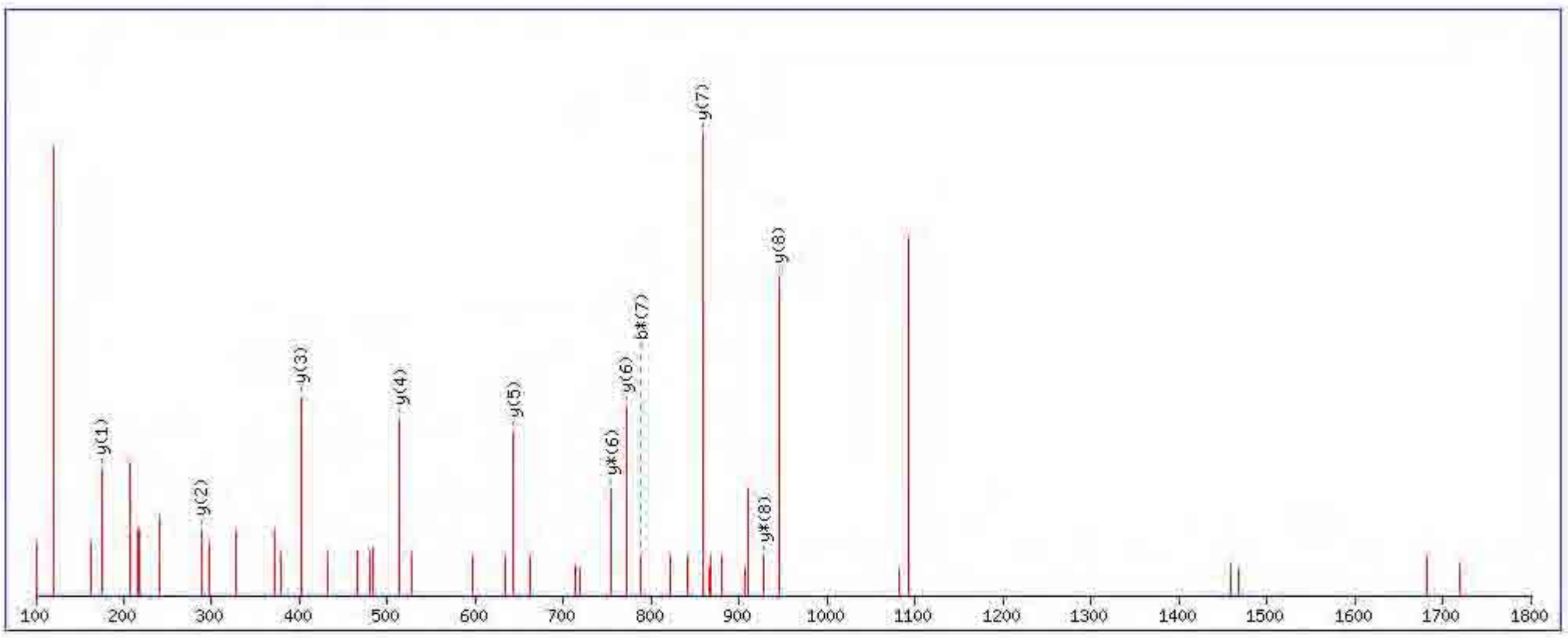
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSSQELILR**
Found in **TGM3_HUMAN**, Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4

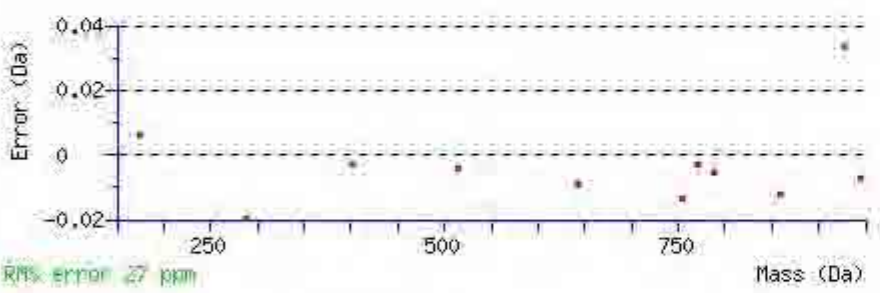
Match to Query 5898: 1091.598188 from(546.806370,2+) rtinseconds(1581) index(9098)
Title: Locus:1.1.1.1656.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

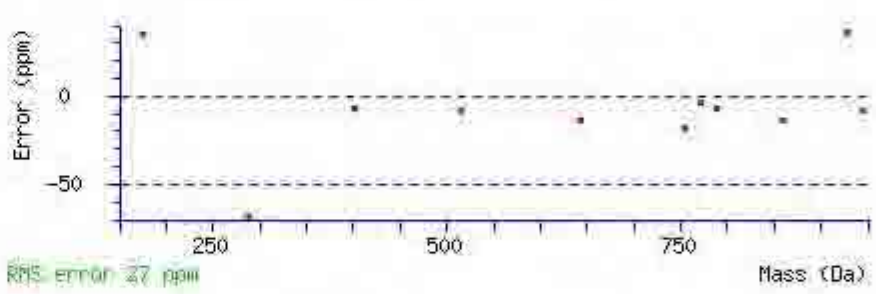
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1091.597488
Ions Score: 46 **Expect:** 0.0011
Matches : 11/80 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							9
2	235.107718	118.057497			217.097153	109.052214	S	*945.536371*	473.271824	928.509822	464.758549	927.525806	464.266541	8
3	322.139746	161.573511			304.129181	152.568229	S	*858.504343*	429.755810	841.477794	421.242535	840.493778	420.750527	7
4	450.198324	225.602800	433.171775	217.089526	432.187759	216.597518	Q	*771.472315*	386.239796	754.445766	377.726521	753.461750	377.234513	6
5	579.240917	290.124097	562.214368	281.610822	561.230352	281.118814	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	L	*514.371144*	257.689210	497.344595	249.175936			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	*401.287080*	201.147178	384.260531	192.633904			3
8	918.493109	459.750193	901.466560	451.236918	900.482544	450.744910	L	*288.203016*	144.605146	271.176467	136.091872			2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FSSQELILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1091.597488	0.000700	FSSQELILR
13.5	1091.608734	-0.010546	FSQSVQKIR
11.9	1091.597488	0.000700	FSLASADLLR
11.9	1091.608719	-0.010531	FSQKSNLIR
10.4	1091.597473	0.000715	YSAKPEILR
7.1	1091.597473	0.000715	AYSQSPAIKK
7.1	1091.597504	0.000684	SFSQKGNLVL
6.5	1091.608734	-0.010546	FSVQKTNLR
6.4	1091.608261	-0.010073	MKLCSLAVLV
5.4	1091.597504	0.000684	FSTLDIQLR

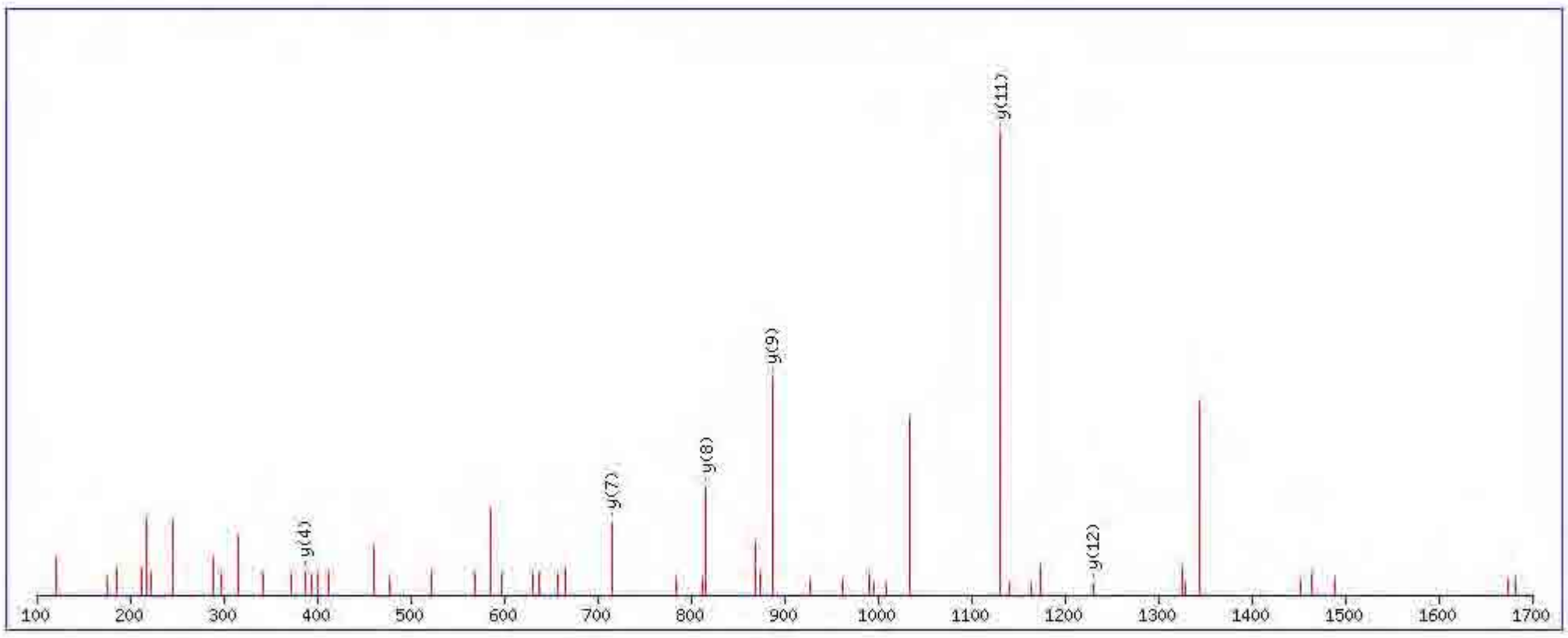
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLMATDRGSPAL**
Found in **PCD16_HUMAN**, Protocadherin-16 OS=Homo sapiens GN=DCHS1 PE=2 SV=1

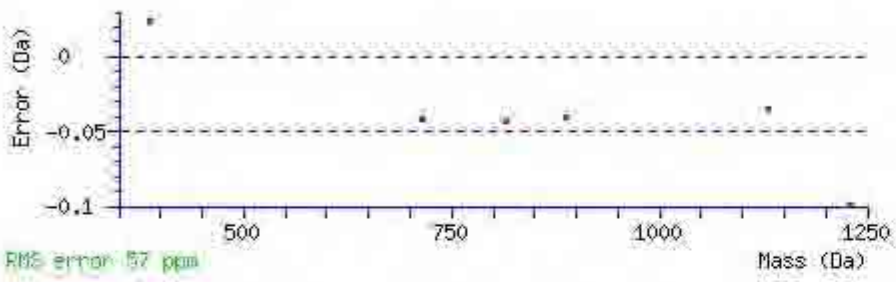
Match to Query 11014: 1342.718408 from(672.366480,2+) rtinseconds(1795) index(11753)
Title: Locus:1.1.1.1772.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

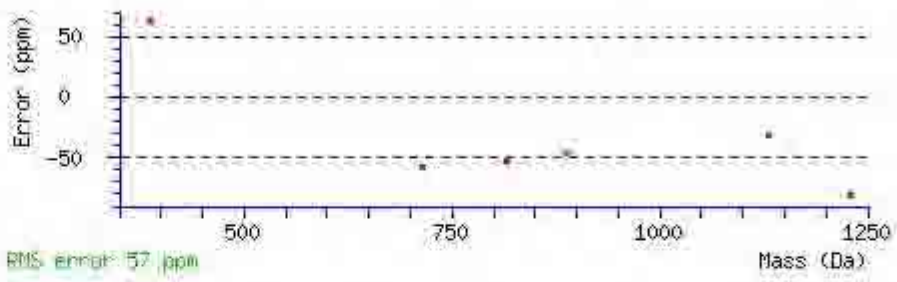
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1342.727859
Ions Score: 37 **Expect:** 0.0039
Matches : 6/104 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							13
2	213.159754	107.083515					V	*1230.651085*	615.829181	1213.624536	607.315906	1212.640520	606.823898	12
3	326.243818	163.625547					L	*1131.582671*	566.294973	1114.556122	557.781699	1113.572106	557.289691	11
4	457.284303	229.145789					M	1018.498607	509.752941	1001.472058	501.239667	1000.488042	500.747659	10
5	528.321417	264.664347					A	*887.458122*	444.232699	870.431573	435.719424	869.447557	435.227416	9
6	629.369096	315.188186			611.358531	306.182904	T	*816.421008*	408.714142	799.394459	400.200867	798.410443	399.708859	8
7	744.396039	372.701658			726.385474	363.696375	D	*715.373329*	358.190302	698.346780	349.677028	697.362764	349.185020	7
8	900.497150	450.752213	883.470601	442.238938	882.486585	441.746930	R	600.346386	300.676831	583.319837	292.163556	582.335821	291.671548	6
9	957.518614	479.262945	940.492065	470.749670	939.508049	470.257662	G	444.245275	222.626275			426.234710	213.620993	5
10	1044.550642	522.778959	1027.524093	514.265685	1026.540077	513.773676	S	*387.223811*	194.115543			369.213246	185.110261	4
11	1141.603406	571.305341	1124.576857	562.792067	1123.592841	562.300058	P	300.191783	150.599529					3
12	1212.640520	606.823898	1195.613971	598.310624	1194.629955	597.818615	A	203.139019	102.073147					2
13							L	132.101905	66.554590					1





NCBI **BLAST** search of LVLMATDRGSPAL
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1342.727859	-0.009451	LVLMATDRGSPAL
10.7	1342.716660	0.001748	LMVSPTSVAAVPVG
9.0	1342.709229	0.009179	LVDEEPQLTKR
8.9	1342.713272	0.005136	LVPLVQATFPEN
3.7	1342.710754	0.007654	LVAMGSAWPWLL
3.7	1342.724503	-0.006095	IVPNGDNVFAAVK
3.7	1342.724472	-0.006064	LVPSYEAPAAAVR
3.6	1342.713287	0.005121	VLPPQPQPPLPP
3.6	1342.717972	0.000436	LVVEWMPTRGR
3.1	1342.709244	0.009164	PVSGTKPDLIER

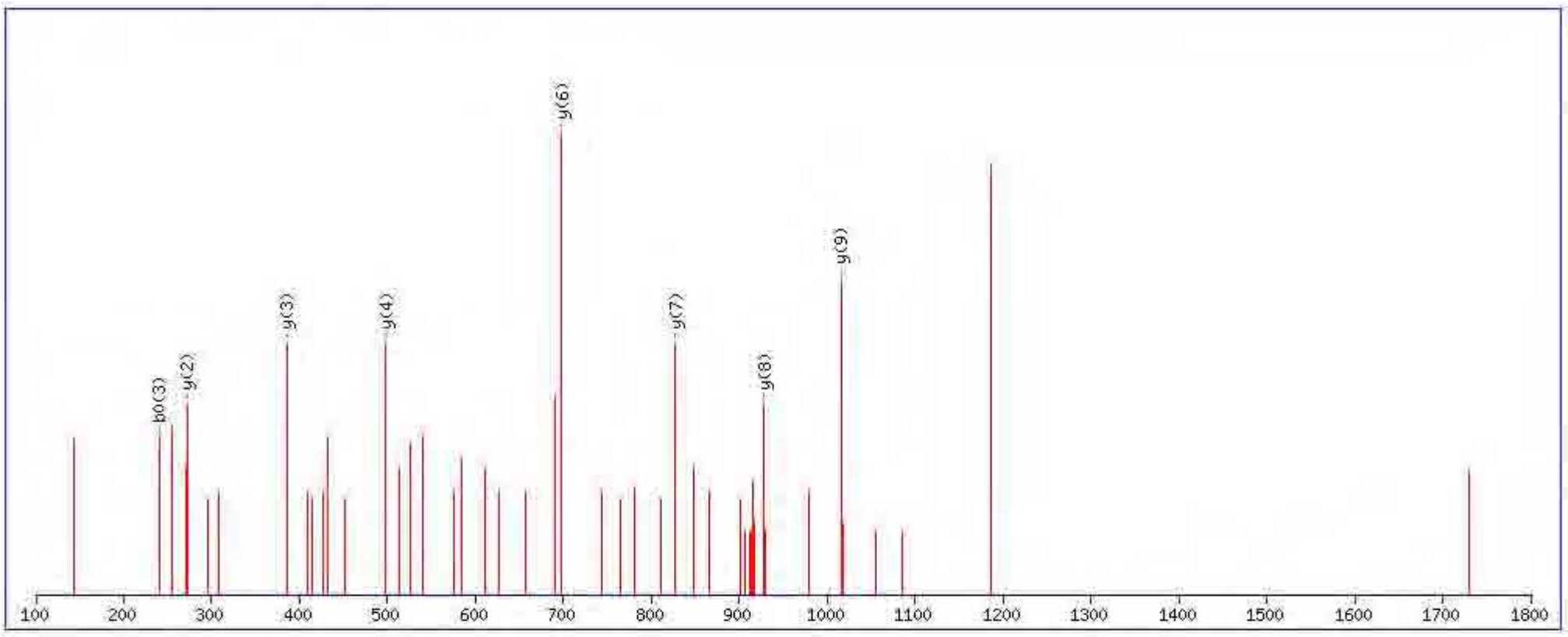
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

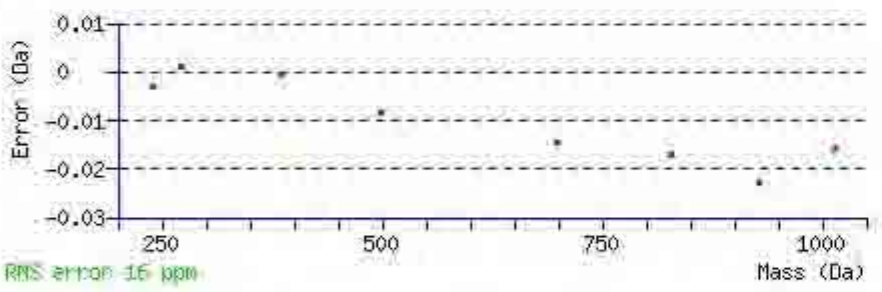
Match to Query 8082: 1184.673408 from(593.343980,2+) rtinseconds(1733) index(10922)
Title: Locus:1.1.1.1739.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

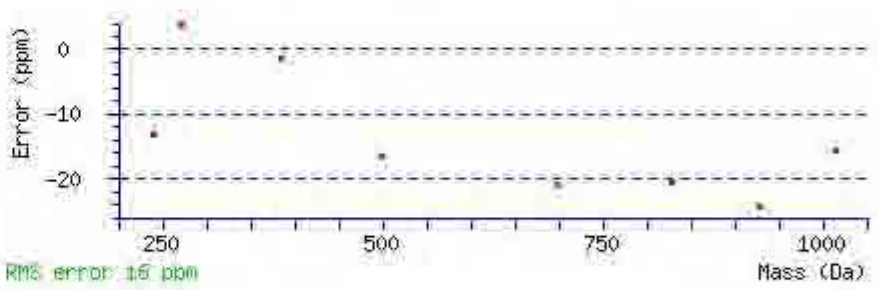
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 63 **Expect:** 5.1e-005
Matches : 8/86 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	*1015.578236*	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	*928.546208*	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	*827.498529*	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	*698.455936*	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	611.423908	306.215592	594.397359	297.702318			5
8	801.435260	401.221268	783.424695	392.215986	L	*498.339844*	249.673560	481.313295	241.160285			4
9	914.519324	457.763300	896.508759	448.758018	I	*385.255780*	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	*272.171716*	136.589496	255.145167	128.076221			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.1	1184.676468	-0.003060	GLSTESILIPR
18.3	1184.677795	-0.004387	PRHPEALLPR
17.2	1184.676468	-0.003060	KEDLTTLLPR
12.9	1184.662552	0.010856	RGQTSASILPR
6.7	1184.680496	-0.007088	AIWDGLILLAT
6.7	1184.666580	0.006828	DPKHLPPLPR
6.4	1184.680527	-0.007119	GLTLPPVPFTK
5.3	1184.662552	0.010856	VATVGRENLAR
5.1	1184.665237	0.008171	SSPIIIQLLSD
5.0	1184.676468	-0.003060	APSILSVLKQN

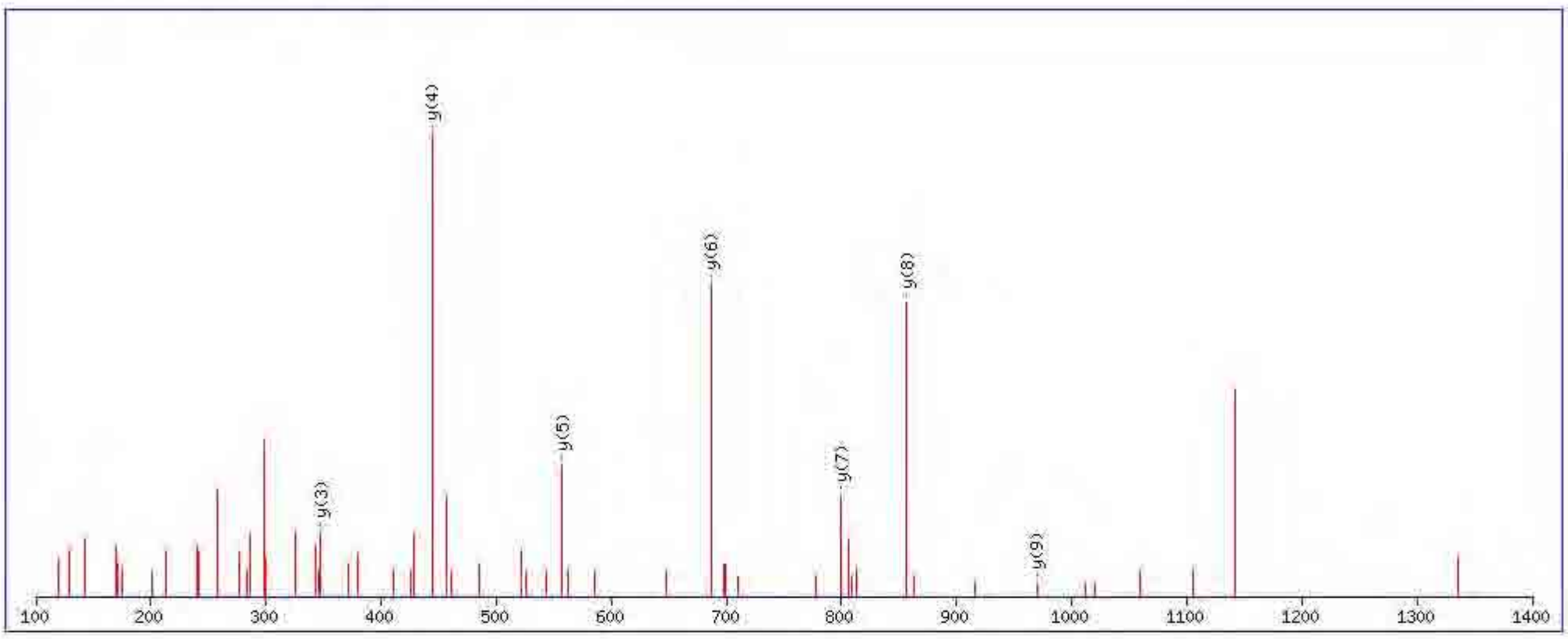
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDLGIEIPAEK**
Found in **KPYM_HUMAN**, Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4

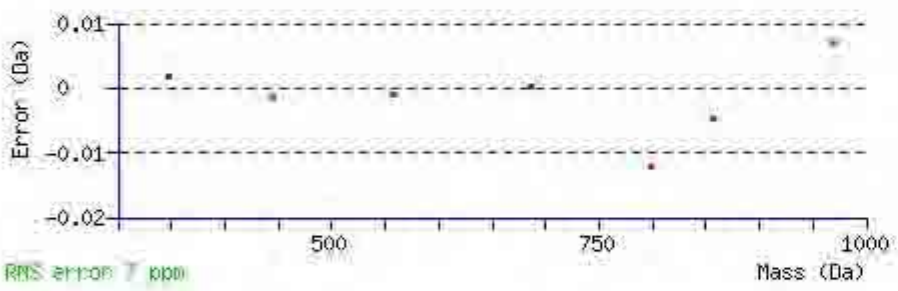
Match to Query 6899: 1140.601528 from(571.308040,2+) rtinseconds(1587) index(9179)
Title: Locus:1.1.1.1659.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

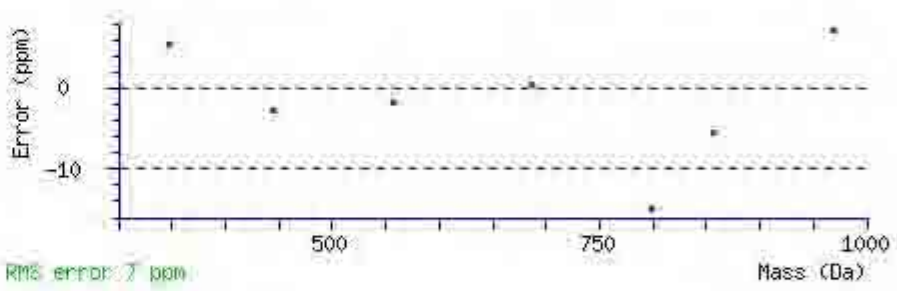
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1140.602631
Ions Score: 60 **Expect:** 0.00014
Matches : 7/96 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	173.055683	87.031479	155.045118	78.026197	D	1084.588467	542.797872	1067.561918	534.284597	1066.577902	533.792589	10
3	286.139747	143.573512	268.129182	134.568229	L	*969.561524*	485.284400	952.534975	476.771126	951.550959	476.279118	9
4	343.161211	172.084243	325.150646	163.078961	G	*856.477460*	428.742368	839.450911	420.229094	838.466895	419.737086	8
5	456.245275	228.626275	438.234710	219.620993	I	*799.455996*	400.231636	782.429447	391.718362	781.445431	391.226354	7
6	585.287868	293.147572	567.277303	284.142290	E	*686.371932*	343.689604	669.345383	335.176330	668.361367	334.684322	6
7	698.371932	349.689604	680.361367	340.684322	I	*557.329339*	279.168308	540.302790	270.655033	539.318774	270.163025	5
8	795.424696	398.215986	777.414131	389.210704	P	*444.245275*	222.626275	427.218726	214.113001	426.234710	213.620993	4
9	866.461810	433.734543	848.451245	424.729261	A	*347.192511*	174.099893	330.165962	165.586619	329.181946	165.094611	3
10	995.504403	498.255840	977.493838	489.250557	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GDLGIEIPAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.8	1140.602631	-0.001103	GDLGIEIPAEK
21.7	1140.603973	-0.002445	RTWLEPAPR
20.0	1140.596115	0.005413	ICRAPEPPVK
12.7	1140.603973	-0.002445	RTWLEPAPR
10.6	1140.602631	-0.001103	LQLTELQEPA
9.9	1140.596115	0.005413	ICRAPEPPVK
8.2	1140.602646	-0.001118	DLKVEPPPAK
8.1	1140.592743	0.008785	ERIWPALQP
8.1	1140.592743	0.008785	REPWLLPSQ
7.9	1140.592773	0.008755	DGLPGRVPLW

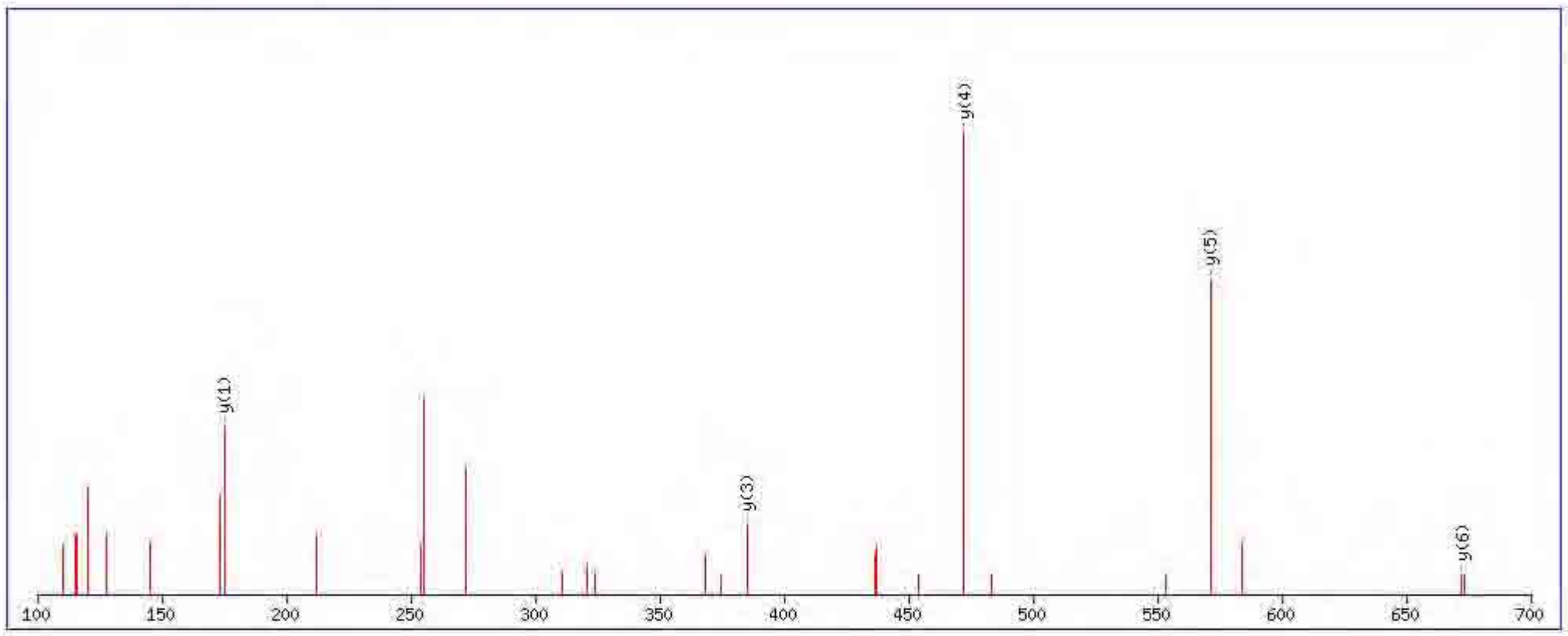
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATVSPLR**
Found in **SH3R3_HUMAN**, SH3 domain-containing RING finger protein 3 OS=Homo sapiens GN=SH3RF3 PE=1 SV=2

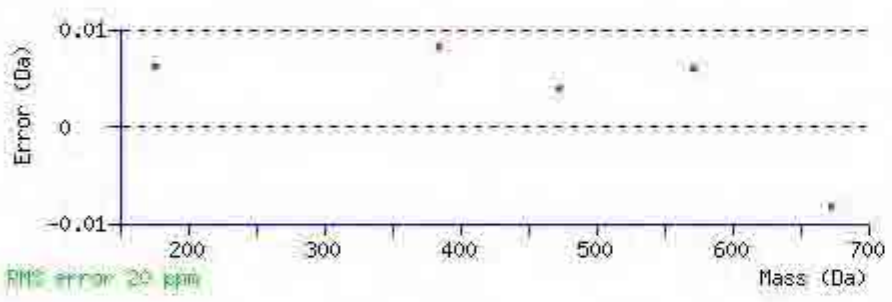
Match to Query 298: 742.435208 from(372.224880,2+) rtinseconds(942) index(2894)
Title: Locus:1.1.1.1299.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

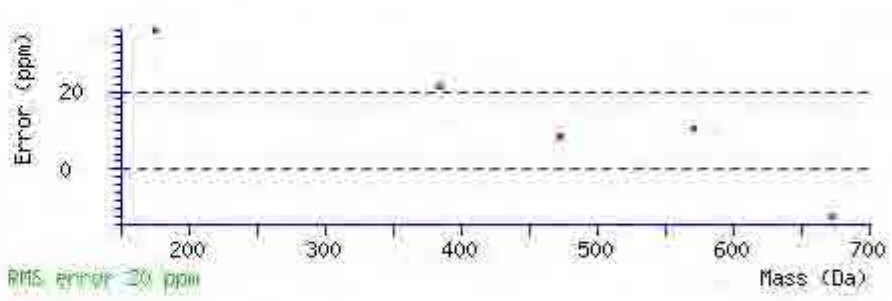
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 742.433731
Ions Score: 49 **Expect:** 0.0031
Matches : 5/52 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							7
2	173.092069	87.049672	155.081504	78.044390	T	*672.403901*	336.705589	655.377352	328.192314	654.393336	327.700306	6
3	272.160483	136.583879	254.149918	127.578597	V	*571.356222*	286.181749	554.329673	277.668475	553.345657	277.176467	5
4	359.192511	180.099894	341.181946	171.094611	S	*472.287808*	236.647542	455.261259	228.134267	454.277243	227.642259	4
5	456.245275	228.626276	438.234710	219.620993	P	*385.255780*	193.131528	368.229231	184.618253			3
6	569.329339	285.168308	551.318774	276.163025	L	288.203016	144.605146	271.176467	136.091871			2
7					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ATVSPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	742.433731	0.001477	ATVSPLR
41.8	742.433731	0.001477	ATSVLPR
36.1	742.433731	0.001477	ATVIPSR
30.4	742.433716	0.001492	ALSSPLR
30.4	742.433716	0.001492	ASLSPLR
24.6	742.433731	0.001477	ATISVPR
24.5	742.433731	0.001477	VATSLPR
20.9	742.433731	0.001477	DGVLALR
20.9	742.433731	0.001477	GDVLLAR
19.4	742.433701	0.001507	AAEILAR

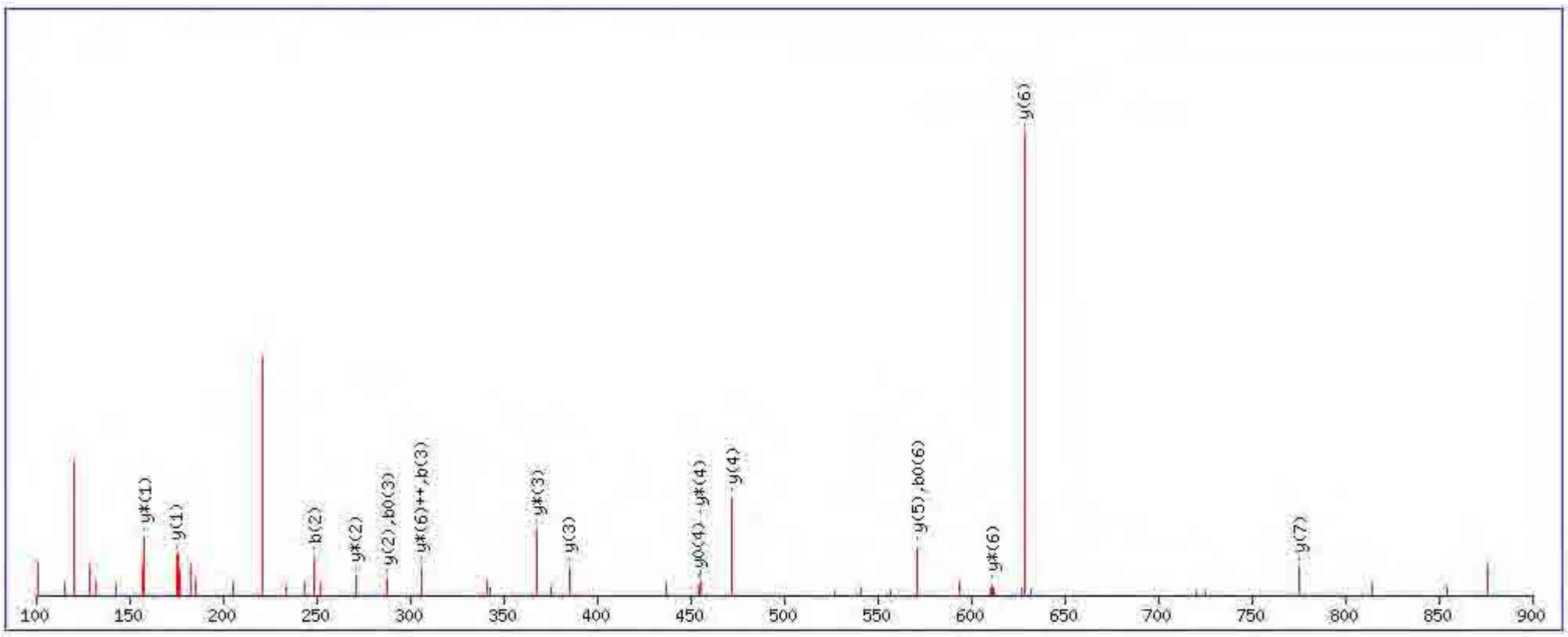
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFGVSPLR**
Found in **XP32_HUMAN**, Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1

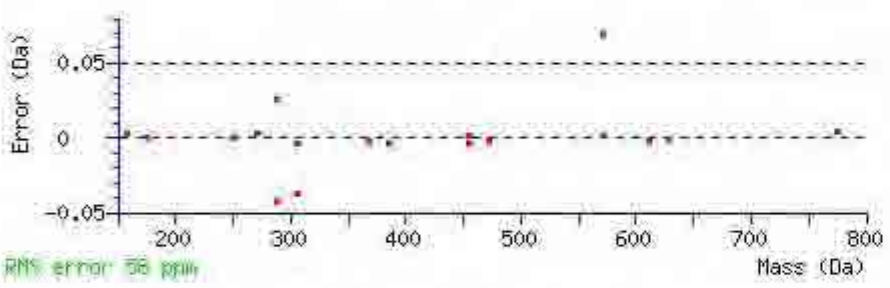
Match to Query 2109: 875.484608 from(438.749580,2+) rtinseconds(1324) index(6271)
Title: Locus:1.1.1.1515.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

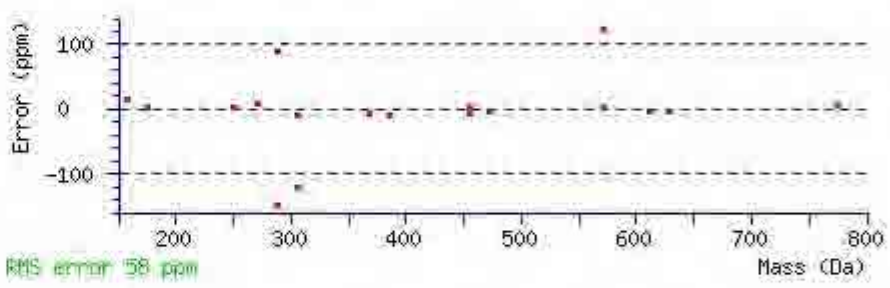
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 875.486511
Ions Score: 50 **Expect:** 0.00045
Matches : 18/64 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							8
2	249.123369	125.065322	231.112804	116.060040	F	775.446100	388.226688	758.419551	379.713414	757.435535	379.221406	7
3	306.144833	153.576054	288.134268	144.570772	G	628.377686	314.692481	611.351137	306.179207	610.367121	305.687199	6
4	405.213247	203.110261	387.202682	194.104979	V	571.356222	286.181749	554.329673	277.668475	553.345657	277.176467	5
5	492.245275	246.626275	474.234710	237.620993	S	472.287808	236.647542	455.261259	228.134268	454.277243	227.642260	4
6	589.298039	295.152658	571.287474	286.147375	P	385.255780	193.131528	368.229231	184.618254			3
7	702.382103	351.694690	684.371538	342.689407	L	288.203016	144.605146	271.176467	136.091872			2
8					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TFGVSPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	875.486511	-0.001903	TFGVSPLR
13.6	875.486481	-0.001873	TYNIPIR
11.0	875.486496	-0.001888	FTAPTAIR
9.3	875.478653	0.005955	KPVMVIGI
9.2	875.486481	-0.001873	FEKSPLR
9.2	875.486496	-0.001888	PPPLSPPR
9.2	875.486496	-0.001888	SGLFSPIR
8.2	875.489868	-0.005260	RILGLCTT
7.7	875.486511	-0.001903	FGTVPISR
6.6	875.489868	-0.005260	RSVTALMV

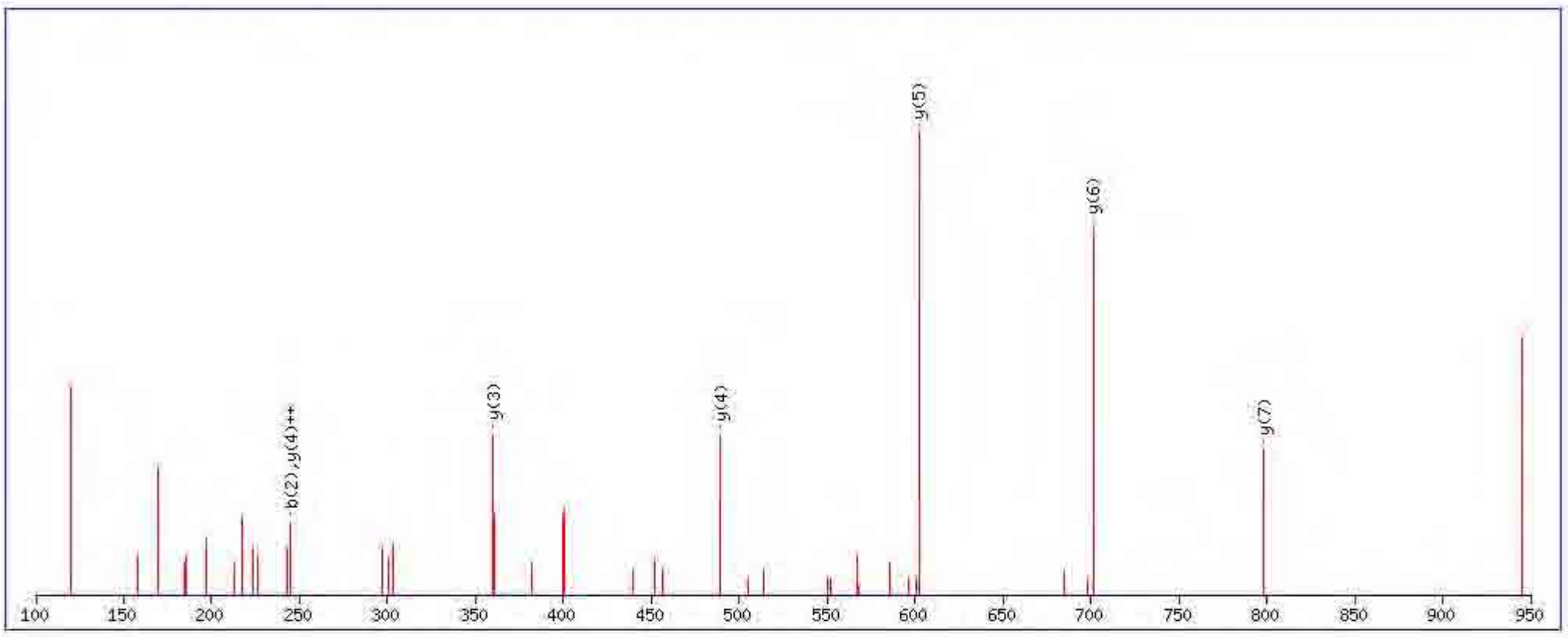
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPVLEGQR**
Found in **QSOX1_HUMAN**, Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3

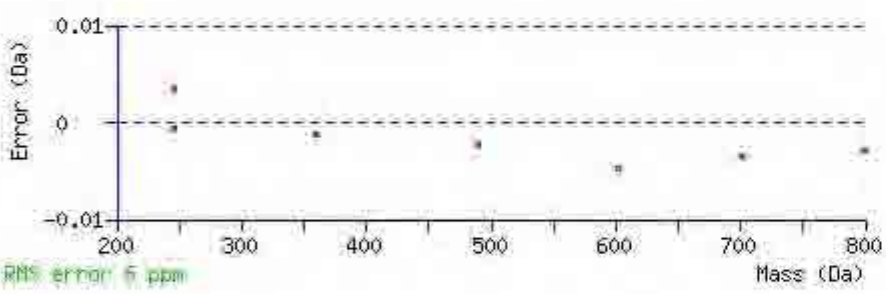
Match to Query 3310: 944.509808 from(473.262180,2+) rtinseconds(1275) index(5841)
Title: Locus:1.1.1.1487.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

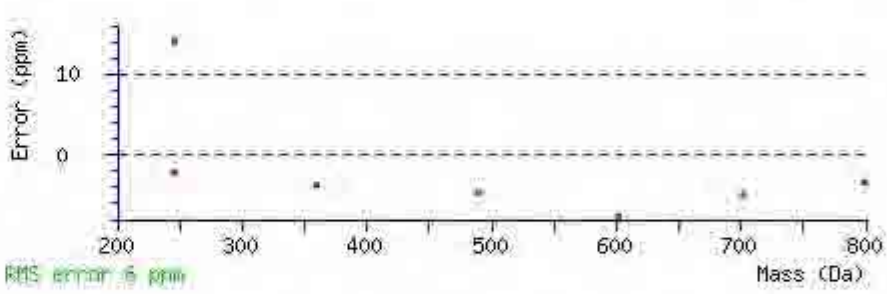
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 944.507965
Ions Score: 46 **Expect:** 0.0053
Matches : 7/58 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							8
2	245.128454	123.067865					P	*798.446829*	399.727053	781.420280	391.213778	780.436264	390.721770	7
3	344.196868	172.602072					V	*701.394065*	351.200671	684.367516	342.687396	683.383500	342.195388	6
4	457.280932	229.144104					L	*602.325651*	301.666464	585.299102	293.153189	584.315086	292.661181	5
5	586.323525	293.665401			568.312960	284.660118	E	*489.241587*	245.124431	472.215038	236.611157	471.231022	236.119149	4
6	643.344989	322.176133			625.334424	313.170850	G	*360.198994*	180.603135	343.172445	172.089860			3
7	771.403567	386.205422	754.377018	377.692147	753.393002	377.200139	Q	303.177530	152.092403	286.150981	143.579128			2
8							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FPVLEGQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	944.507965	0.001843	FPVLEGQR
30.1	944.517853	-0.008045	DEVLAVAKT
18.7	944.517838	-0.008030	NTKIEVLE
17.6	944.511337	-0.001529	MLVGNAGVGK
15.4	944.507980	0.001828	FVPPTNVR
11.1	944.517853	-0.008045	TEIIKVDQ
10.2	944.507965	0.001843	FPDGLQLR
10.2	944.507950	0.001858	FPDLNRLA
9.8	944.507950	0.001858	EPTIKWR
8.9	944.517853	-0.008045	DPDLKLTK

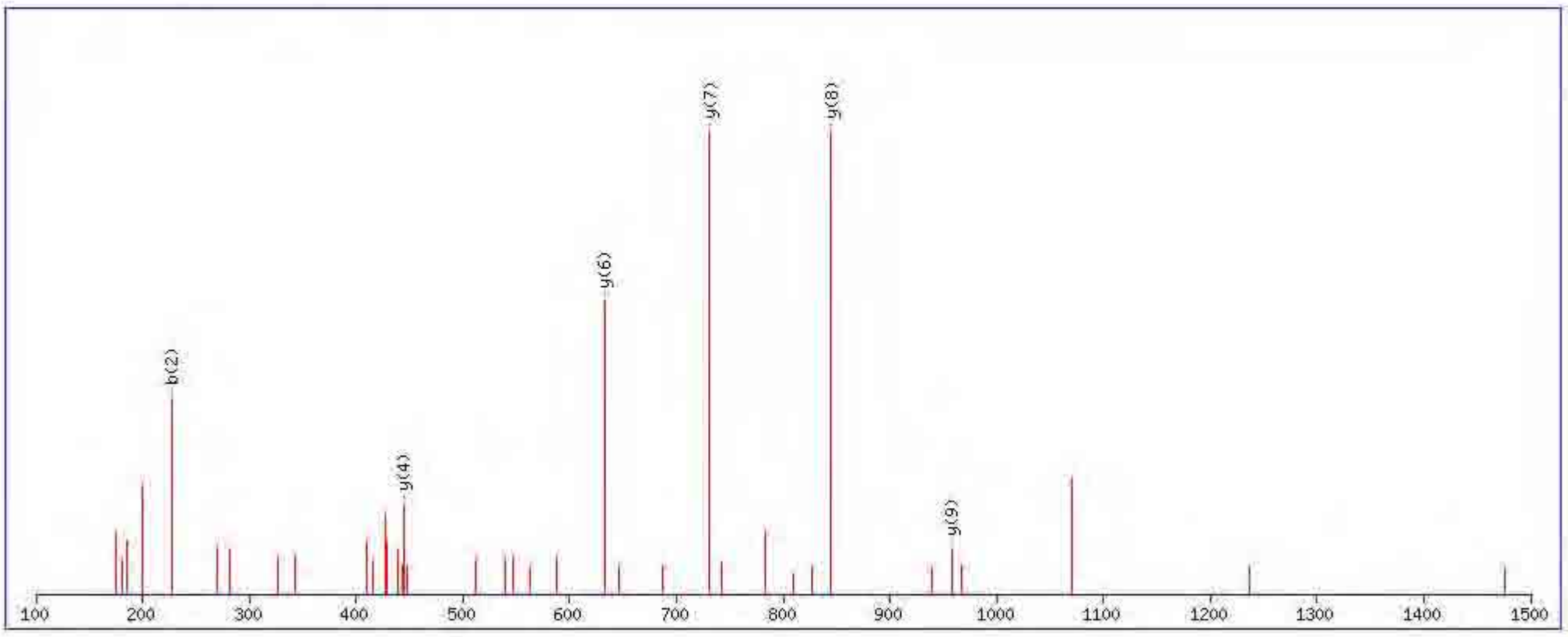
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

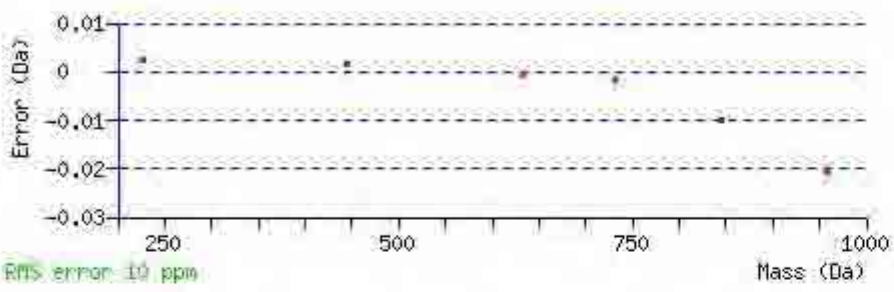
Match to Query 5452: 1069.646228 from(535.830390,2+) rtinseconds(1408) index(7172)
Title: Locus:1.1.1.1561.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

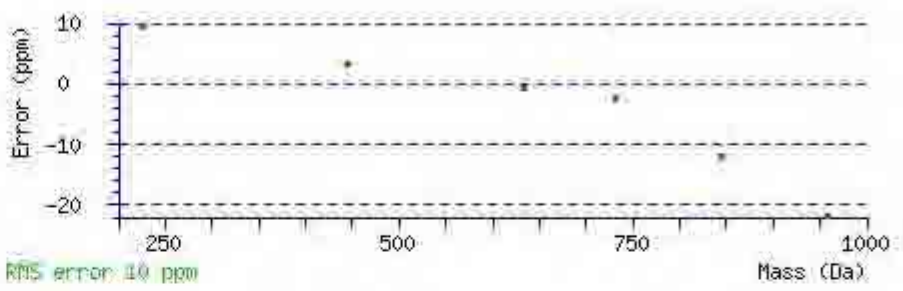
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 38 **Expect:** 0.0097
Matches : 6/78 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	*957.572758*	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	*844.488694*	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	*731.404630*	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	*632.336216*	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	*444.256509*	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	1069.649536	-0.003308	LLIVSTPTAR
24.1	1069.638321	0.007907	IPLVPSKVSV
24.1	1069.638306	0.007922	LLPVLLSTAQ
18.5	1069.649521	-0.003293	PLLSVKELR
14.9	1069.649521	-0.003293	LLIIRSAPAT
14.6	1069.638321	0.007907	LPLTVTSVPK
14.3	1069.649506	-0.003278	LILLSENLR
13.2	1069.639633	0.006595	LLWPTRLR
13.1	1069.635605	0.010623	ILLSRQQGR
13.1	1069.649521	-0.003293	LLLQDSLLR

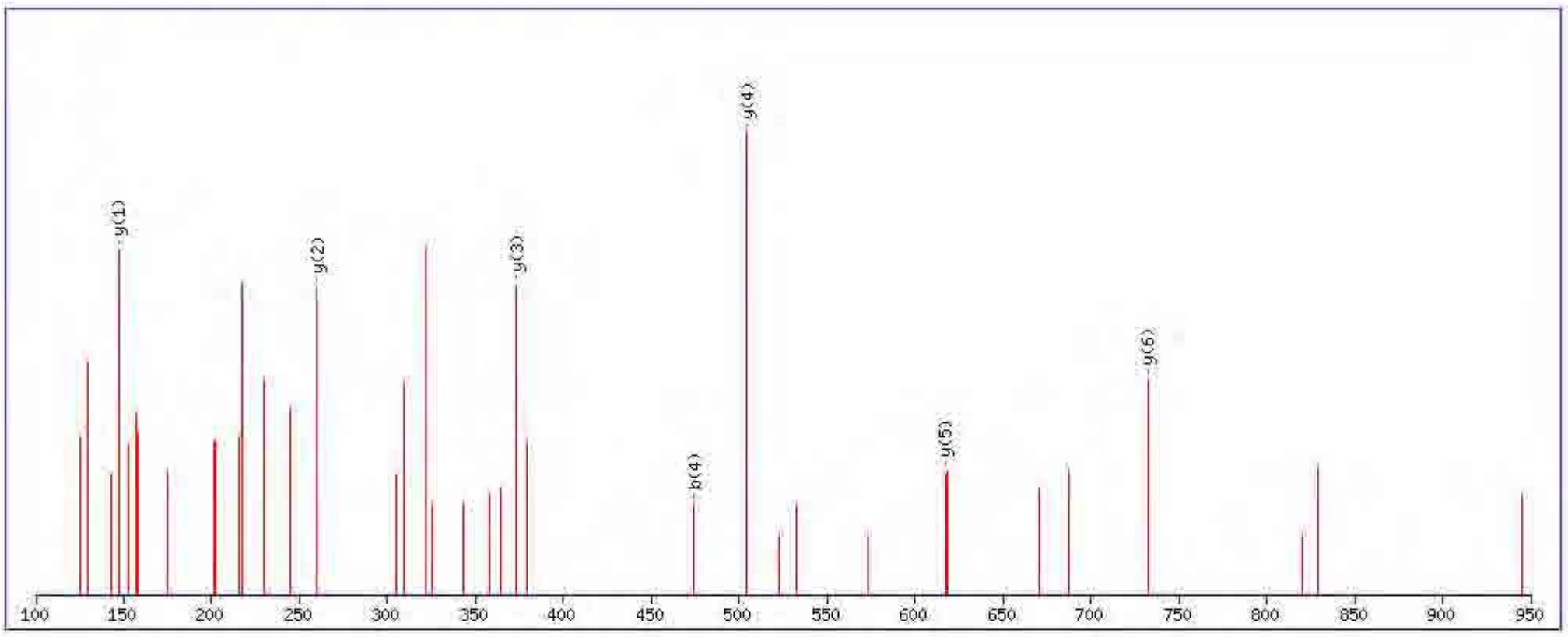
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDIMLIK**
Found in **TRY1_HUMAN**, Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1

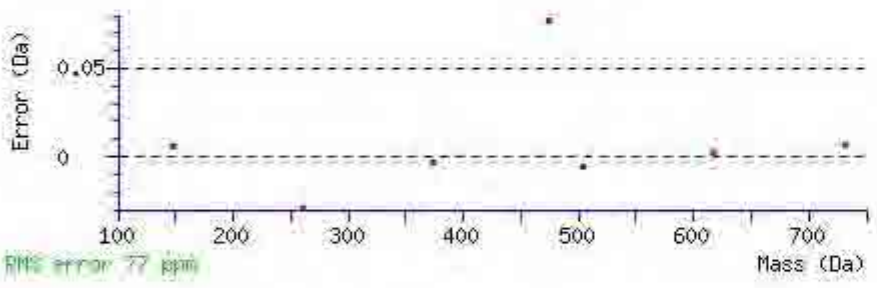
Match to Query 1540: 845.464988 from(423.739770,2+) rtinseconds(1398) index(7083)
Title: Locus:1.1.1.1556.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

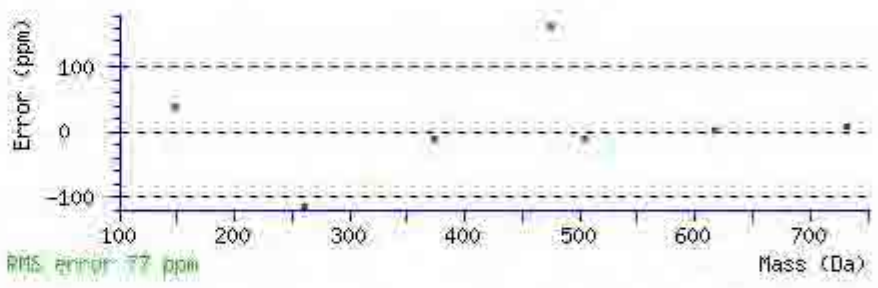
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 845.468048
Ions Score: 40 **Expect:** 0.019
Matches : 7/60 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							7
2	230.077146	115.542211	213.050597	107.028937	212.066581	106.536928	D	*732.432424*	366.719850	715.405875	358.206576	714.421859	357.714568	6
3	343.161210	172.084243	326.134661	163.570968	325.150645	163.078960	I	*617.405481*	309.206379	600.378932	300.693104			5
4	474.201695	237.604485	457.175146	229.091211	456.191130	228.599203	M	*504.321417*	252.664346	487.294868	244.151072			4
5	587.285759	294.146518	570.259210	285.633243	569.275194	285.141235	L	*373.280932*	187.144104	356.254383	178.630829			3
6	700.369823	350.688550	683.343274	342.175275	682.359258	341.683267	I	*260.196868*	130.602072	243.170319	122.088798			2
7							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NDIMLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.9	845.468048	-0.003060	NDIMLIK
39.9	845.468048	-0.003060	NDLMLIK
26.5	845.468048	-0.003060	NVEMILK
17.9	845.458160	0.006828	WRMLIQ
16.7	845.464706	0.000282	VSWTLPK
15.6	845.464706	0.000282	DGGFPLLK
15.6	845.468063	-0.003075	TAGMILPK
15.6	845.464706	0.000282	TQFPLPK
15.1	845.468063	-0.003075	VTAAMLLQ
14.4	845.460678	0.004310	EDKTVVR

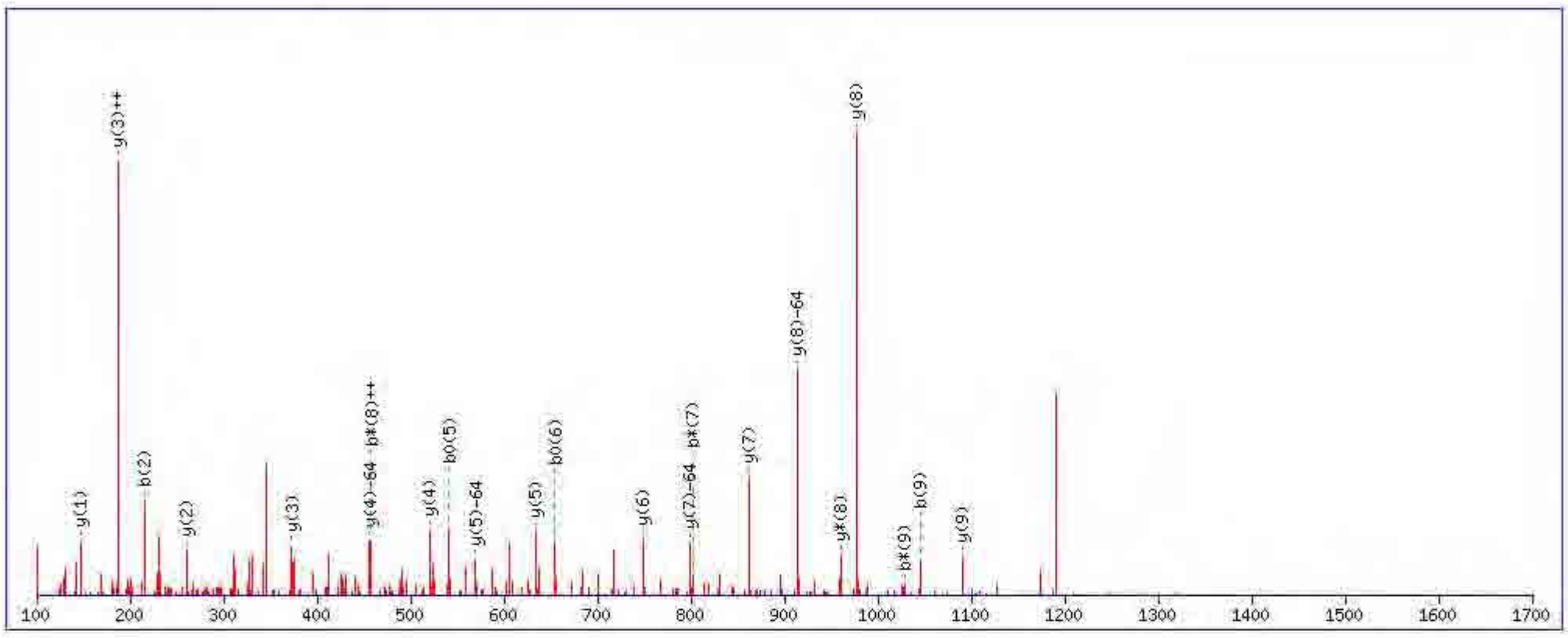
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLDNDIMLIK**
Found in **TRY3_HUMAN**, Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2

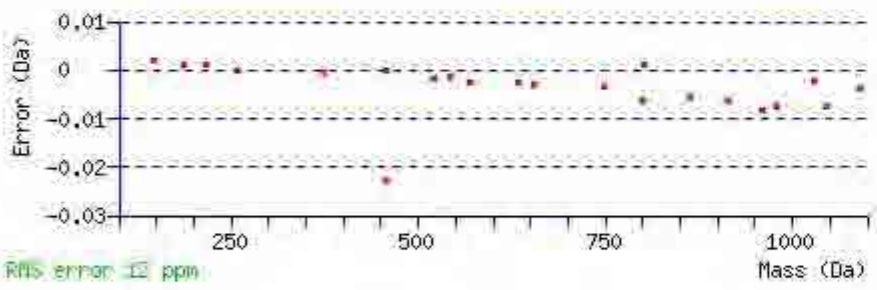
Match to Query 8242: 1190.618868 from(596.316710,2+) rtinseconds(1633) index(9687)
Title: Locus:1.1.1.1684.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

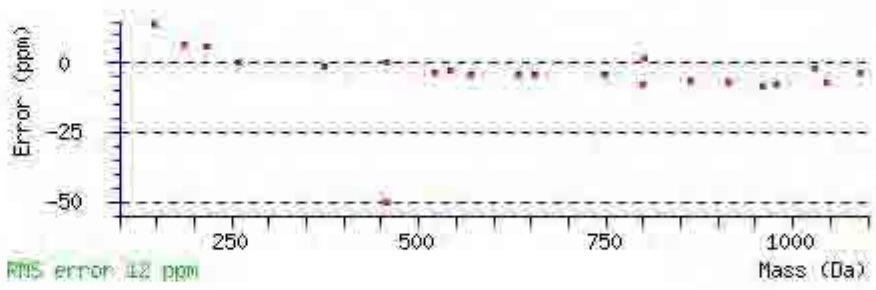
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1190.621658
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 77 **Expect:** 4.1e-006
Matches : 22/142 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	215.139019	108.073147			197.128454	99.067865	L	*1090.581273*	545.794275	1073.554724	537.281000	1072.570708	536.788992	9
3	330.165962	165.586619			312.155397	156.581336	D	*977.497209*	489.252243	960.470660	480.738968	959.486644	480.246960	8
4	444.208889	222.608082	427.182340	214.094808	426.198324	213.602800	N	*862.470266*	431.738771	845.443717	423.225497	844.459701	422.733489	7
5	559.235832	280.121554	542.209283	271.608280	541.225267	271.116272	D	*748.427339*	374.717308	731.400790	366.204033	730.416774	365.712025	6
6	672.319896	336.663586	655.293347	328.150312	654.309331	327.658304	I	*633.400396*	317.203836	616.373847	308.690562			5
7	819.355296	410.181286	802.328747	401.668012	801.344731	401.176004	M	*520.316332*	260.661804	503.289783	252.148530			4
8	932.439360	466.723318	915.412811	458.210044	914.428795	457.718036	L	*373.280932*	187.144104	356.254383	178.630829			3
9	1045.523424	523.265350	1028.496875	514.752076	1027.512859	514.260067	I	*260.196868*	130.602072	243.170319	122.088797			2
10							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TLDNDIMLIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.3	1190.621658	-0.002790	TLDNDIMLIK
22.5	1190.618332	0.000536	TPPPPPVPPTK
21.2	1190.618332	0.000536	TPPPPPVPPTK
19.6	1190.615128	0.003740	EMPMGRTILK
18.7	1190.621628	-0.002760	KTEAELEMLK
17.9	1190.621689	-0.002821	DVATSMPVVIK
16.5	1190.618332	0.000536	TPPPPPVPPTK
16.2	1190.621689	-0.002821	TLVLVSPGDMK
16.2	1190.621674	-0.002806	VDAGLLTDIMK
15.5	1190.615128	0.003740	EMPMGRTILK

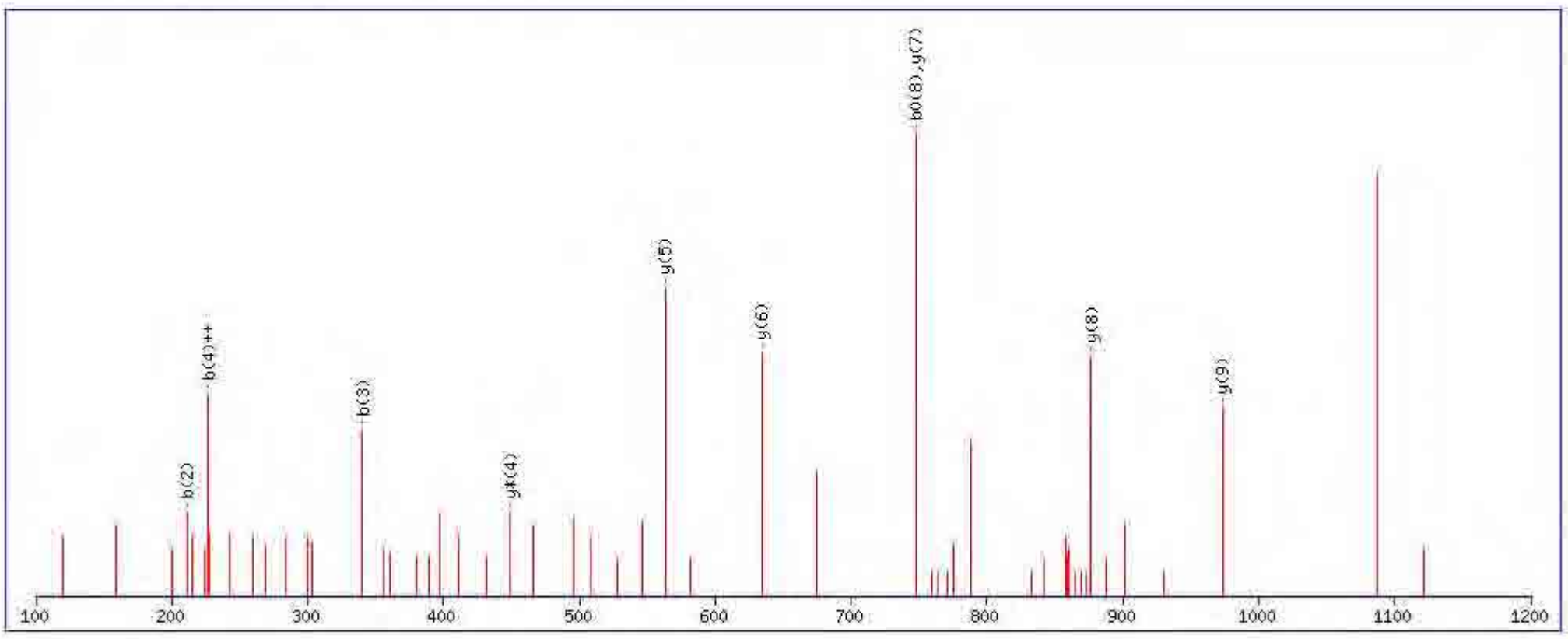
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPELAPSGFR**
Found in **TSK_HUMAN**, Tsukushin OS=Homo sapiens GN=TSKU PE=2 SV=3

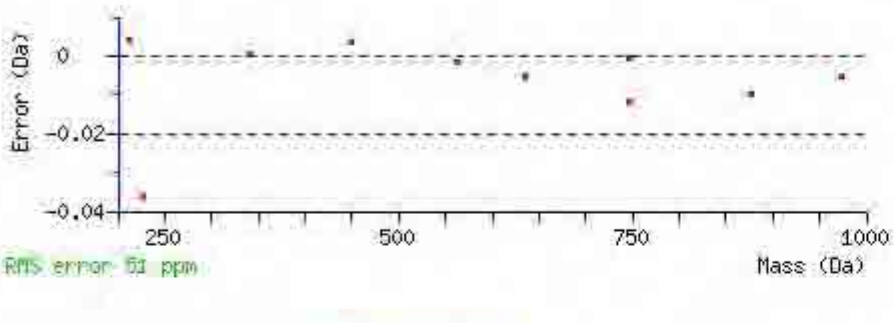
Match to Query 5781: 1085.585868 from(543.800210,2+) rtinseconds(1627) index(9641)
Title: Locus:1.1.1.1681.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

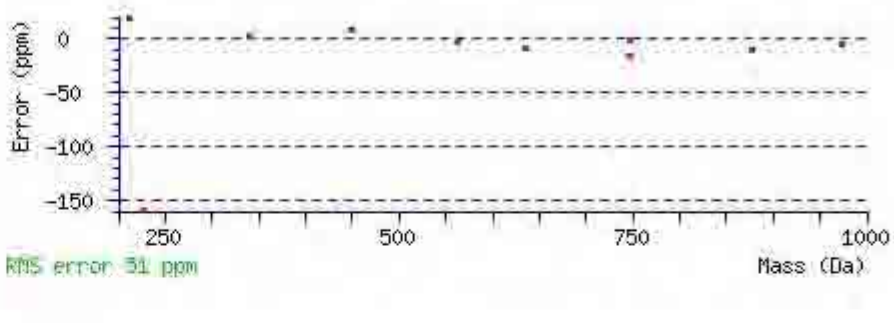
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1085.586929
Ions Score: 45 **Expect:** 0.008
Matches : 10/80 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	211.144104	106.075690			P	973.510157	487.258717	956.483608	478.745442	955.499592	478.253434	9
3	340.186697	170.596986	322.176132	161.591704	E	876.457393	438.732335	859.430844	430.219060	858.446828	429.727052	8
4	453.270761	227.139018	435.260196	218.133736	L	747.414800	374.211038	730.388251	365.697764	729.404235	365.205756	7
5	524.307875	262.657576	506.297310	253.652293	A	634.330736	317.669006	617.304187	309.155732	616.320171	308.663724	6
6	621.360639	311.183958	603.350074	302.178675	P	563.293622	282.150449	546.267073	273.637175	545.283057	273.145167	5
7	708.392667	354.699972	690.382102	345.694689	S	466.240858	233.624067	449.214309	225.110792	448.230293	224.618784	4
8	765.414131	383.210704	747.403566	374.205421	G	379.208830	190.108053	362.182281	181.594778			3
9	912.482545	456.744911	894.471980	447.739628	F	322.187366	161.597321	305.160817	153.084046			2
10					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPELAPSGFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	1085.586929	-0.001061	LPELAPSGFR
26.2	1085.579071	0.006797	LPEPVKLQM
25.8	1085.590286	-0.004418	IPEALLAGMR
25.4	1085.577042	0.008826	LPYHHVIHA
17.8	1085.579071	0.006797	LPLPMDPKK
14.9	1085.594315	-0.008447	LILLPSHMY
14.9	1085.590286	-0.004418	LLIIPECNR
14.9	1085.585571	0.000297	LLLLEEEDL
14.9	1085.579071	0.006797	LPLPMDPKK
14.9	1085.590302	-0.004434	LPLPPAMKR

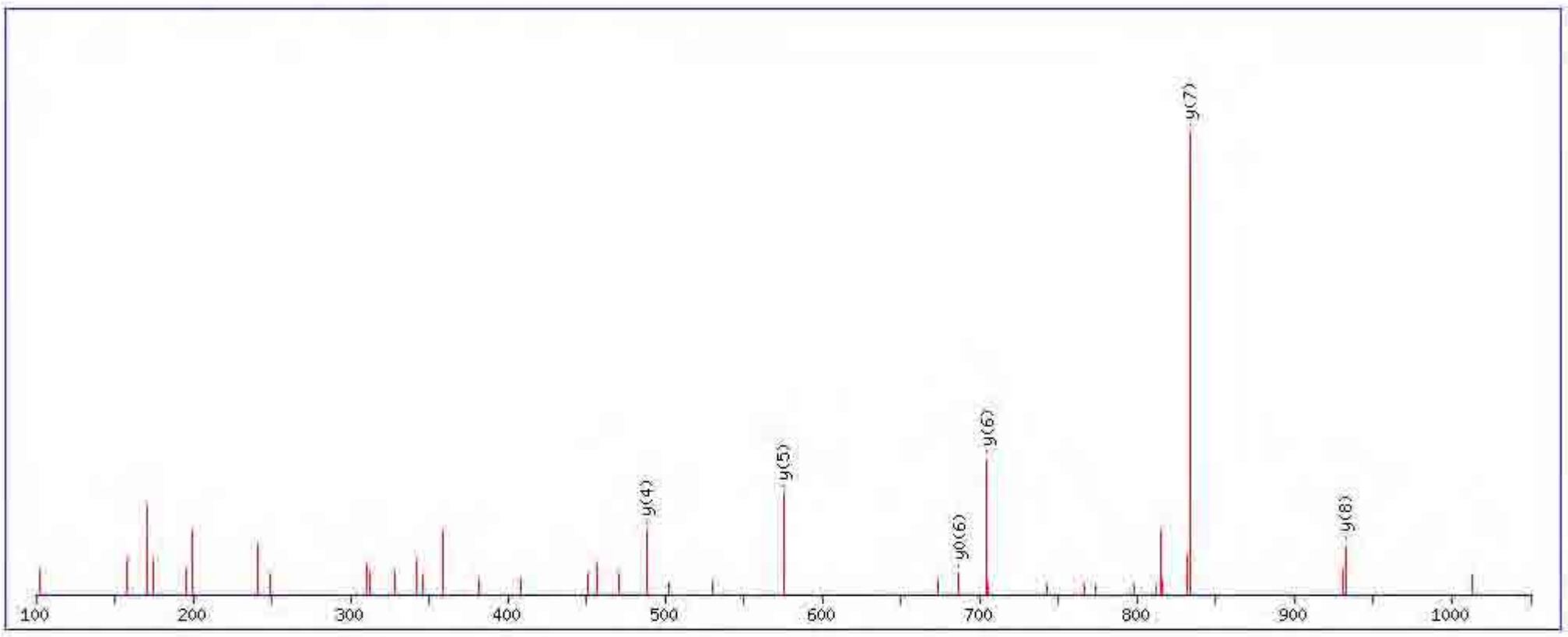
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PVEESALER**
Found in **TYDP2_HUMAN**, Tyrosyl-DNA phosphodiesterase 2 OS=Homo sapiens GN=TDP2 PE=1 SV=1

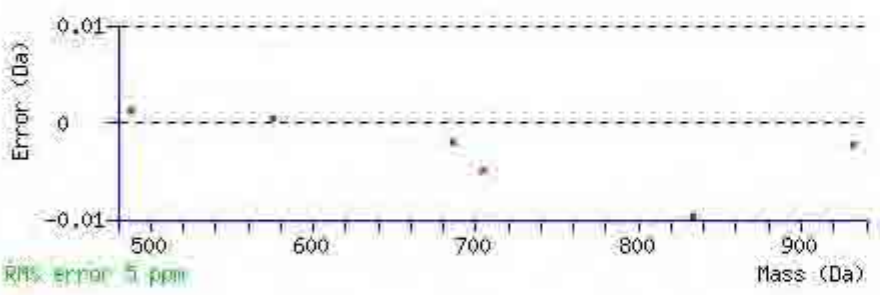
Match to Query 4670: 1028.515528 from(515.265040,2+) rtinseconds(859) index(2231)
Title: Locus:1.1.1.1251.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_2.mgf

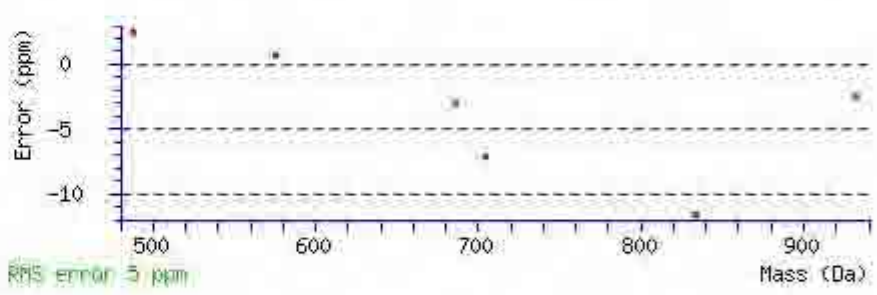
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1028.513809
Ions Score: 38 **Expect:** 0.0036
Matches : 6/74 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.060040	49.533658			P							9
2	197.128454	99.067865			V	*932.468351*	466.737814	915.441802	458.224539	914.457786	457.732531	8
3	326.171047	163.589161	308.160482	154.583879	E	*833.399937*	417.203607	816.373388	408.690332	815.389372	408.198324	7
4	455.213640	228.110458	437.203075	219.105176	E	*704.357344*	352.682310	687.330795	344.169036	686.346779	343.677028	6
5	542.245668	271.626472	524.235103	262.621190	S	*575.314751*	288.161014	558.288202	279.647739	557.304186	279.155731	5
6	613.282782	307.145029	595.272217	298.139747	A	*488.282723*	244.644999	471.256174	236.131725	470.272158	235.639717	4
7	726.366846	363.687061	708.356281	354.681779	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
8	855.409439	428.208358	837.398874	419.203075	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PVEESALER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	1028.513809	0.001719	PVEESALER
11.5	1028.513824	0.001704	PTEEDLGLR
11.1	1028.525055	-0.009527	VVEEERPR
10.4	1028.507309	0.008219	VPCPEGQKR
10.3	1028.513840	0.001688	VEVDVEAPR
10.1	1028.525070	-0.009542	PVQVSSADAR
9.6	1028.513824	0.001704	PLDSENVQK
9.2	1028.507294	0.008234	VPQRMAAEGA
9.0	1028.515167	0.000361	VPAHEPSHR
7.9	1028.513824	0.001704	TPEAETPIR

Sibling 2 – technical replicate # 3

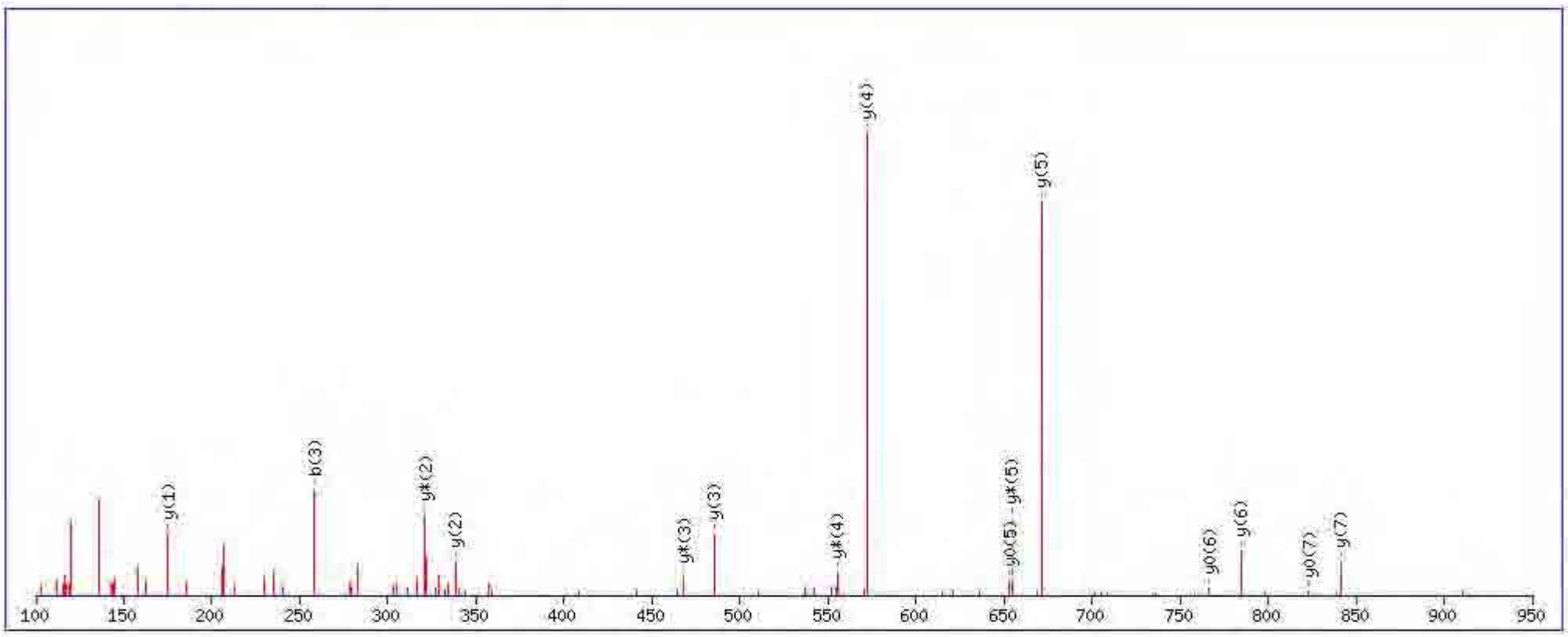
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGLVSFYR**
Found in **ANGL7_HUMAN**, Angiopoietin-related protein 7 OS=Homo sapiens GN=ANGPTL7 PE=1 SV=1

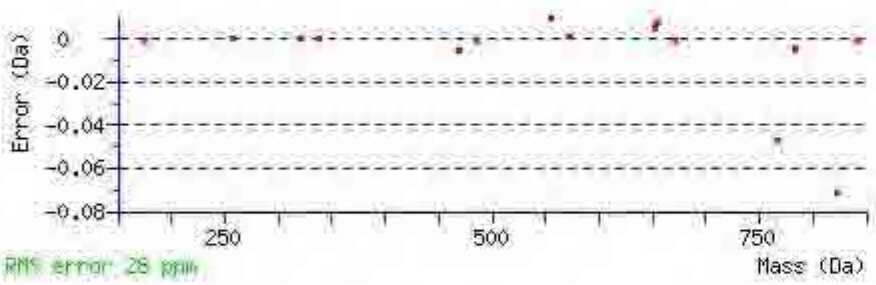
Match to Query 2580: 927.482228 from(464.748390,2+) rtinseconds(1502) index(7522)
Title: Locus:1.1.1.1665.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

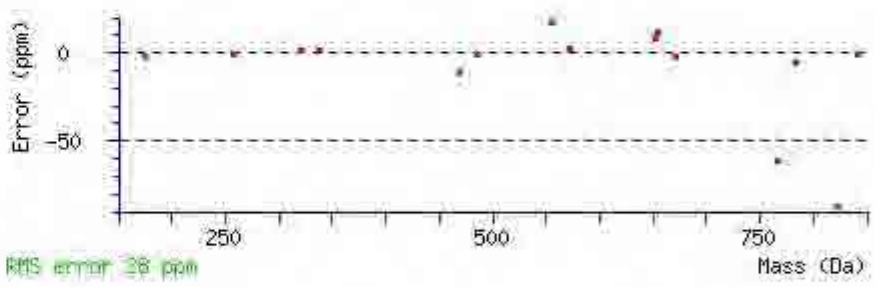
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 927.481415
Ions Score: 53 **Expect:** 0.00081
Matches : 15/64 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							8
2	145.060768	73.034022	127.050203	64.028740	G	*841.456665*	421.231971	824.430116	412.718696	823.446100	412.226688	7
3	258.144832	129.576054	240.134267	120.570772	L	*784.435201*	392.721239	767.408652	384.207964	766.424636	383.715956	6
4	357.213246	179.110261	339.202681	170.104979	V	*671.351137*	336.179207	654.324588	327.665932	653.340572	327.173924	5
5	444.245274	222.626275	426.234709	213.620993	S	*572.282723*	286.645000	555.256174	278.131725	554.272158	277.639717	4
6	591.313688	296.160482	573.303123	287.155200	F	*485.250695*	243.128985	468.224146	234.615711			3
7	754.377017	377.692147	736.366452	368.686864	Y	*338.182281*	169.594778	321.155732	161.081504			2
8					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SGLVSFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	927.481415	0.000813	SGLVSFYR
26.1	927.473557	0.008671	SGIVMEVPP
15.6	927.488617	-0.006389	SGDPRKPR
15.2	927.488617	-0.006389	SGPDQRLR
13.4	927.477386	0.004842	SGPPGNKGAK
12.7	927.477386	0.004842	SGLQSPPSR
12.4	927.488617	-0.006389	GLSEGPRGR
12.4	927.488632	-0.006404	GSPGAVRPR
11.8	927.488617	-0.006389	SPRSNPVR
11.2	927.488617	-0.006389	SPGAAPRTR

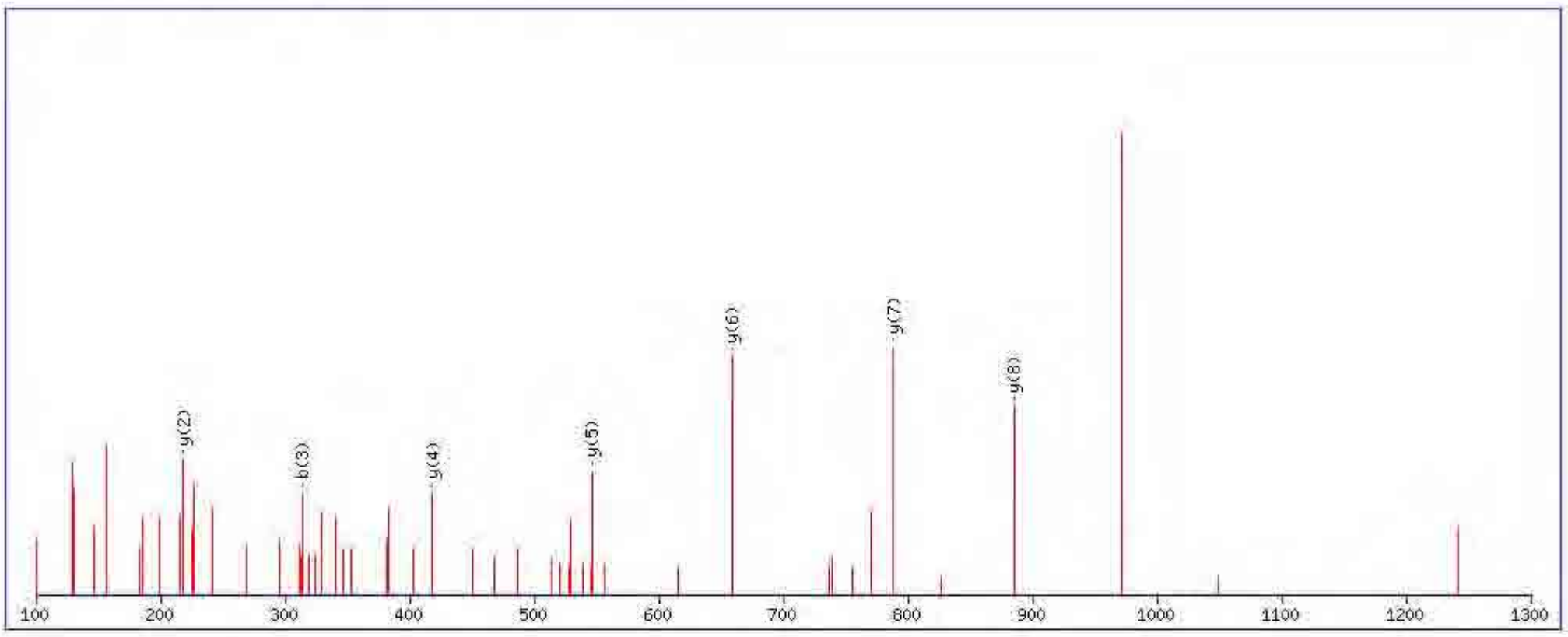
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPELQAEAK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

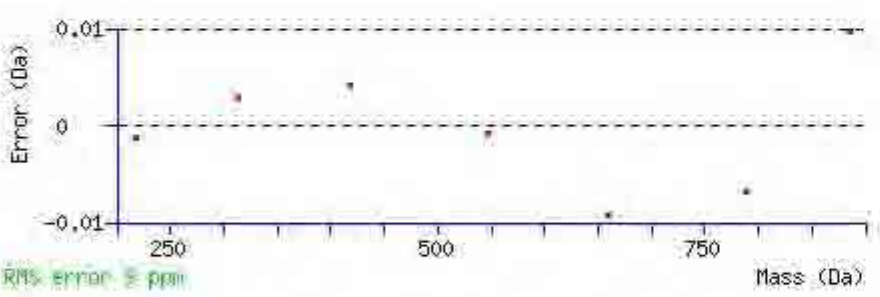
Match to Query 3167: 971.499748 from(486.757150,2+) rtinseconds(588) index(695)
Title: Locus:1.1.1.1150.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

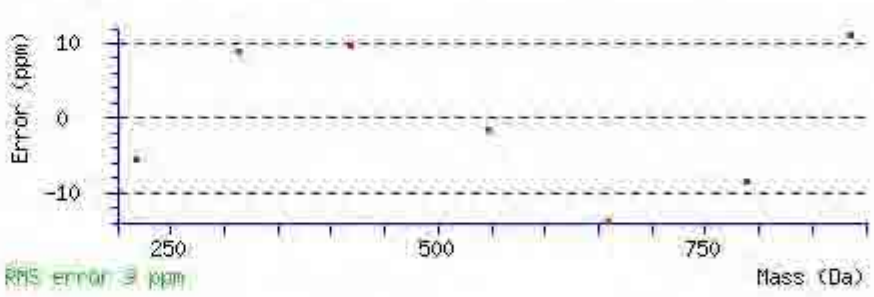
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 971.492340
Ions Score: 53 **Expect:** 0.0012
Matches : 7/84 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	185.092068	93.049672			167.081503	84.044389	P	*885.467624*	443.237450	868.441075	434.724176	867.457059	434.232168	8
3	314.134661	157.570968			296.124096	148.565686	E	*788.414860*	394.711068	771.388311	386.197794	770.404295	385.705786	7
4	427.218725	214.113001			409.208160	205.107718	L	*659.372267*	330.189772	642.345718	321.676497	641.361702	321.184489	6
5	555.277303	278.142290	538.250754	269.629015	537.266738	269.137007	Q	*546.288203*	273.647740	529.261654	265.134465	528.277638	264.642457	5
6	626.314417	313.660847	609.287868	305.147572	608.303852	304.655564	A	*418.229625*	209.618450	401.203076	201.105176	400.219060	200.613168	4
7	755.357010	378.182143	738.330461	369.668869	737.346445	369.176861	E	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	826.394124	413.700700	809.367575	405.187426	808.383559	404.695418	A	*218.149918*	109.578597	201.123369	101.065322			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SPELQAEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	971.492340	0.007408	SPELQAEAK
21.7	971.503571	-0.003823	SPEKLENR
21.7	971.492355	0.007393	SPEKLPQSS
20.3	971.492340	0.007408	EPSAEQIAK
20.1	971.503601	-0.003853	APGGQKSPSK
18.6	971.492371	0.007377	SSENGALPVV
17.1	971.492371	0.007377	QPSVTPEKA
15.2	971.503601	-0.003853	PQSVQQAAK
14.1	971.492371	0.007377	SPVASPSSPK
13.7	971.492371	0.007377	EPTVQPASK

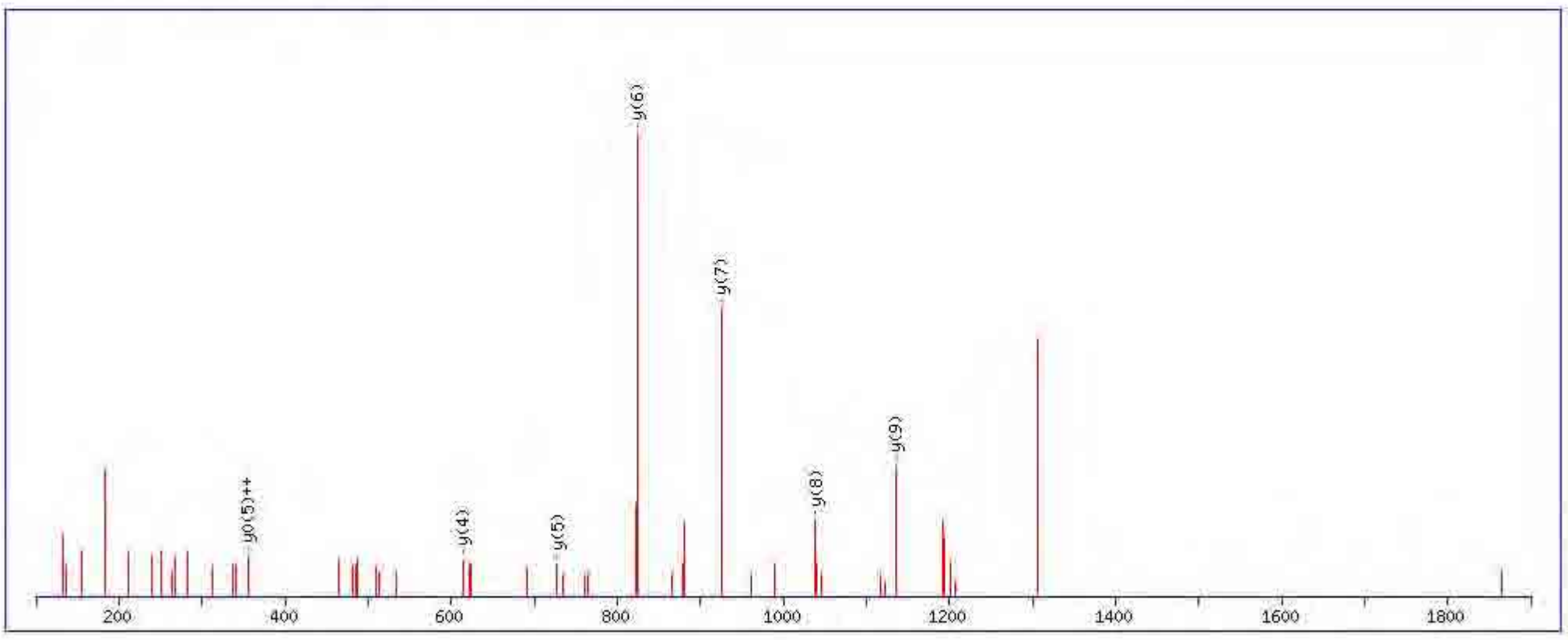
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGPITPLEFYR**
Found in **BLMH_HUMAN**, Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1

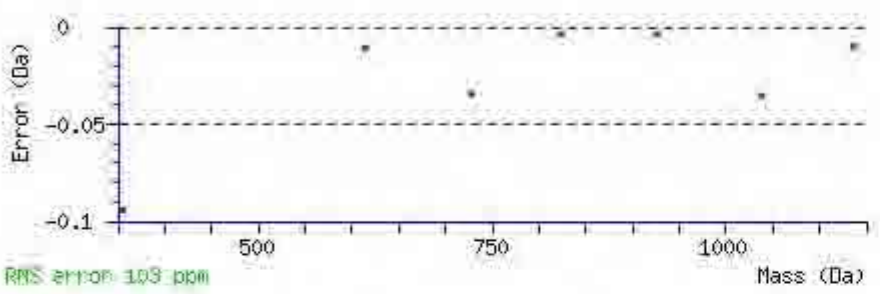
Match to Query 9732: 1304.719988 from(653.367270,2+) rtinseconds(2099) index(14230)
Title: Locus:1.1.1.1994.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

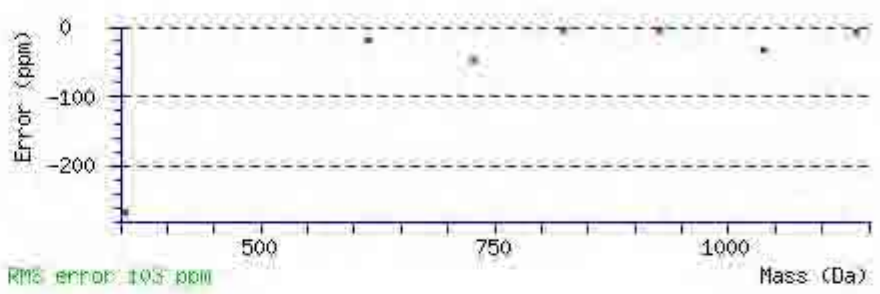
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1304.712860
Ions Score: 43 **Expect:** 0.00041
Matches : 7/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	1192.636087	596.821682	1175.609538	588.308407	1174.625522	587.816399	10
3	268.165568	134.586422			P	*1135.614623*	568.310949	1118.588074	559.797675	1117.604058	559.305667	9
4	381.249632	191.128454			I	*1038.561859*	519.784568	1021.535310	511.271293	1020.551294	510.779285	8
5	482.297311	241.652293	464.286746	232.647011	T	*925.477795*	463.242536	908.451246	454.729261	907.467230	454.237253	7
6	579.350075	290.178676	561.339510	281.173393	P	*824.430116*	412.718696	807.403567	404.205422	806.419551	403.713414	6
7	692.434139	346.720708	674.423574	337.715425	L	*727.377352*	364.192314	710.350803	355.679039	709.366787	355.187031	5
8	821.476732	411.242004	803.466167	402.236722	E	*614.293288*	307.650282	597.266739	299.137007	596.282723	298.644999	4
9	968.545146	484.776211	950.534581	475.770929	F	485.250695	243.128985	468.224146	234.615711			3
10	1131.608475	566.307876	1113.597910	557.302593	Y	338.182281	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IGPITPLEFYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1304.712860	0.007128	IGPITPLEFYR
6.5	1304.720078	-0.000090	LGPVESLQGHLR
2.3	1304.724106	-0.004118	PAGPPPPPPPPLR
2.3	1304.731323	-0.011335	RPPVPPRGPLR
2.0	1304.731308	-0.011320	VAPLPGRNGTPAR
0.4	1304.724106	-0.004118	WPPTLQPPTLR
0.3	1304.712189	0.007799	VLAKNNALTMSK
0.2	1304.708862	0.011126	PGTKPTPIPPPR
0.0	1304.708832	0.011156	NASPVQVKTAYK

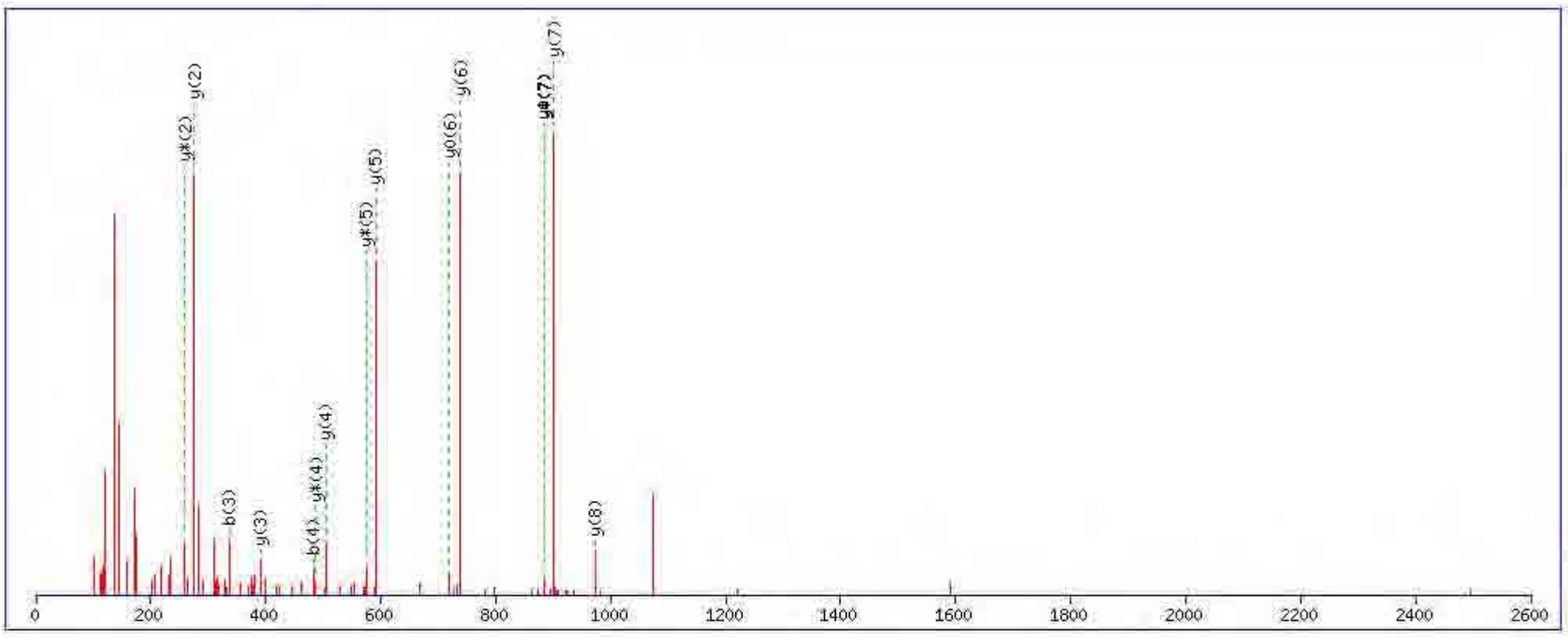
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAYFSLDTR**
Found in **CADH1_HUMAN**, Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3

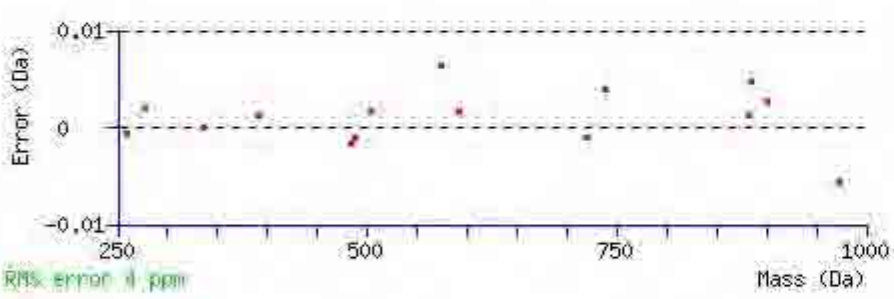
Match to Query 4824: 1072.525768 from(537.270160,2+) rtinseconds(1520) index(7687)
Title: Locus:1.1.1.1675.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

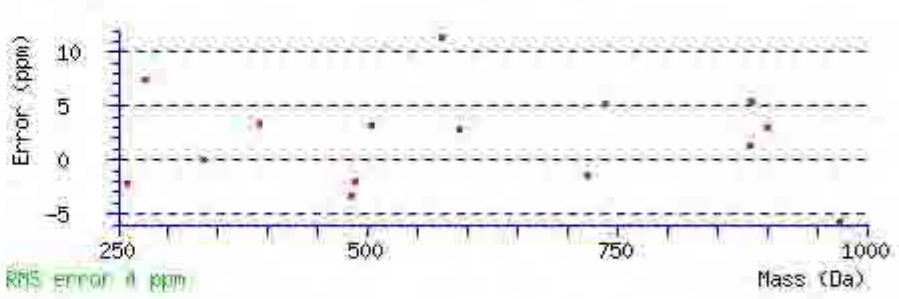
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1072.518921
Ions Score: 50 **Expect:** 0.00025
Matches : 15/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	173.092069	87.049672	155.081504	78.044390	A	*972.478523*	486.742900	955.451974	478.229625	954.467958	477.737617	8
3	**336.155398**	168.581337	318.144833	159.576055	Y	*901.441409*	451.224343	884.414860	442.711068	883.430844	442.219060	7
4	**483.223812**	242.115544	465.213247	233.110262	F	*738.378080*	369.692678	721.351531	361.179403	720.367515	360.687395	6
5	570.255840	285.631558	552.245275	276.626276	S	*591.309666*	296.158471	574.283117	287.645197	573.299101	287.153189	5
6	683.339904	342.173590	665.329339	333.168308	L	*504.277638*	252.642457	487.251089	244.129182	486.267073	243.637174	4
7	798.366847	399.687062	780.356282	390.681779	D	*391.193574*	196.100425	374.167025	187.587150	373.183009	187.095142	3
8	899.414526	450.210901	881.403961	441.205619	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TAYFSLDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1072.518921	0.006847	TAYFSLDTR
11.3	1072.533508	-0.007740	MSTALHELR
6.7	1072.522308	0.003460	TANVPQTVPM
6.7	1072.522308	0.003460	TANVPQTVPM
6.4	1072.522278	0.003490	QLAGPLAMEQ
5.8	1072.533508	-0.007740	MENLRAAVPG
5.5	1072.533539	-0.007771	SGMVPRGPTAT
4.5	1072.533524	-0.007756	AGAGIPPMSTR
3.9	1072.519791	0.005977	TAFFLCCLR
1.5	1072.518936	0.006832	TPHDLFSSGL

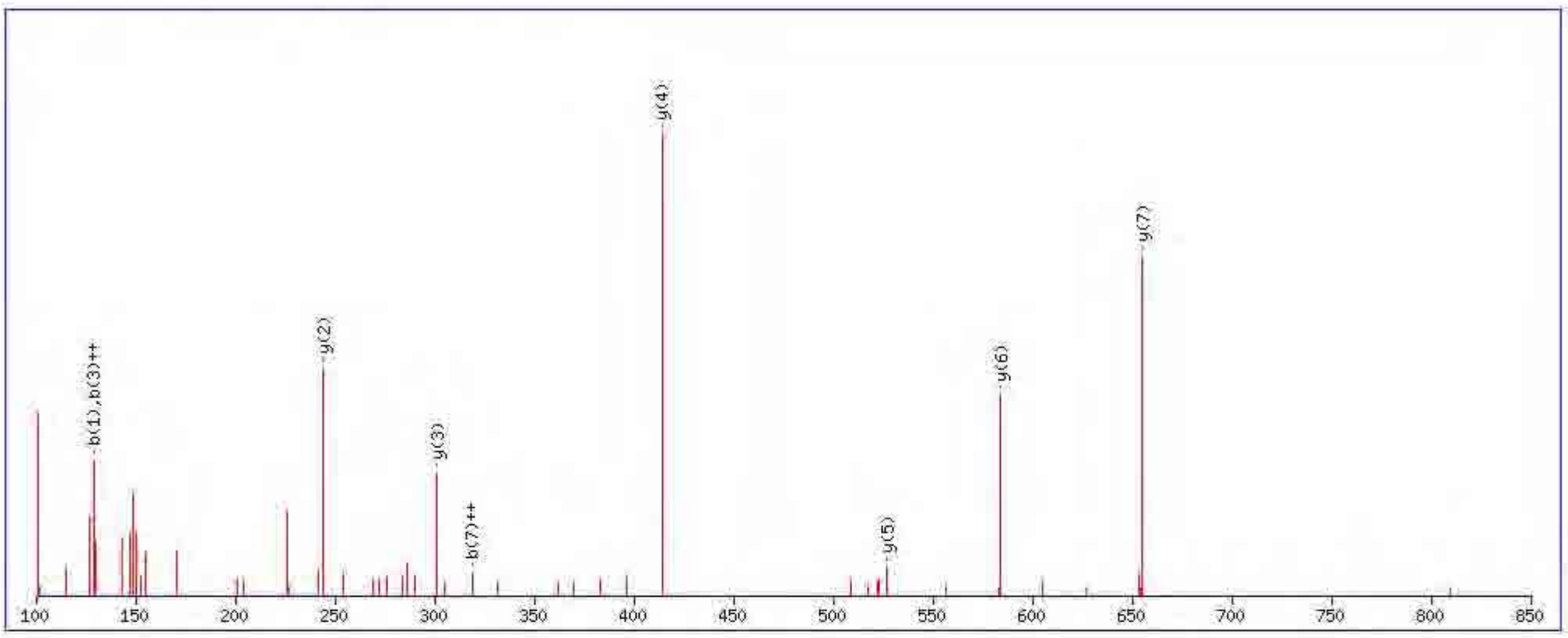
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAGPPGPK**
Found in **CO9A2_HUMAN**, Collagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2

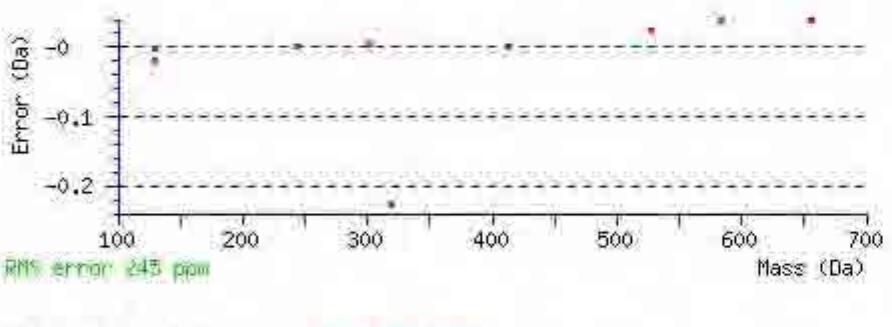
Match to Query 506: 782.430808 from(392.222680,2+) rtinseconds(508) index(514)
Title: Locus:1.1.1.1104.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

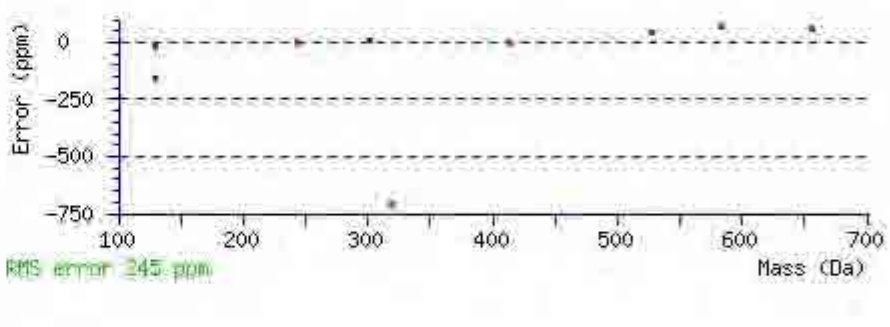
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 782.428650
Variable modifications:
P4 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 55 **Expect:** 0.00025
Matches : 9/56 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	129.102239	65.054757	112.075690	56.541483	K					8
2	200.139353	100.573315	183.112804	92.060040	A	*655.340968*	328.174122	638.314419	319.660848	7
3	257.160817	**129.084047**	240.134268	120.570772	G	*584.303854*	292.655565	567.277305	284.142291	6
4	370.208496	185.607886	353.181947	177.094612	P	*527.282390*	264.144833	510.255841	255.631559	5
5	483.256175	242.131726	466.229626	233.618451	P	*414.234711*	207.620994	397.208162	199.107719	4
6	540.277639	270.642458	523.251090	262.129183	G	*301.187032*	151.097154	284.160483	142.583880	3
7	637.330403	**319.168840**	620.303854	310.655565	P	*244.165568*	122.586422	227.139019	114.073148	2
8					K	147.112804	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of KAGPPGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	782.428650	0.002158	KAGPPGPK
52.8	782.428650	0.002158	GAAGLPGPK
38.2	782.428650	0.002158	AKGPPGPK
30.5	782.428650	0.002158	KPKPGPGA
24.8	782.428650	0.002158	KAGPPGPK
24.0	782.428635	0.002173	AANLPGPK
23.7	782.428650	0.002158	GAAGLPGPK
15.0	782.428665	0.002143	GAPGVTGPK
14.2	782.428650	0.002158	QGAPPAVK
13.5	782.428650	0.002158	AKGPPGPK

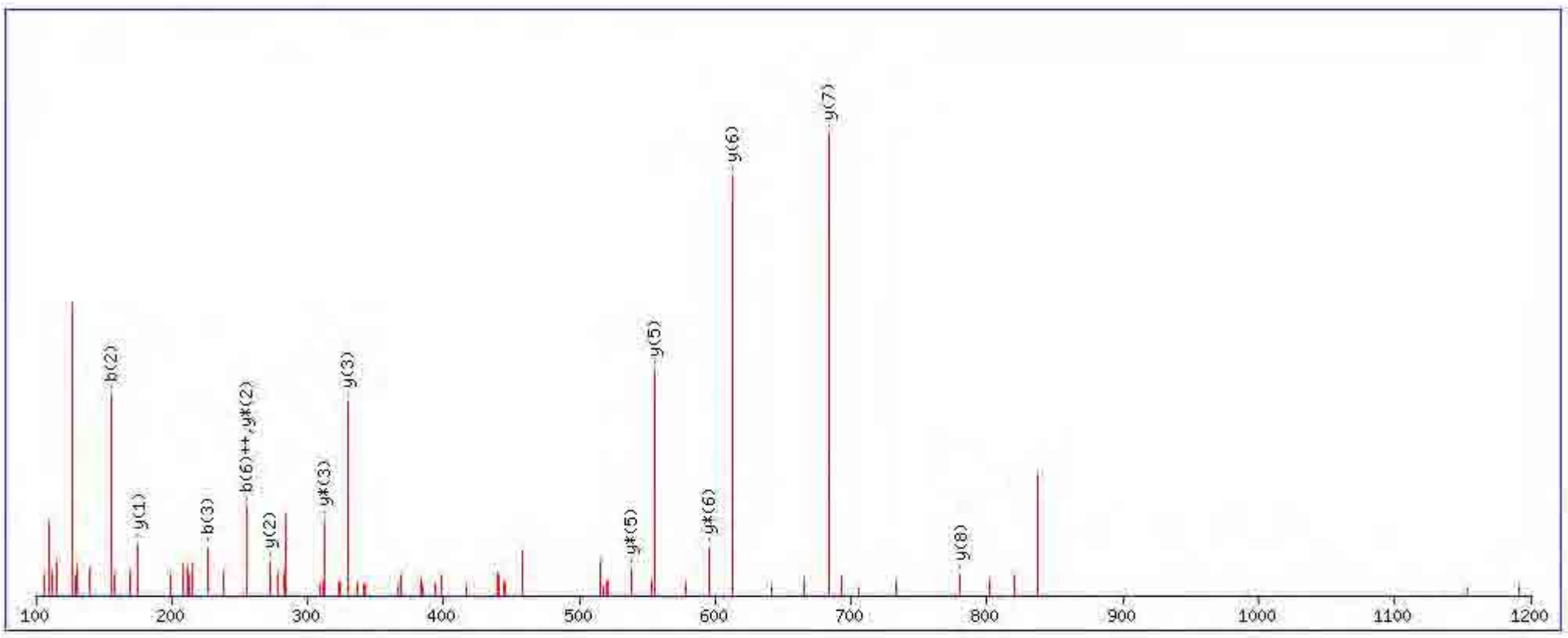
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPAGPPGPR**
Found in **CO4A3_HUMAN**, Collagen alpha-3(IV) chain OS=Homo sapiens GN=COL4A3 PE=1 SV=3

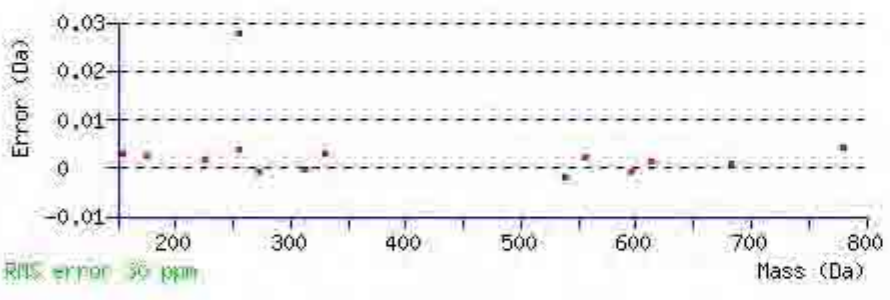
Match to Query 1058: 836.416148 from(419.215350,2+) rtinseconds(351) index(142)
Title: Locus:1.1.1.1014.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

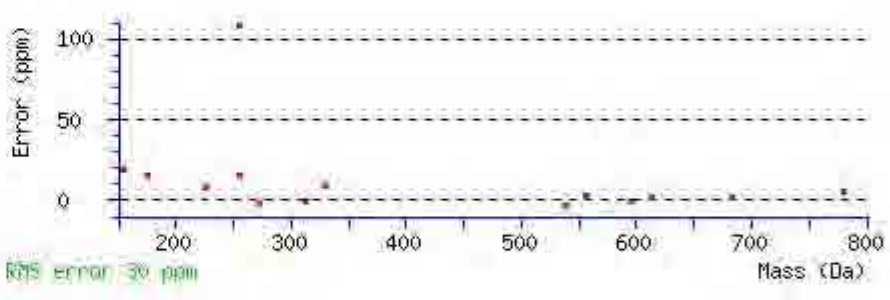
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 836.414078
Variable modifications:
P5 : Oxidation (P)
P6 : Oxidation (P)
Ions Score: 47 **Expect:** 0.0023
Matches : 14/48 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008	G					9
2	155.081504	78.044390	P	*780.399880*	390.703578	763.373331	382.190304	8
3	226.118618	113.562947	A	*683.347116*	342.177196	666.320567	333.663922	7
4	283.140082	142.073679	G	*612.310002*	306.658639	595.283453	298.145365	6
5	396.187761	198.597518	P	*555.288538*	278.147907	538.261989	269.634633	5
6	509.235440	255.121358	P	442.240859	221.624068	425.214310	213.110793	4
7	566.256904	283.632090	G	*329.193180*	165.100228	312.166631	156.586953	3
8	663.309668	332.158472	P	*272.171716*	136.589496	255.145167	128.076221	2
9			R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of GPAGPPGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	836.414078	0.002070	GPAGPPGPR
37.2	836.414063	0.002086	GPAGPPGER
32.5	836.414078	0.002070	GPAGPPGPR
29.8	836.414078	0.002070	GAPGPPGPR
21.6	836.414063	0.002086	GPAPPPNR
21.0	836.414078	0.002070	GPPGPSGPR
20.8	836.414078	0.002070	GPAGPPGPR
19.9	836.414063	0.002086	PGPAGEPGR
19.7	836.414078	0.002070	GPPGPSGPR
19.6	836.414063	0.002086	GPPGEAGPR

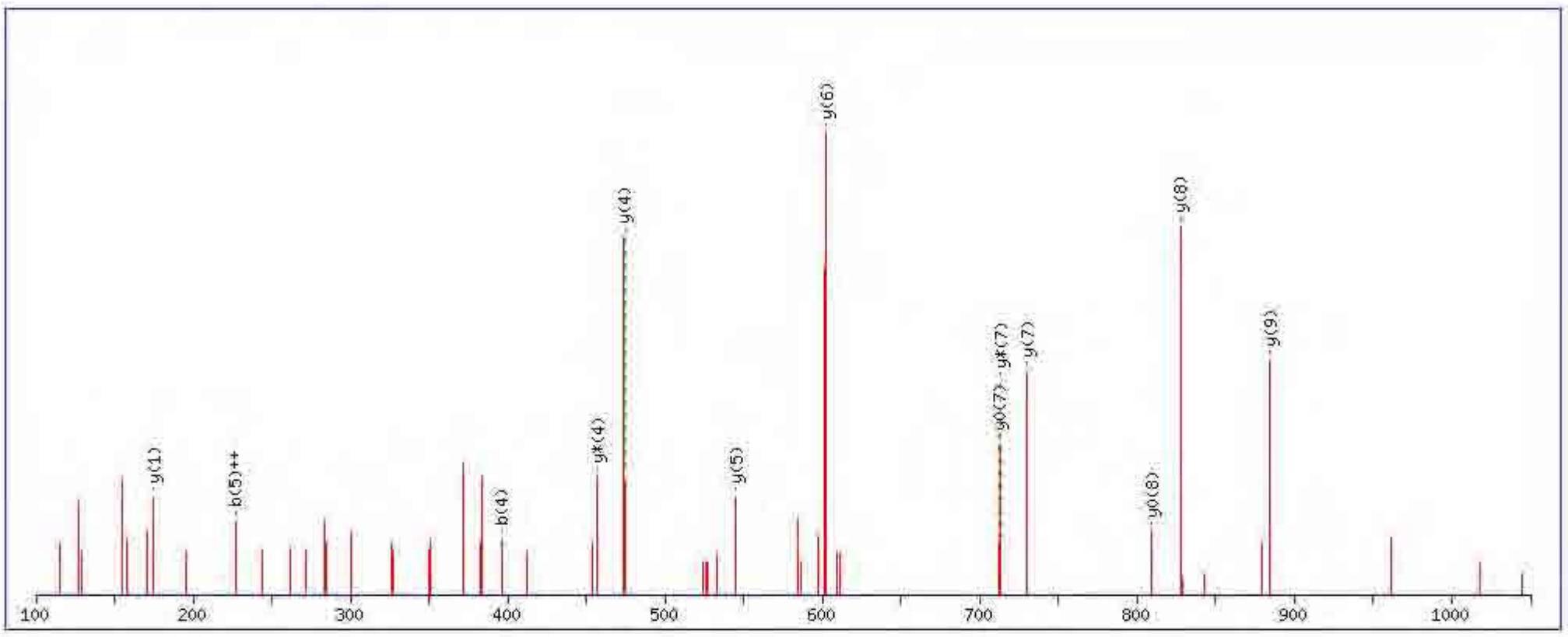
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPKGAPGER**
Found in **CO9A3_HUMAN**, Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2

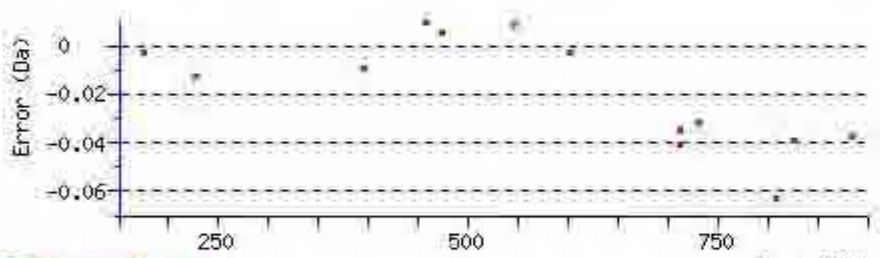
Match to Query 3546: 996.507428 from(499.260990,2+) rtinseconds(526) index(554)
Title: Locus:1.1.1.1114.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

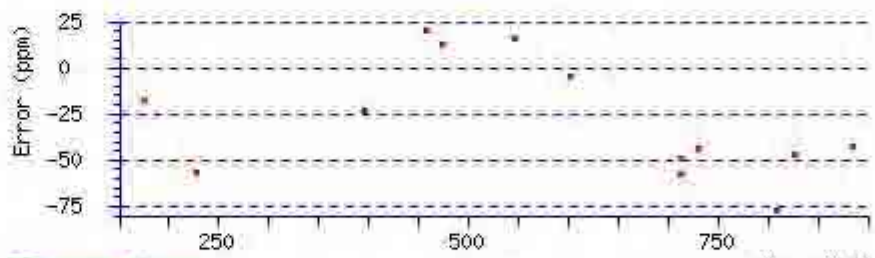
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 996.498856
Variable modifications:
P1 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 44 Expect: 0.0057
Matches : 13/84 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.054955	57.531116					P							10
2	171.076419	86.041847					G	*884.458457*	442.732867	867.431908	434.219592	866.447892	433.727584	9
3	268.129183	134.568229					P	*827.436993*	414.222135	810.410444	405.708860	809.426428	405.216852	8
4	396.224146	198.615711	379.197597	190.102436			K	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	7
5	453.245610	227.126443	436.219061	218.613168			G	*602.289266*	301.648271	585.262717	293.134997	584.278701	292.642989	6
6	524.282724	262.645000	507.256175	254.131726			A	*545.267802*	273.137539	528.241253	264.624265	527.257237	264.132257	5
7	637.330403	319.168840	620.303854	310.655565			P	*474.230688*	237.618982	457.204139	229.105708	456.220123	228.613700	4
8	694.351867	347.679572	677.325318	339.166297			G	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
9	823.394460	412.200868	806.367911	403.687594	805.383895	403.195586	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PGPKGAPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	996.498856	0.008572	PGPKGAPGER
26.0	996.498856	0.008572	PGPAGPKGER
25.8	996.498871	0.008557	PGPSGPPGKR
24.3	996.498871	0.008557	PGQPGLPGSR
23.9	996.512756	-0.005328	VAPKEPVEE
23.8	996.498856	0.008572	PGPKGAPGER
21.5	996.498871	0.008557	LGPPQGGSPR
16.1	996.498856	0.008572	PGPQAGAGAGAK
15.8	996.498856	0.008572	PGPAGPRGEK
15.3	996.512772	-0.005344	LGPELSPSPT

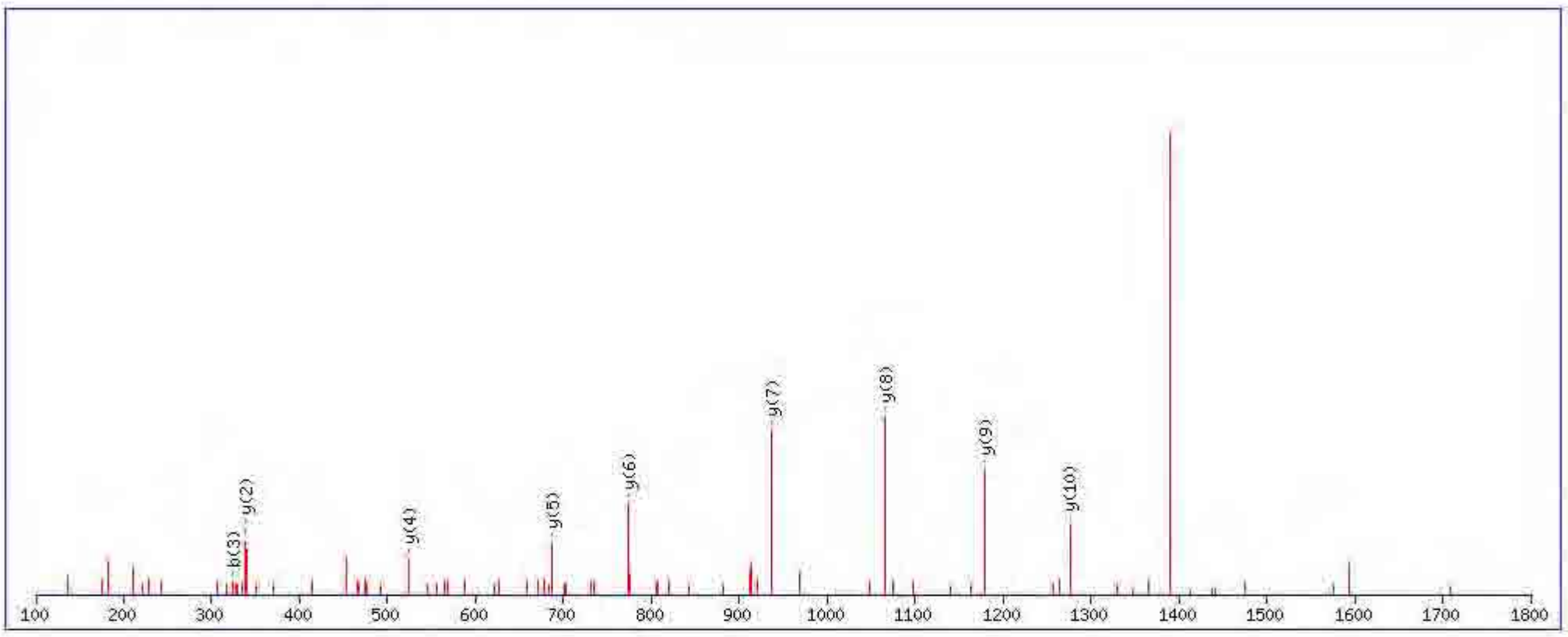
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLEYSYGEYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

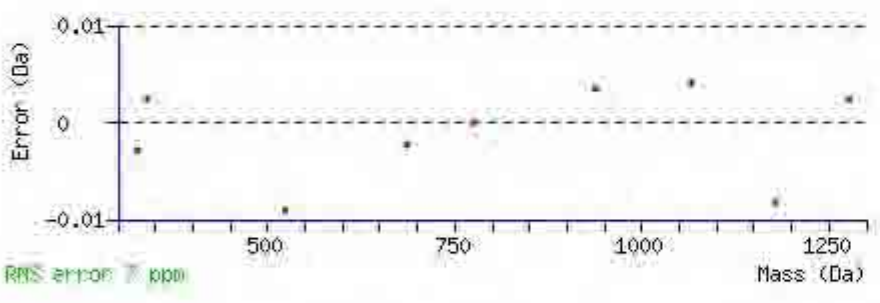
Match to Query 10964: 1388.665888 from(695.340220,2+) rtinseconds(1605) index(8565)
Title: Locus:1.1.1.1721.16
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

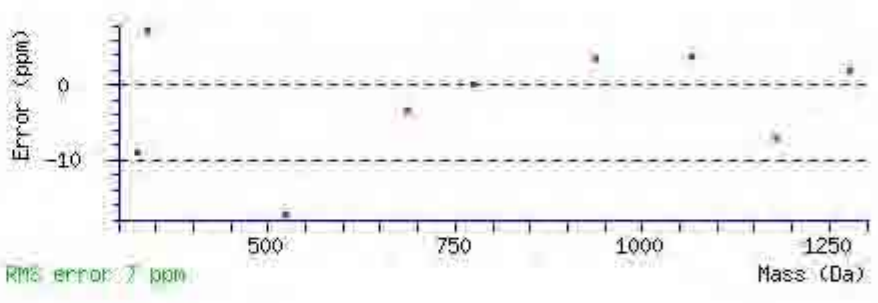
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1388.661194
Ions Score: 62 **Expect:** 2.6e-005
Matches : 9/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							11
2	211.144104	106.075690			P	*1276.584445*	638.795861	1259.557896	630.282586	1258.573880	629.790578	10
3	324.228168	162.617722			L	*1179.531681*	590.269479	1162.505132	581.756204	1161.521116	581.264196	9
4	453.270761	227.139018	435.260196	218.133736	E	*1066.447617*	533.727447	1049.421068	525.214172	1048.437052	524.722164	8
5	616.334090	308.670683	598.323525	299.665401	Y	*937.405024*	469.206150	920.378475	460.692876	919.394459	460.200868	7
6	703.366118	352.186697	685.355553	343.181415	S	*774.341695*	387.674486	757.315146	379.161211	756.331130	378.669203	6
7	866.429447	433.718362	848.418882	424.713079	Y	*687.309667*	344.158472	670.283118	335.645197	669.299102	335.153189	5
8	923.450911	462.229094	905.440346	453.223811	G	*524.246338*	262.626807	507.219789	254.113533	506.235773	253.621525	4
9	1052.493504	526.750390	1034.482939	517.745108	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
10	1215.556833	608.282055	1197.546268	599.276772	Y	*338.182281*	169.594778	321.155732	161.081504			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LPLEYSYGEYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.4	1388.661194	0.004694	LPLEYSYGEYR
12.8	1388.667114	-0.001226	PPPELTDTATSTK
9.8	1388.657227	0.008661	PPPPAPPAPPAPR
9.3	1388.667953	-0.002065	IPELLASGMVDNM
8.1	1388.657227	0.008661	PPPPAPPAPPAPR
7.3	1388.667114	-0.001226	PPPELTDTATSTK
7.2	1388.657227	0.008661	PPPPAPPAPPAPR
6.8	1388.672485	-0.006597	PPPVFADSPFQR
5.4	1388.657211	0.008677	LPEDQPPGPAALH
5.3	1388.658051	0.007837	LPEHCIEYVRM

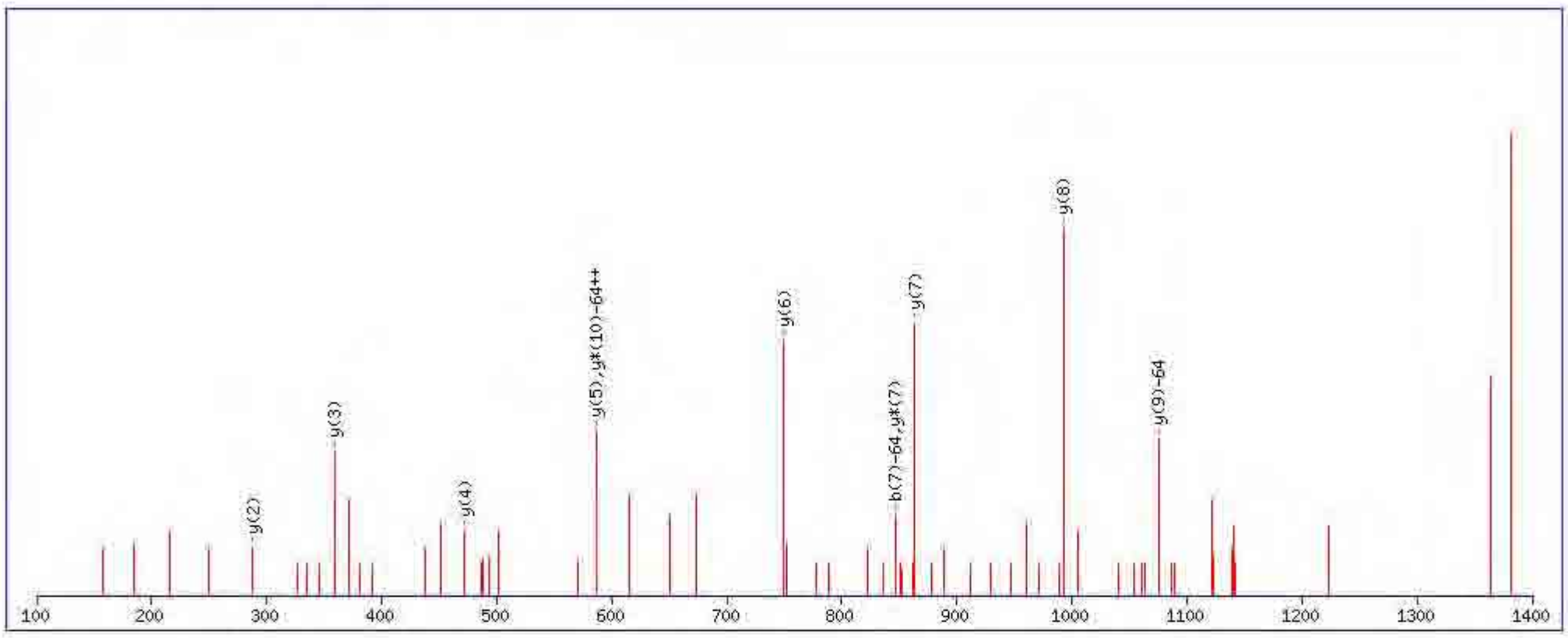
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

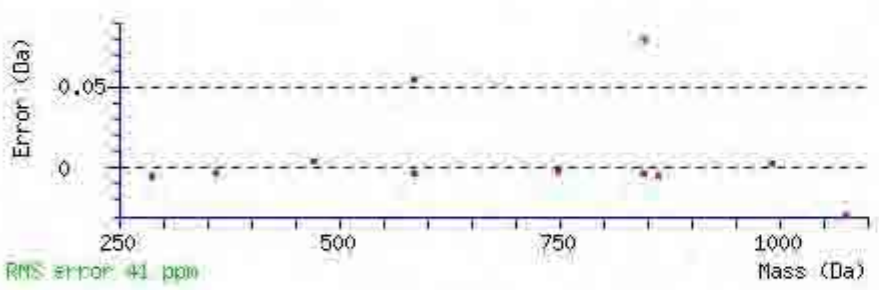
Match to Query 10834: 1380.675248 from(691.344900,2+) rtinseconds(1473) index(7190)
Title: Locus:1.1.1.1648.24
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

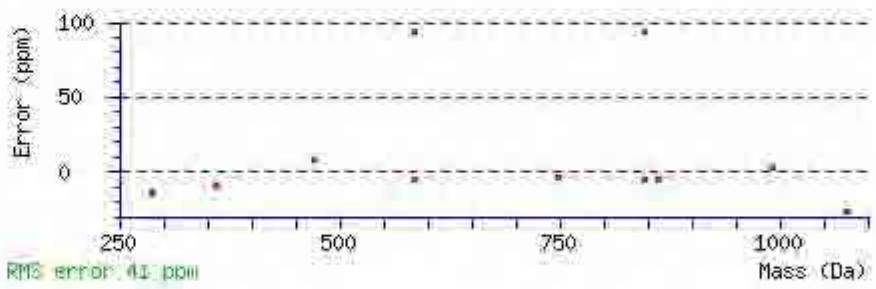
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 69 **Expect:** 1.9e-005
Matches : 11/154 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1188.637149	594.822213	1171.610600	586.308938	1170.626584	585.816930	10
3	326.171048	163.589162			308.160483	154.583879	M	*1075.553085*	538.280181	1058.526536	529.766906	1057.542520	529.274898	9
4	455.213641	228.110458			437.203076	219.105176	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	569.256568	285.131922	552.230019	276.618648	551.246003	276.126640	N	*863.473377*	432.240326	846.446828	423.727052			7
6	732.319897	366.663587	715.293348	358.150312	714.309332	357.658304	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	846.362824	423.685050	829.336275	415.171775	828.352259	414.679767	N	*586.367121*	293.687199	569.340572	285.173924			5
8	959.446888	480.227082	942.420339	471.713807	941.436323	471.221799	I	*472.324194*	236.665735	455.297645	228.152460			4
9	1030.484002	515.745639	1013.457453	507.232365	1012.473437	506.740357	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1143.568066	572.287671	1126.541517	563.774397	1125.557501	563.282389	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.0	1380.670700	0.004548	EIMENYNIALR
17.5	1380.688492	-0.013244	YIPENVSSSTLR
12.2	1380.674103	0.001145	TLGSLMNIKNMSG
6.8	1380.684647	-0.009399	EELFTMKLIEP
6.3	1380.667374	0.007874	INFSGPDYPSIR
5.7	1380.667389	0.007859	PFNVQYPGQTSK
5.6	1380.663330	0.011918	ESAAAFSSQPSRK
5.6	1380.688507	-0.013259	SPSAPAPGPVPAAAK
5.6	1380.688507	-0.013259	SPSAPAPGPVPAAAK
5.6	1380.688507	-0.013259	SPSAPAPGPVPAAAK

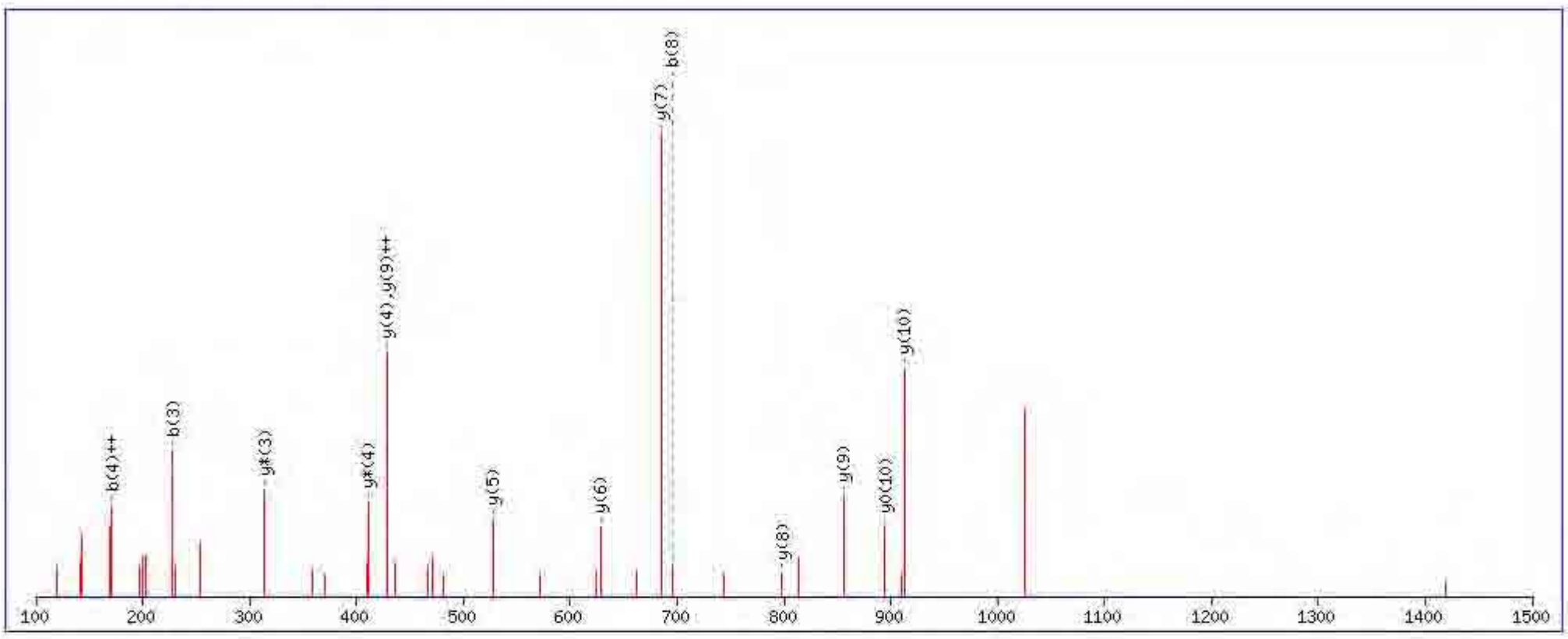
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **EF1A1_HUMAN**, Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

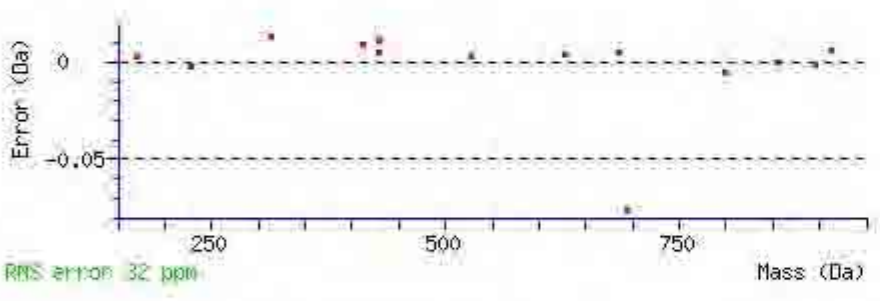
Match to Query 3953: 1024.612968 from(513.313760,2+) rtinseconds(1283) index(5218)
Title: Locus:1.1.1.1543.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

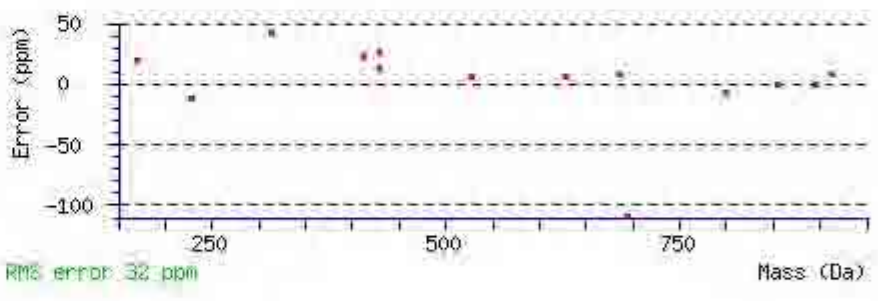
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1024.602951
Ions Score: 48 **Expect:** 0.00049
Matches : 15/80 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	912.526143	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	228.134268	114.570772			G	855.504679	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	341.218332	171.112804			I	798.483215	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	685.399151	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	628.377687	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	598.355889	299.681583	580.345324	290.676300	V	527.330008	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	428.261594	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	232.140416	116.573846	215.113867	108.060572			2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IGGIGTVPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	1024.602951	0.010017	IGGIGTVPVGR
12.0	1024.614166	-0.001198	LVLTGGGRPR
11.6	1024.602921	0.010047	IVQGPREVK
11.4	1024.602936	0.010032	LVQPGIVQR
11.2	1024.614151	-0.001183	LVQPGRSLR
11.2	1024.602921	0.010047	PVKPAVDRK
11.2	1024.614151	-0.001183	PVQRPKLR
10.8	1024.602905	0.010063	PGAVAAAAILR
10.5	1024.616837	-0.003869	LNPLVLLLD
9.3	1024.614166	-0.001198	LVGGATRVPR

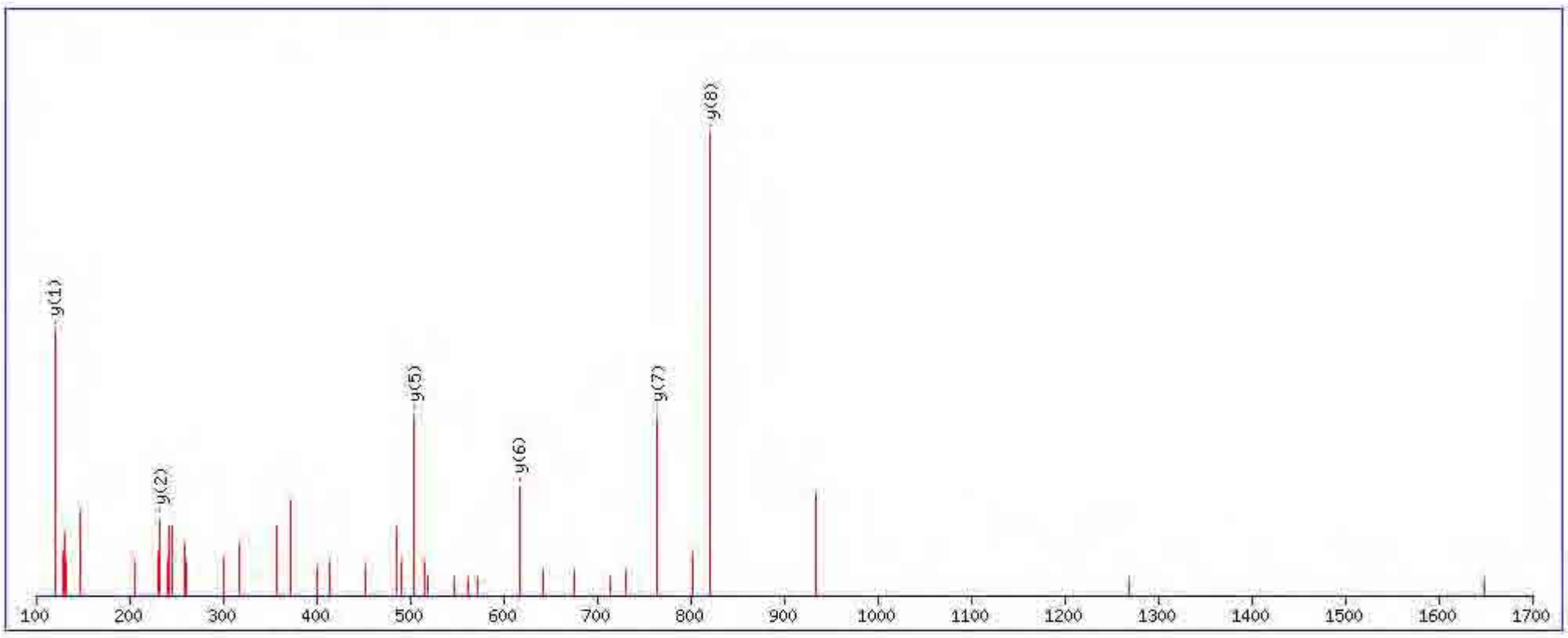
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFLAEALT**
Found in **EPHAA_HUMAN**, Ephrin type-A receptor 10 OS=Homo sapiens GN=EPHA10 PE=2 SV=1

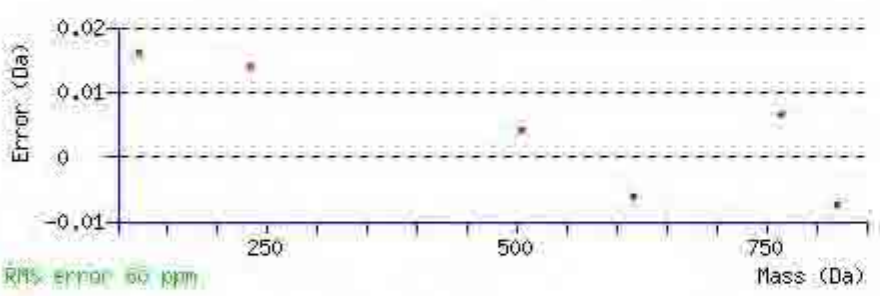
Match to Query 2689: 933.520028 from(467.767290,2+) rtinseconds(1514) index(7625)
Title: Locus:1.1.1.1672.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

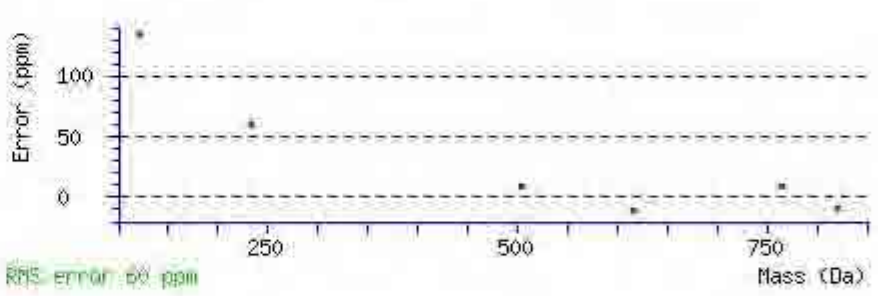
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 933.517120
Ions Score: 55 **Expect:** 0.0006
Matches : 6/54 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L					9
2	171.112804	86.060040			G	*821.440347*	411.223812	803.429782	402.218529	8
3	318.181218	159.594247			F	*764.418883*	382.713080	746.408318	373.707797	7
4	431.265282	216.136279			L	*617.350469*	309.178873	599.339904	300.173590	6
5	502.302396	251.654836			A	*504.266405*	252.636840	486.255840	243.631558	5
6	631.344989	316.176133	613.334424	307.170850	E	433.229291	217.118283	415.218726	208.113001	4
7	702.382103	351.694690	684.371538	342.689407	A	304.186698	152.596987	286.176133	143.591704	3
8	815.466167	408.236722	797.455602	399.231439	L	*233.149584*	117.078430	215.139019	108.073148	2
9					T	*120.065520*	60.536398	102.054955	51.531116	1





NCBI **BLAST** search of LGFLAEALT
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.9	933.517120	0.002908	LGFLAEALT
33.7	933.517120	0.002908	IGFIEEVK
29.1	933.528351	-0.008323	IGFIDKNK
22.9	933.517151	0.002877	LGFTPSVTI
20.5	933.528366	-0.008338	IGFEGVKGK
15.3	933.517120	0.002908	IGFELVEK
14.9	933.528381	-0.008353	IGVKFNVGT
13.6	933.517120	0.002908	VAFLLDEK
12.1	933.517151	0.002877	IGSVVVYPT
11.8	933.517151	0.002877	IFGVLAVDT

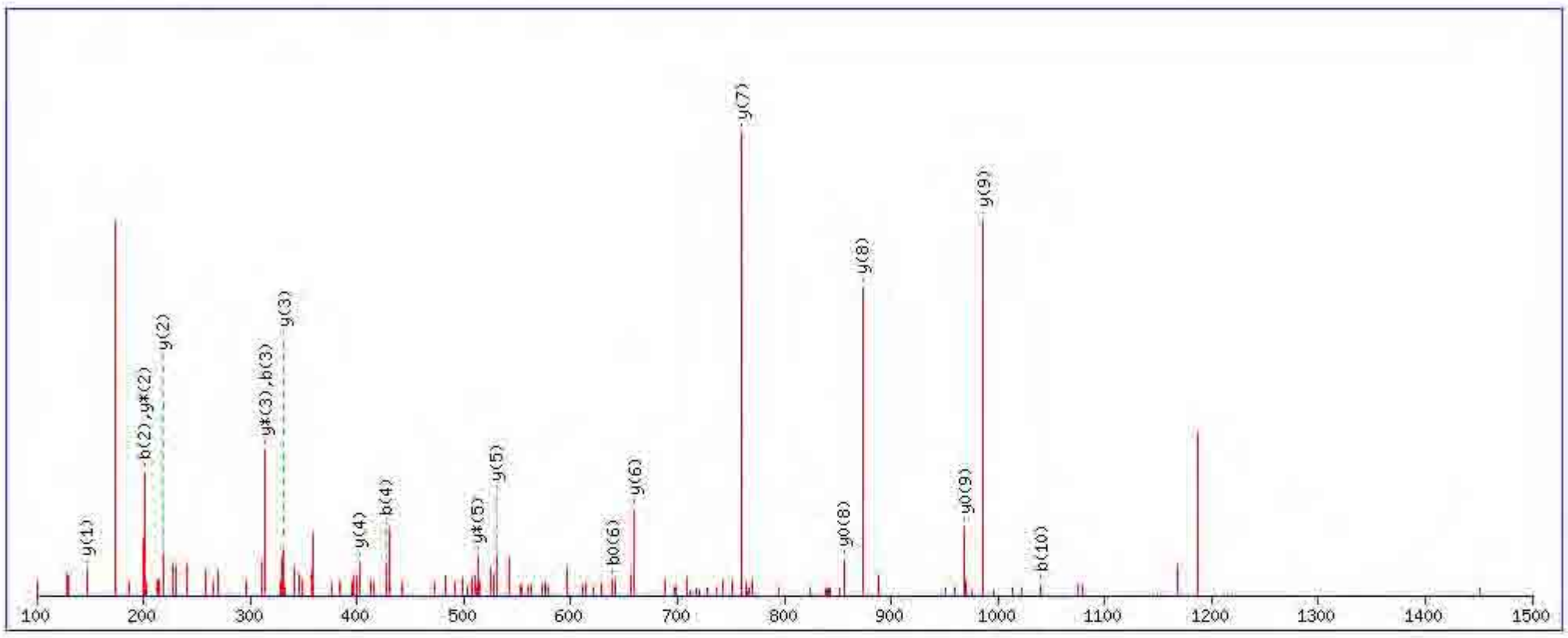
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILLTEQALAK**
Found in **LACRT_HUMAN**, Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1

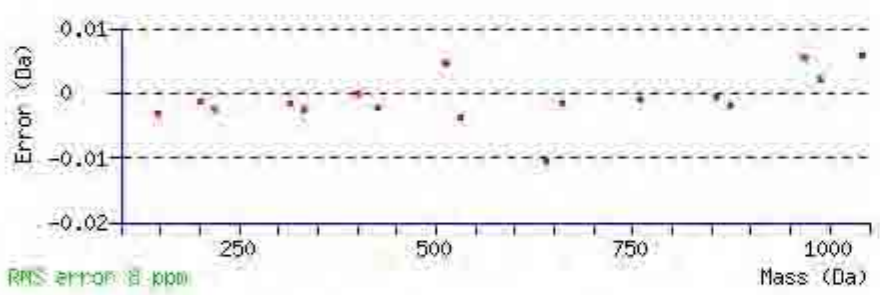
Match to Query 7388: 1185.702868 from(593.858710,2+) rtinseconds(1599) index(8505)
Title: Locus:1.1.1.1718.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

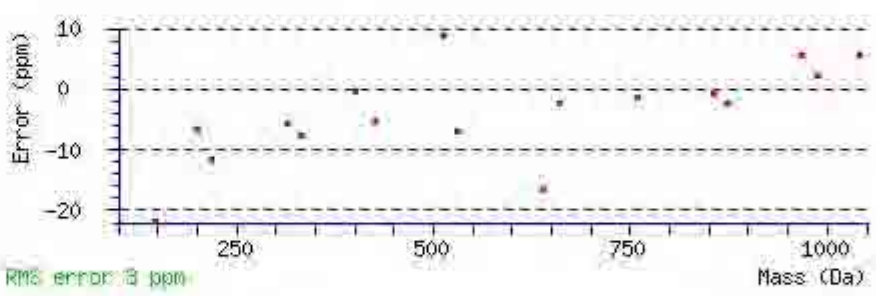
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1185.696854
Ions Score: 66 **Expect:** 9.2e-006
Matches : 19/98 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	201.123368	101.065322			183.112803	92.060039	I	1099.672138	550.339707	1082.645589	541.826433	1081.661573	541.334425	10
3	314.207432	157.607354			296.196867	148.602071	L	*986.588074*	493.797675	969.561525	485.284401	968.577509	484.792393	9
4	427.291496	214.149386			409.280931	205.144104	L	*873.504010*	437.255643	856.477461	428.742369	855.493445	428.250361	8
5	528.339175	264.673226			510.328610	255.667943	T	*760.419946*	380.713611	743.393397	372.200337	742.409381	371.708329	7
6	657.381768	329.194522			639.371203	320.189240	E	*659.372267*	330.189772	642.345718	321.676497	641.361702	321.184489	6
7	785.440346	393.223811	768.413797	384.710537	767.429781	384.218529	Q	*530.329674*	265.668475	513.303125	257.155201			5
8	856.477460	428.742368	839.450911	420.229094	838.466895	419.737086	A	*402.271096*	201.639186	385.244547	193.125912			4
9	969.561524	485.284400	952.534975	476.771126	951.550959	476.279118	L	*331.233982*	166.120629	314.207433	157.607355			3
10	1040.598638	520.802957	1023.572089	512.289683	1022.588073	511.797675	A	*218.149918*	109.578597	201.123369	101.065323			2
11							K	*147.112804*	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SILLTEQALAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.4	1185.696854	0.006014	SILLTEQALAK
24.1	1185.698212	0.004656	LSILTPRHHL
23.6	1185.708084	-0.005216	ISASALLKQQK
19.3	1185.696869	0.005999	TVLTELQAKIA
15.2	1185.708099	-0.005231	SIIPRGSLSLK
13.4	1185.700882	0.001986	ISLLLIESWL
13.4	1185.708084	-0.005216	ISLLNLTERK
13.4	1185.712128	-0.009260	PSLIFKQLPK
13.4	1185.696854	0.006014	SILILQEKDK
13.4	1185.712158	-0.009290	TVPIVLFPIR

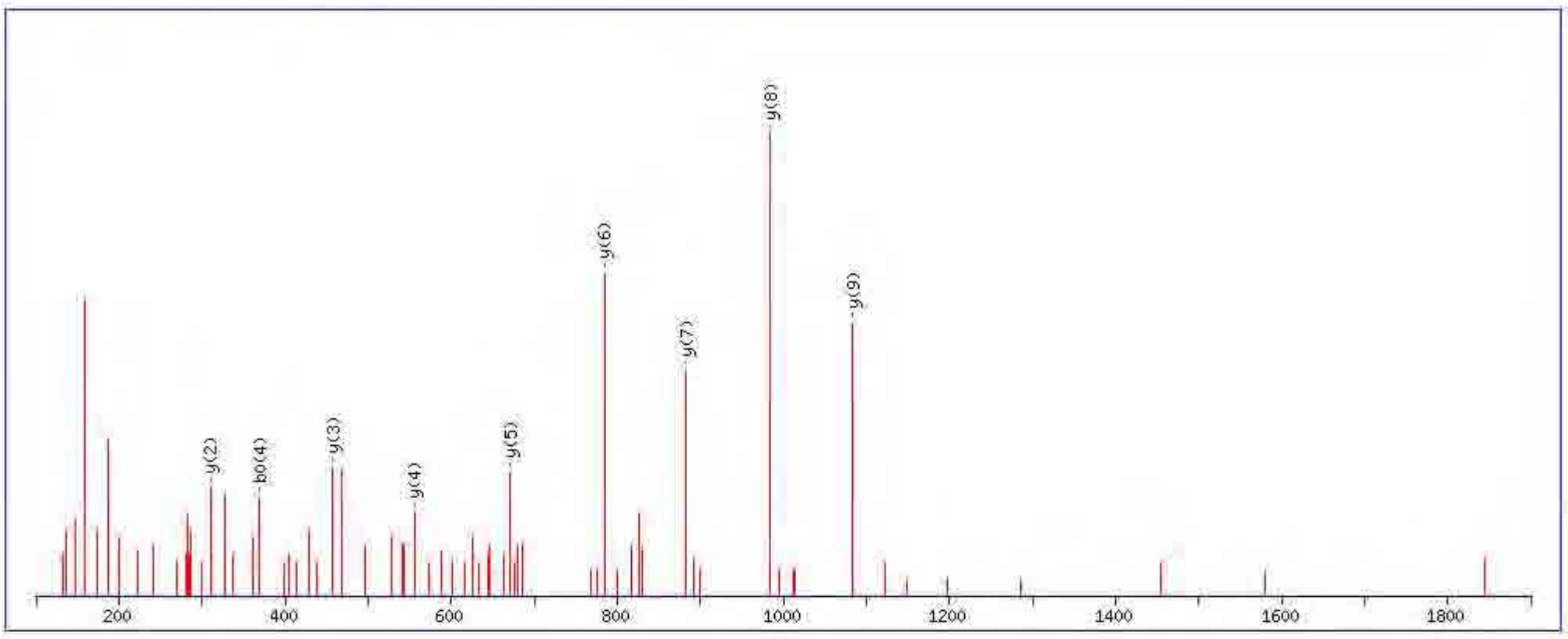
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVVTVIDVFYK**
Found in **FIL2_HUMAN**, Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1

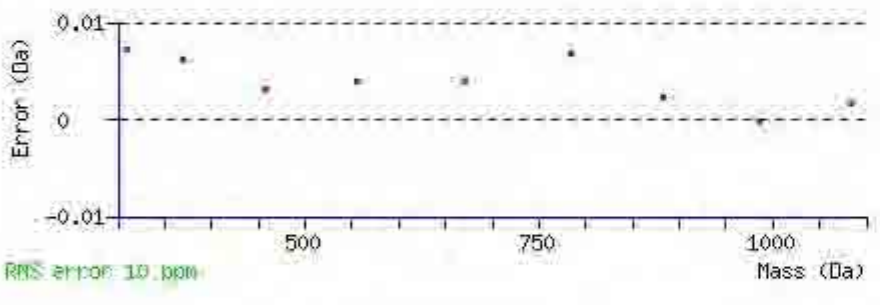
Match to Query 9075: 1268.713668 from(635.364110,2+) rtinseconds(2253) index(16173)
Title: Locus:1.1.1.2078.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

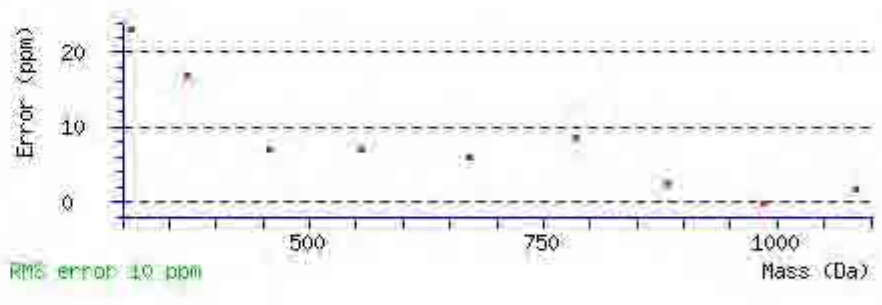
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1268.701660
Ions Score: 70 **Expect:** 1.6e-006
Matches : 9/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	187.107718	94.057497	169.097153	85.052214	V	1182.676889	591.842082	1165.650340	583.328808	1164.666324	582.836800	10
3	286.176132	143.591704	268.165567	134.586422	V	*1083.608475*	542.307876	1066.581926	533.794601	1065.597910	533.302593	9
4	387.223811	194.115544	369.213246	185.110261	T	*984.540061*	492.773668	967.513512	484.260394	966.529496	483.768386	8
5	486.292225	243.649751	468.281660	234.644468	V	*883.492382*	442.249829	866.465833	433.736554	865.481817	433.244546	7
6	599.376289	300.191783	581.365724	291.186500	I	*784.423968*	392.715622	767.397419	384.202347	766.413403	383.710339	6
7	714.403232	357.705254	696.392667	348.699972	D	*671.339904*	336.173590	654.313355	327.660315	653.329339	327.168307	5
8	813.471646	407.239461	795.461081	398.234178	V	*556.312961*	278.660119	539.286412	270.146844			4
9	960.540060	480.773668	942.529495	471.768385	F	*457.244547*	229.125911	440.217998	220.612637			3
10	1123.603389	562.305332	1105.592824	553.300050	Y	*310.176133*	155.591704	293.149584	147.078430			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SVVTVIDVFYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.3	1268.701660	0.012008	SVVTVIDVFYK
8.1	1268.701614	0.012054	KELDLFTYLK
7.8	1268.722748	-0.009080	DVITLLIPEEK
7.0	1268.712875	0.000793	VSLWPVPVAASK
6.8	1268.712845	0.000823	WVIEAKDLPAK
5.1	1268.708832	0.004836	VSPPAGRSLELK
4.8	1268.708801	0.004867	AQKPAQLKEEK
4.7	1268.724091	-0.010423	WSVISLLRQPA
3.5	1268.716248	-0.002580	ATIPGMVGPVIAK
2.9	1268.708832	0.004836	VSPPAGRSLELK

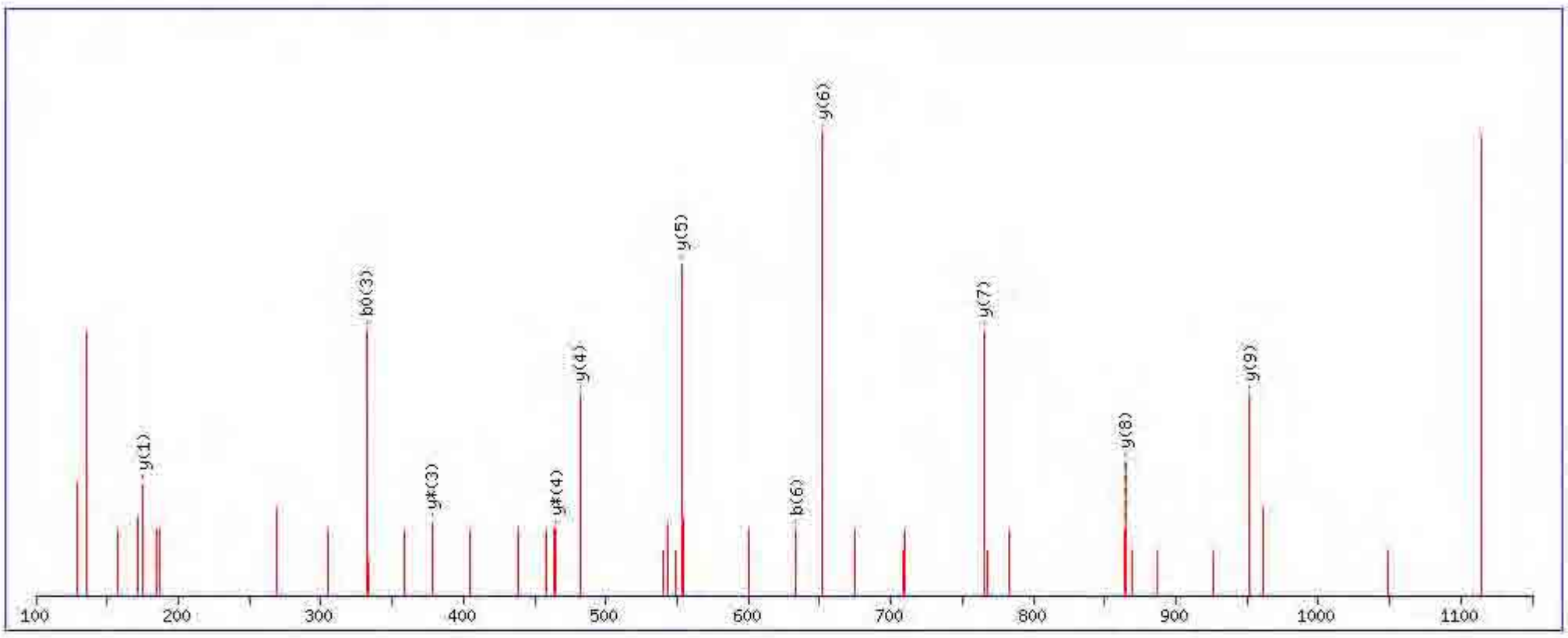
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSVLVASGYR**
Found in **GPHA2_HUMAN**, Glycoprotein hormone alpha-2 OS=Homo sapiens GN=GPHA2 PE=1 SV=1

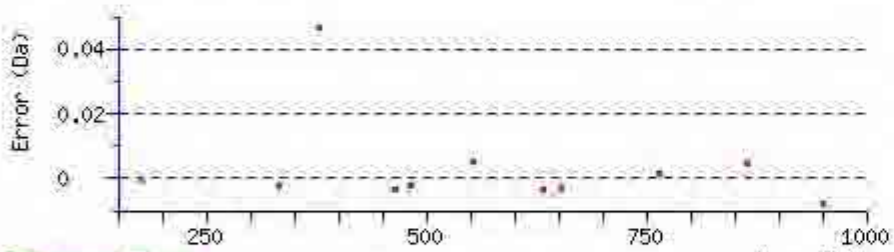
Match to Query 5620: 1113.578248 from(557.796400,2+) rtinseconds(1400) index(6416)
Title: Locus:1.1.1.1608.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

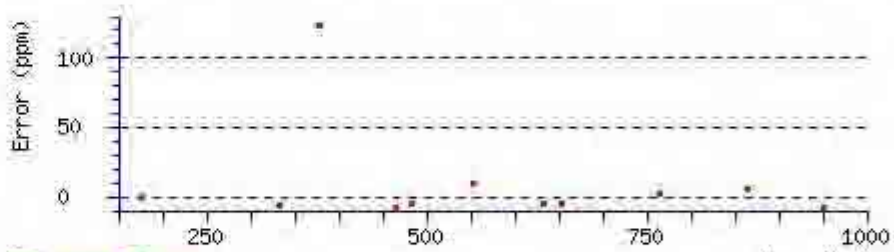
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1113.581848
Ions Score: 34 **Expect:** 0.0032
Matches : 11/82 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							10
2	251.102633	126.054954	233.092068	117.049672	S	*951.525807*	476.266542	934.499258	467.753267	933.515242	467.261259	9
3	350.171047	175.589161	332.160482	166.583879	V	*864.493779*	432.750528	847.467230	424.237253	846.483214	423.745245	8
4	463.255111	232.131193	445.244546	223.125911	L	*765.425365*	383.216321	748.398816	374.703046	747.414800	374.211038	7
5	562.323525	281.665401	544.312960	272.660118	V	*652.341301*	326.674289	635.314752	318.161014	634.330736	317.669006	6
6	633.360639	317.183958	615.350074	308.178675	A	*553.272887*	277.140082	536.246338	268.626807	535.262322	268.134799	5
7	720.392667	360.699972	702.382102	351.694689	S	*482.235773*	241.621524	465.209224	233.108250	464.225208	232.616242	4
8	777.414131	389.210704	759.403566	380.205421	G	395.203745	198.105511	378.177196	189.592236			3
9	940.477460	470.742368	922.466895	461.737086	Y	338.182281	169.594778	321.155732	161.081504			2
10					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YSVLVASGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1113.581848	-0.003600	YSVLVASGYR
7.4	1113.578705	-0.000457	MVCIVHLQR
6.8	1113.574005	0.004243	LPSMTGPLLPG
6.8	1113.574005	0.004243	TLALMGPPGLP
6.8	1113.570633	0.007615	TPLAVPGPYPA
3.7	1113.574005	0.004243	TLALMGPPGLP
3.2	1113.581863	-0.003615	APFTPSPLPR
0.5	1113.571304	0.006944	MGGRPGSLAPR
0.2	1113.574005	0.004243	LPSMTGPLLPG

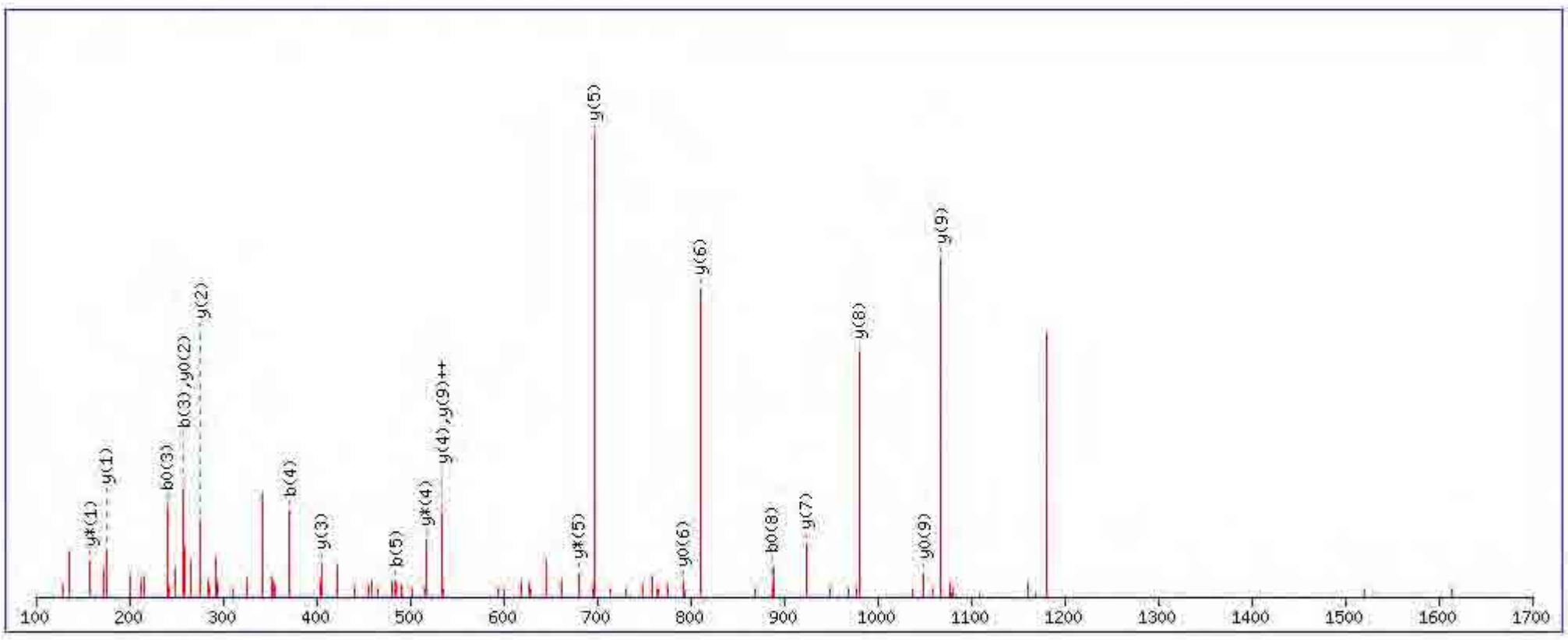
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISGLIYEETR**
Found in **H4_HUMAN**, Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

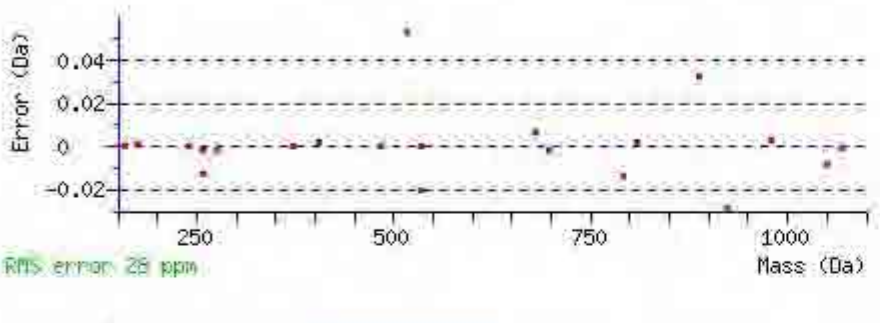
Match to Query 7201: 1179.613788 from(590.814170,2+) rtinseconds(1396) index(6385)
Title: Locus:1.1.1.1606.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

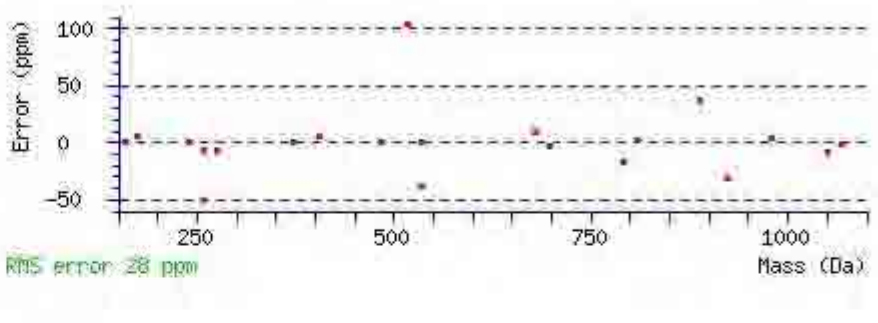
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1179.613525
Ions Score: 69 **Expect:** 1.9e-005
Matches : 21/86 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							10
2	201.123368	101.065322	183.112803	92.060039	S	*1067.536766*	534.272021	1050.510217	525.758747	1049.526201	525.266739	9
3	**258.144832**	129.576054	240.134267	120.570771	G	*980.504738*	490.756007	963.478189	482.242733	962.494173	481.750725	8
4	**371.228896**	186.118086	353.218331	177.112803	L	*923.483274*	462.245275	906.456725	453.732001	905.472709	453.239993	7
5	**484.312960**	242.660118	466.302395	233.654835	I	*810.399210*	405.703243	793.372661	397.189969	792.388645	396.697961	6
6	647.376289	324.191783	629.365724	315.186500	Y	*697.315146*	349.161211	680.288597	340.647937	679.304581	340.155929	5
7	776.418882	388.713079	758.408317	379.707797	E	*534.251817*	267.629547	517.225268	259.116272	516.241252	258.624264	4
8	905.461475	453.234376	887.450910	444.229093	E	*405.209224*	203.108250	388.182675	194.594975	387.198659	194.102967	3
9	1006.509154	503.758215	988.498589	494.752933	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
10					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ISGLIYEETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.4	1179.613525	0.000263	ISGLIYEETR
27.6	1179.610855	0.002933	PSGLHNQQKR
17.7	1179.610840	0.002948	ISGHRPEAASR
16.1	1179.613586	0.000202	SPGPPPPVGVKT
15.4	1179.618256	-0.004468	LSGRGFMLGSR
14.8	1179.624771	-0.010983	ISPPPTANLDR
14.2	1179.613525	0.000263	LKAEPAAPPAAP
13.8	1179.624786	-0.010998	SVAPLPPQRSP
10.9	1179.614883	-0.001095	PSAHSLLFHR
10.1	1179.624771	-0.010983	GAELPTHPSKK

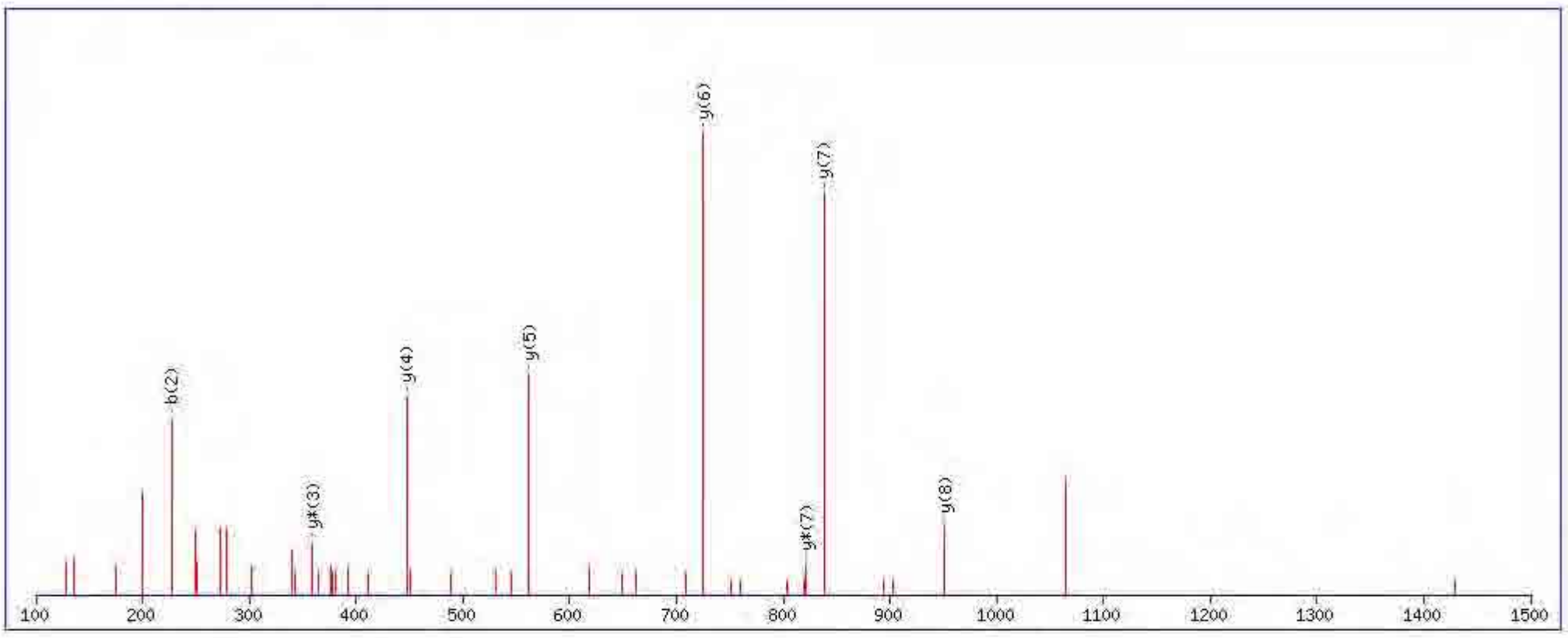
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

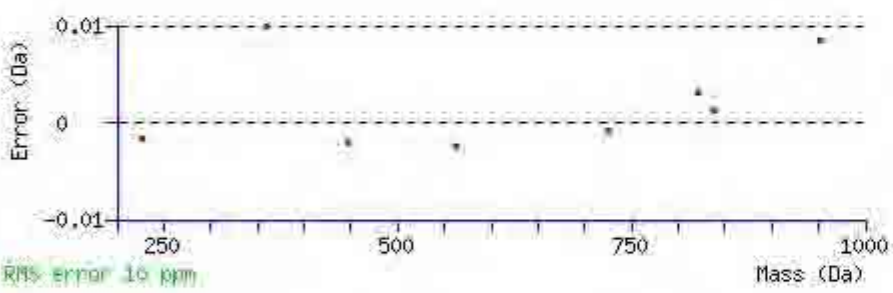
Match to Query 4667: 1063.568608 from(532.791580,2+) rtinseconds(1342) index(5827)
Title: Locus:1.1.1.1576.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

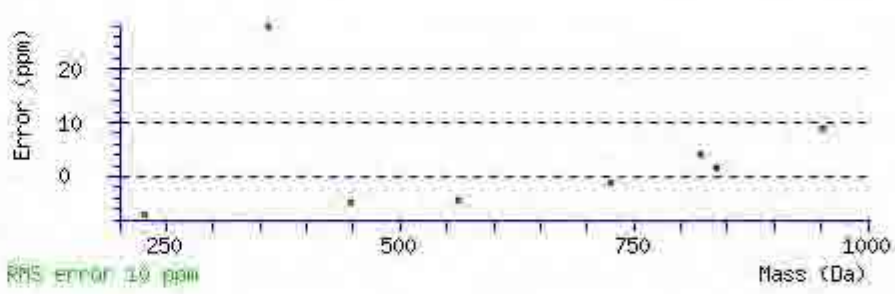
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 42 **Expect:** 0.0088
Matches : 8/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*951.489421*	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	*838.405357*	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	*725.321293*	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	*562.257964*	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	*447.231021*	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	376.193907	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	1063.566177	0.002431	LLIYDASNR
27.8	1063.573593	-0.004985	LLPNFGKML
21.4	1063.559006	0.009602	LLLPPGYFP
16.3	1063.566208	0.002400	LLLQHGADPT
15.4	1063.566208	0.002400	LPLAQVSAHP
14.7	1063.570221	-0.001613	LLNAFFDPK
14.5	1063.573593	-0.004985	LIAQACVSIF
14.3	1063.577438	-0.008830	PLPRPAPPR
14.3	1063.577438	-0.008830	PPPPALRPR
13.6	1063.577438	-0.008830	PPPPALRPR

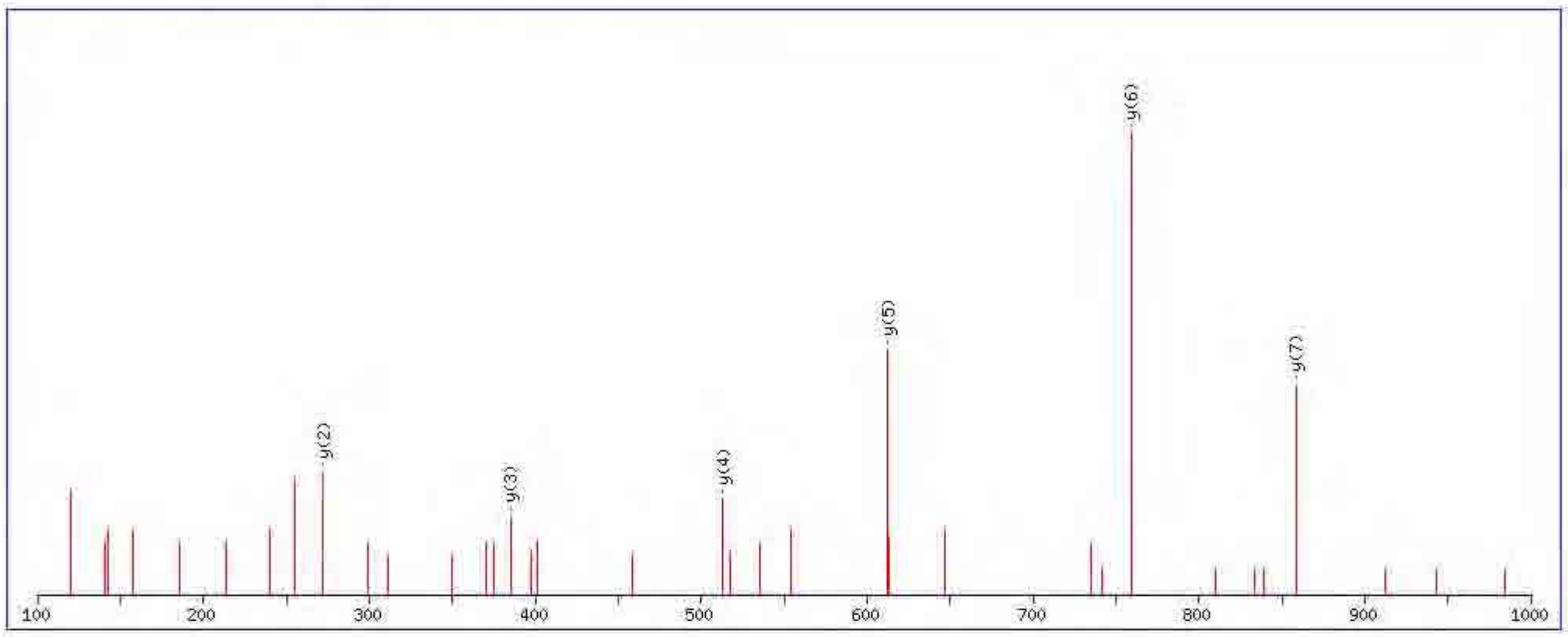
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANVFVQLPR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

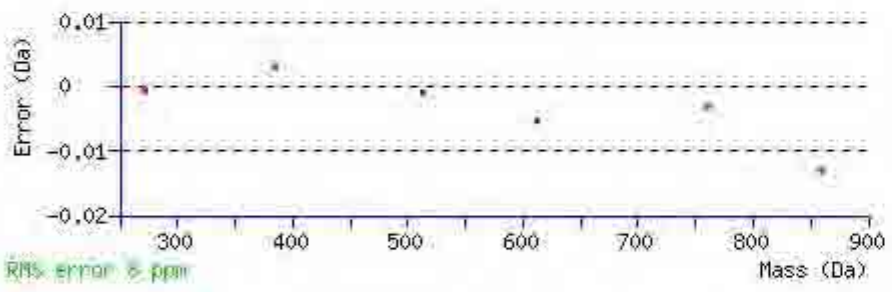
Match to Query 4287: 1042.595488 from(522.305020,2+) rtinseconds(1610) index(8607)
Title: Locus:1.1.1.1724.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

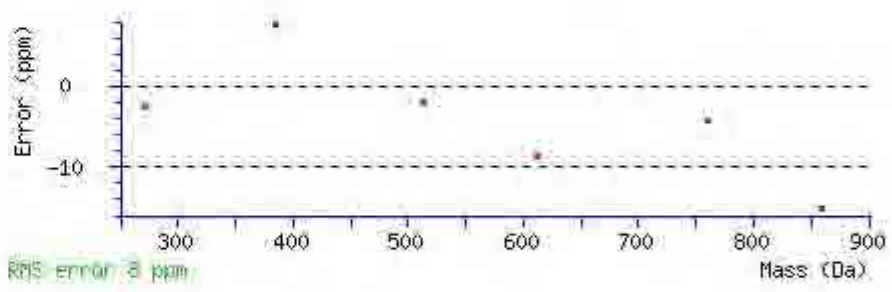
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1042.592361
Ions Score: 49 **Expect:** 0.0003
Matches : 6/62 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	186.087317	93.547296	169.060768	85.034022	N	972.562527	486.784902	955.535978	478.271627	8
3	285.155731	143.081504	268.129182	134.568229	V	*858.519600*	429.763438	841.493051	421.250164	7
4	432.224145	216.615710	415.197596	208.102436	F	*759.451186*	380.229231	742.424637	371.715957	6
5	531.292559	266.149918	514.266010	257.636643	V	*612.382772*	306.695024	595.356223	298.181750	5
6	659.351137	330.179207	642.324588	321.665932	Q	*513.314358*	257.160817	496.287809	248.647543	4
7	772.435201	386.721239	755.408652	378.207964	L	*385.255780*	193.131528	368.229231	184.618253	3
8	869.487965	435.247621	852.461416	426.734346	P	*272.171716*	136.589496	255.145167	128.076221	2
9					R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of ANVFVQLPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	1042.592361	0.003127	ANVFVQLPR
10.7	1042.592377	0.003111	KGVFGPPLGR
10.7	1042.592377	0.003111	KGVFGPPLGR
7.9	1042.588333	0.007155	APSLARTVGR
6.8	1042.602264	-0.006776	PSVTKVTPAK
5.3	1042.602249	-0.006761	ASPIKSTPVK
5.3	1042.588318	0.007170	TGILQEARR
5.0	1042.602264	-0.006776	ISALQSAGVVV
1.0	1042.602249	-0.006761	GKVGSLPLEK
0.8	1042.592346	0.003142	AAAALRFPVQ

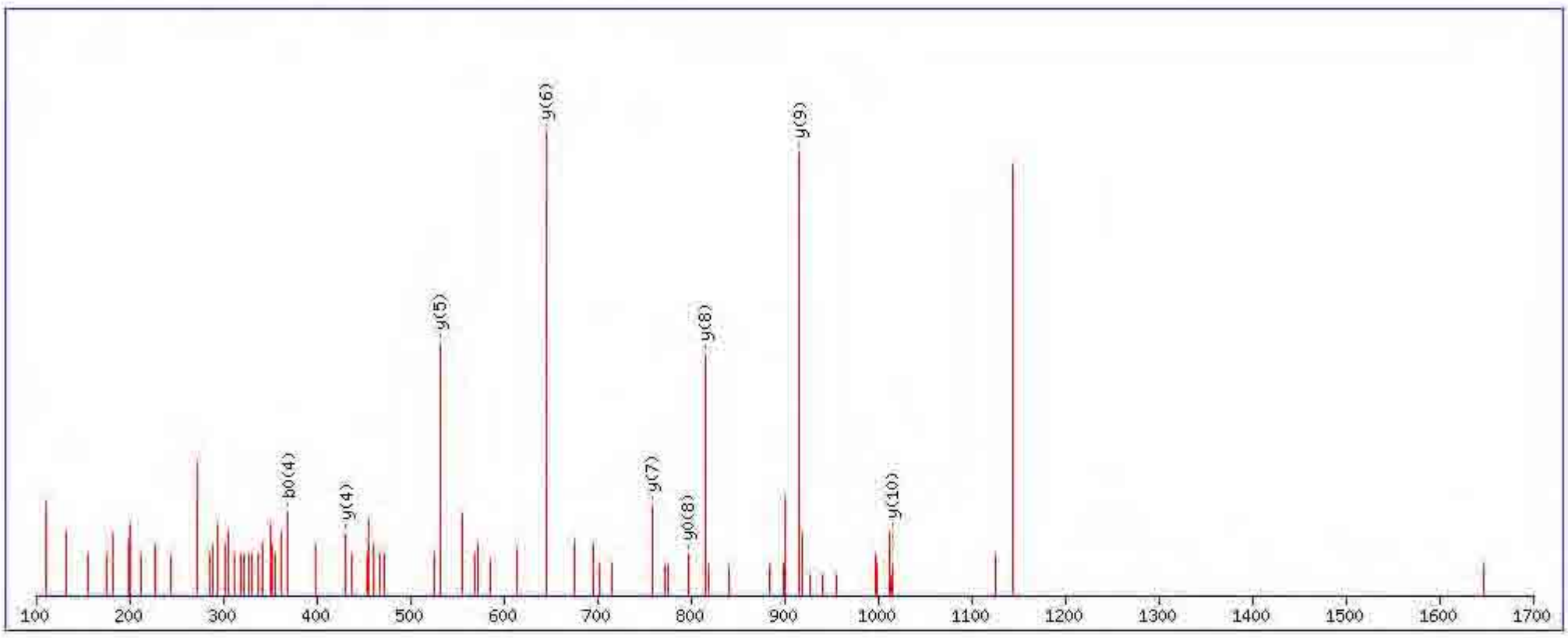
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVTGIITQGAR**
Found in **MFGM_HUMAN**, Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2

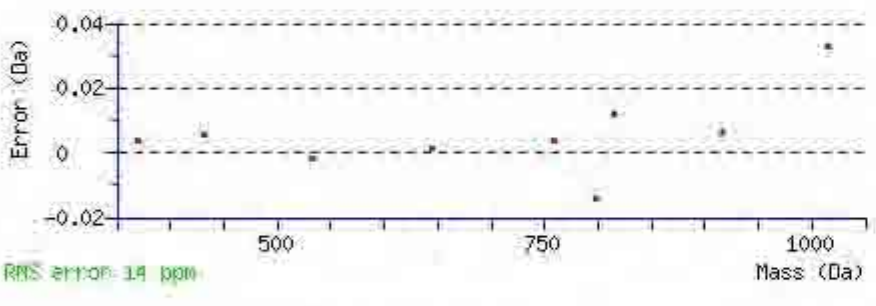
Match to Query 6204: 1143.635128 from(572.824840,2+) rtinseconds(1141) index(4050)
Title: Locus:1.1.1.1462.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

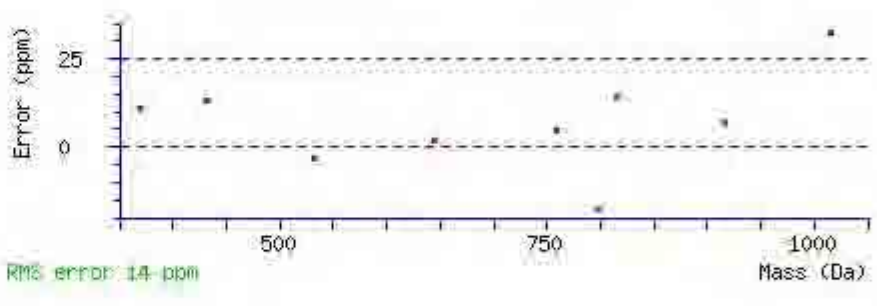
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1143.624786
Ions Score: 40 **Expect:** 0.0091
Matches : 9/98 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	229.118283	115.062780			211.107718	106.057497	V	*1015.589472*	508.298374	998.562923	499.785100	997.578907	499.293092	10
3	330.165962	165.586619			312.155397	156.581337	T	*916.521058*	458.764167	899.494509	450.250893	898.510493	449.758885	9
4	387.187426	194.097351			369.176861	185.092069	G	*815.473379*	408.240328	798.446830	399.727053	797.462814	399.235045	8
5	500.271490	250.639383			482.260925	241.634101	I	*758.451915*	379.729596	741.425366	371.216321	740.441350	370.724313	7
6	613.355554	307.181415			595.344989	298.176133	I	*645.367851*	323.187564	628.341302	314.674289	627.357286	314.182281	6
7	714.403233	357.705255			696.392668	348.699972	T	*532.283787*	266.645532	515.257238	258.132257	514.273222	257.640249	5
8	842.461811	421.734544	825.435262	413.221269	824.451246	412.729261	Q	*431.236108*	216.121692	414.209559	207.608418			4
9	899.483275	450.245276	882.456726	441.732001	881.472710	441.239993	G	303.177530	152.092403	286.150981	143.579129			3
10	970.520389	485.763833	953.493840	477.250558	952.509824	476.758550	A	246.156066	123.581671	229.129517	115.068397			2
11							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EVTGIITQGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.8	1143.624786	0.010342	EVTGIITQGAR
16.9	1143.644058	-0.008930	LSWLPLFPR
14.2	1143.625641	0.009487	LCLGIMGGKPR
10.7	1143.628815	0.006313	KPPSGFKGTIP
9.2	1143.643402	-0.008274	ATVPMLQRTK
9.0	1143.636002	-0.000874	SVPSILRSNR
8.6	1143.628815	0.006313	KPPSGFKGTIP
7.8	1143.628799	0.006329	FRDLLLPPSS
7.7	1143.638672	-0.003544	SAVELLISLAE
7.2	1143.624756	0.010372	GSNQLIEAKGK

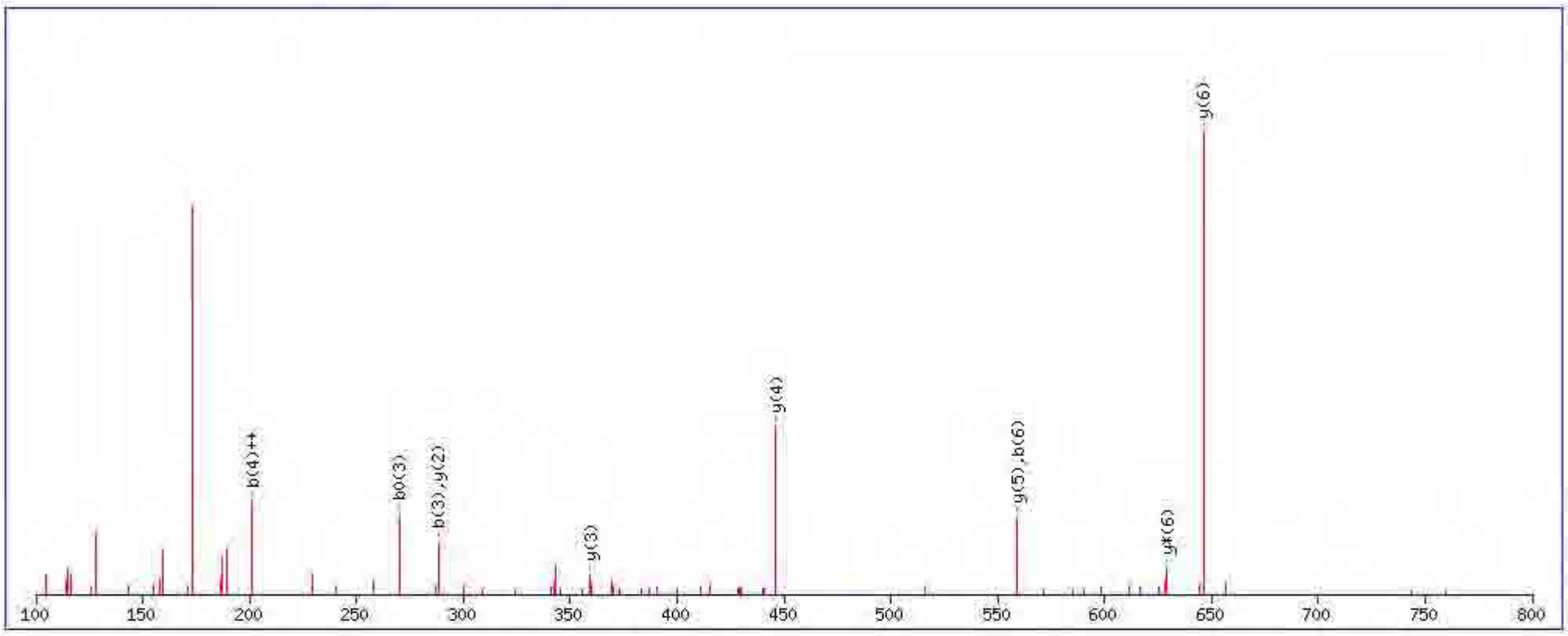
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSLSAIR**
Found in **LRC48_HUMAN**, Leucine-rich repeat-containing protein 48 OS=Homo sapiens GN=LRRC48 PE=2 SV=2

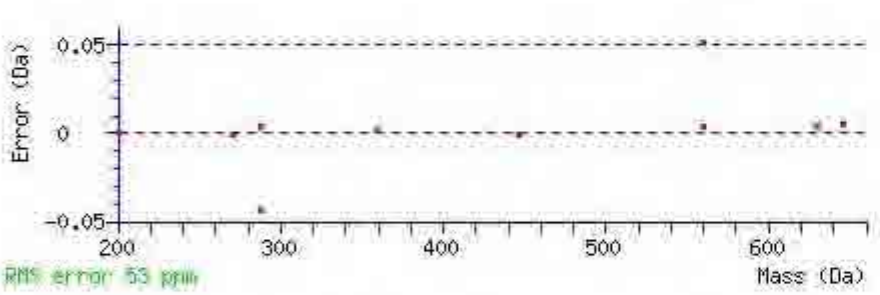
Match to Query 1299: 845.500968 from(423.757760,2+) rtinseconds(1170) index(4290)
Title: Locus:1.1.1.1479.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

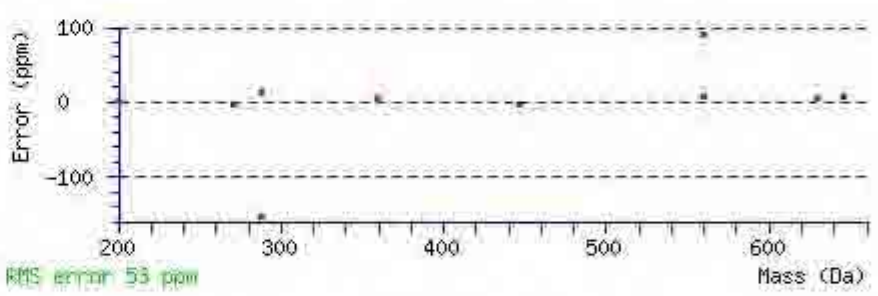
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 845.497040
Ions Score: 37 **Expect:** 0.011
Matches : 11/62 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							8
2	**201.123368**	101.065322	183.112803	92.060039	S	733.420278	367.213777	716.393729	358.700502	715.409713	358.208494	7
3	**288.155396**	144.581336	270.144831	135.576053	S	***646.388250***	323.697763	629.361701	315.184488	628.377685	314.692480	6
4	401.239460	201.123368	383.228895	192.118085	L	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	5
5	488.271488	244.639382	470.260923	235.634099	S	***446.272158***	223.639717	429.245609	215.126442	428.261593	214.634434	4
6	**559.308602**	280.157939	541.298037	271.152656	A	***359.240130***	180.123703	342.213581	171.610428			3
7	672.392666	336.699971	654.382101	327.694688	I	***288.203016***	144.605146	271.176467	136.091871			2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSLSAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	845.497040	0.003928	LSSLSAIR
26.6	845.497040	0.003928	SLSLLASR
23.9	845.497055	0.003913	TVSSLAIR
20.4	845.497040	0.003928	SLSALLSR
18.5	845.497055	0.003913	SLTISGLR
16.3	845.497070	0.003898	TVGSTLIR
15.3	845.497055	0.003913	VTSALLSR
14.8	845.497040	0.003928	SSISLALR
13.8	845.497055	0.003913	LSTVASIR
13.1	845.497055	0.003913	SLGTIISR

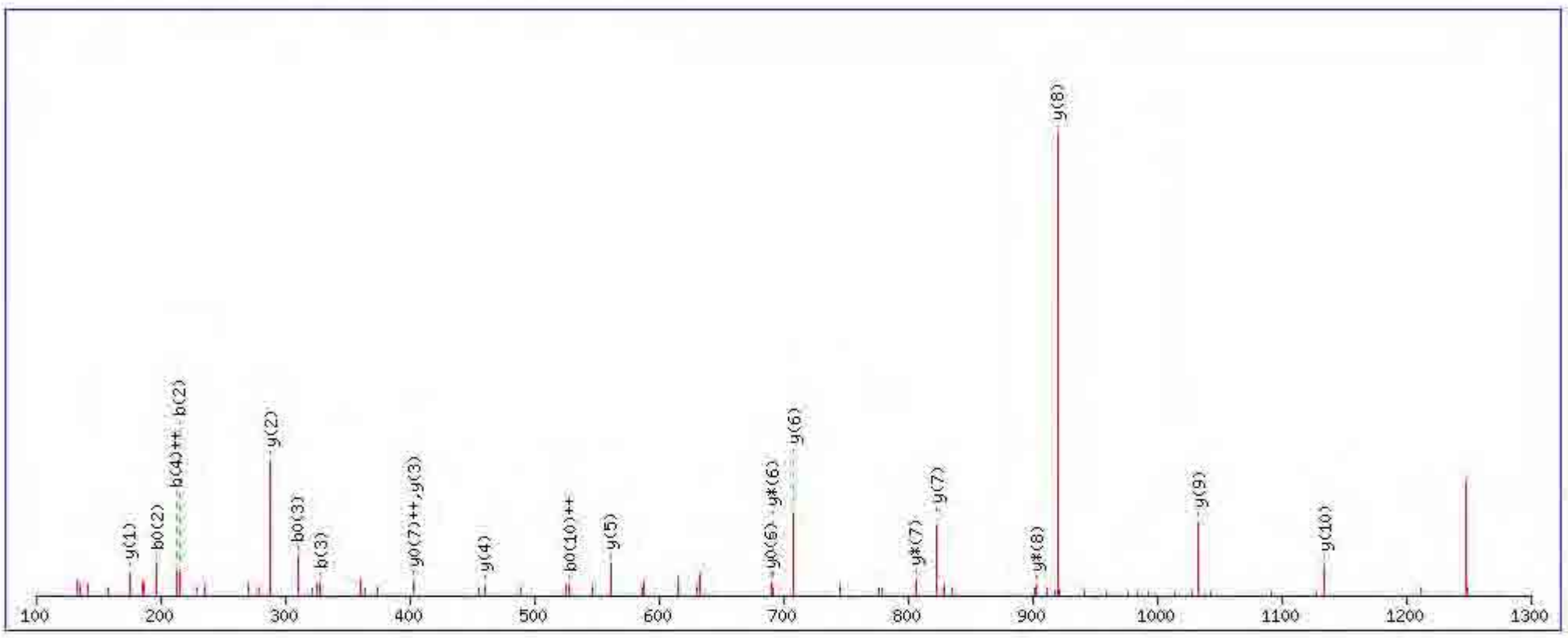
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLPDFTGDLR**
Found in **LBP_HUMAN**, Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3

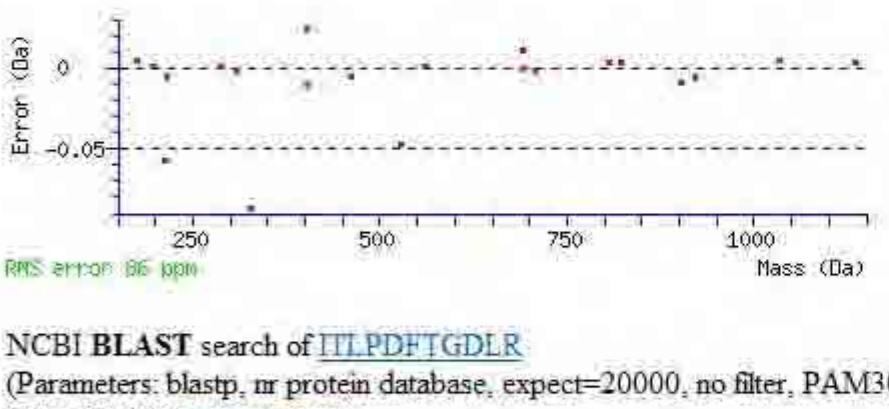
Match to Query 8688: 1246.663208 from(624.338880,2+) rtinseconds(2099) index(14228)
Title: Locus:1.1.1.1994.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

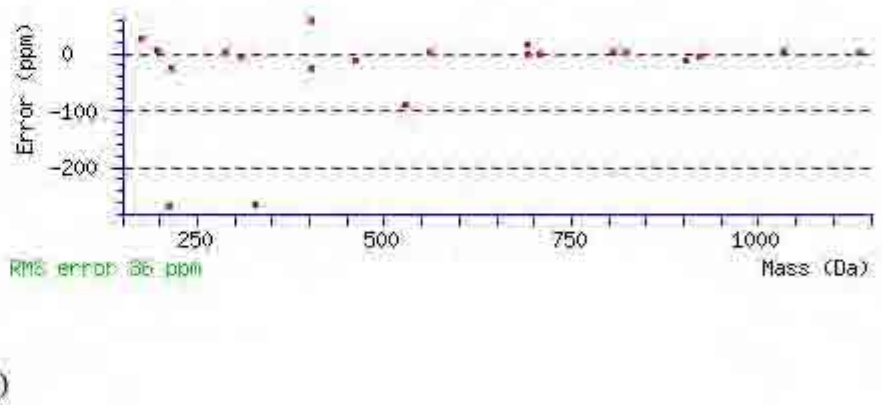
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1246.655762
Ions Score: 69 **Expect:** 1.7e-005
Matches : 21/94 fragment ions using 42 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	1134.578966	567.793121	1117.552417	559.279847	1116.568401	558.787839	10
3	328.223083	164.615179	310.212518	155.609897	L	1033.531287	517.269282	1016.504738	508.756007	1015.520722	508.263999	9
4	425.275847	213.141561	407.265282	204.136279	P	920.447223	460.727249	903.420674	452.213975	902.436658	451.721967	8
5	540.302790	270.655033	522.292225	261.649750	D	823.394459	412.200868	806.367910	403.687593	805.383894	403.195585	7
6	687.371204	344.189240	669.360639	335.183957	F	708.367516	354.687396	691.340967	346.174122	690.356951	345.682114	6
7	788.418883	394.713079	770.408318	385.707797	T	561.299102	281.153189	544.272553	272.639915	543.288537	272.147907	5
8	845.440347	423.223812	827.429782	414.218529	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	960.467290	480.737283	942.456725	471.732000	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1073.551354	537.279315	1055.540789	528.274032	L	288.203016	144.605146	271.176467	136.091871			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLPDFTGDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.9	1246.655762	0.007446	ITLPDFTGDLR
16.9	1246.655762	0.007446	PTPPGQPPISPK
14.3	1246.659103	0.004105	LTPEIMKEVR
14.1	1246.655746	0.007462	LTPLSDPALAPH
11.2	1246.659119	0.004089	PTDTAMLTLLR
10.1	1246.657074	0.006134	AAYRHHSPIPV
9.7	1246.670349	-0.007141	TLLTKLCGQDR
9.3	1246.665634	-0.002426	LTIKDLESIDT
9.2	1246.670334	-0.007126	IVDSILMERR
8.7	1246.671005	-0.007797	TIPPFERPFK

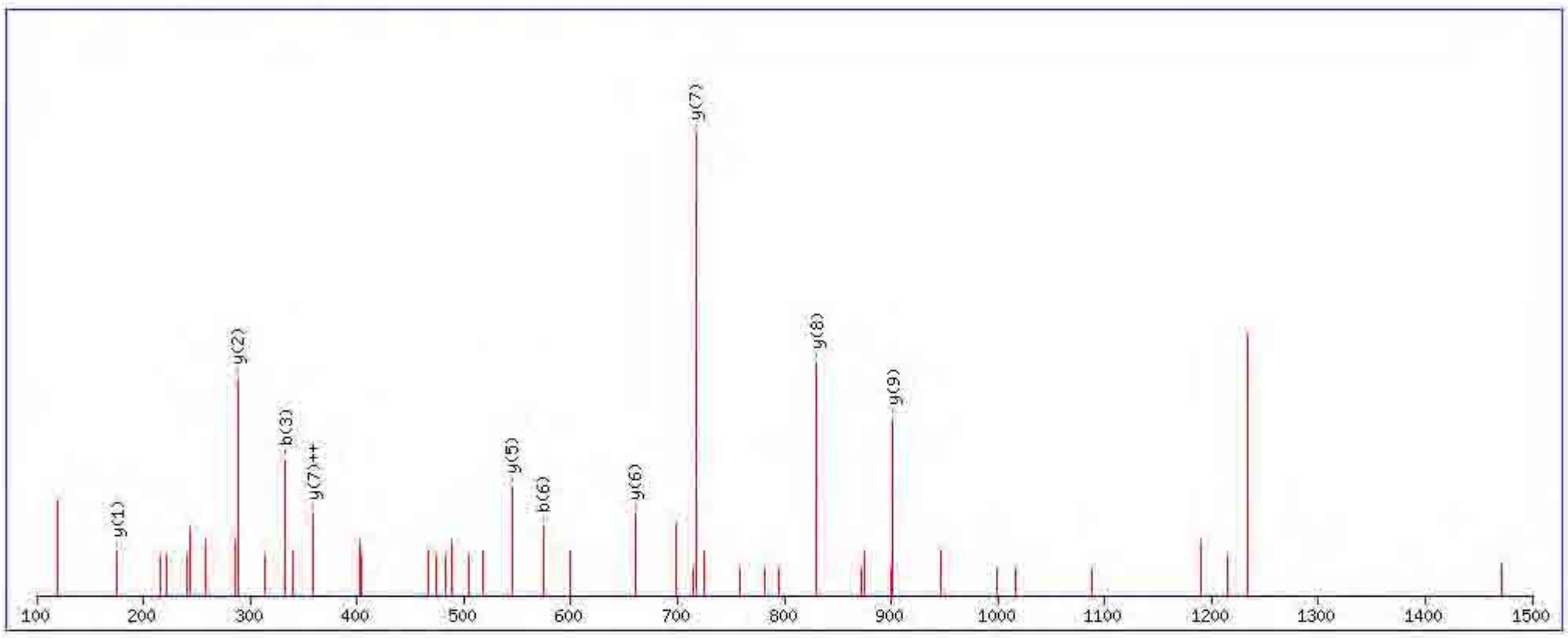
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFQALGDAADIR**
Found in **TIMP1_HUMAN**, Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1

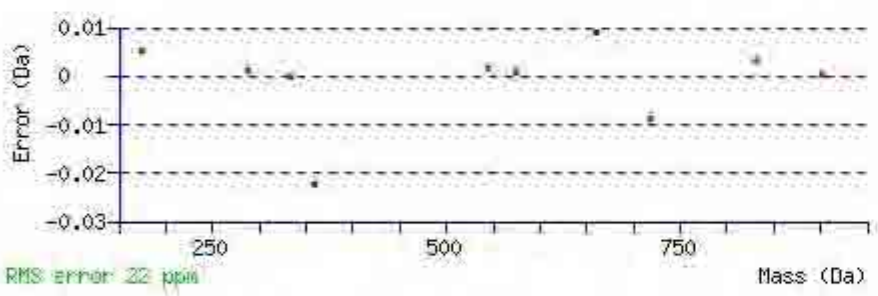
Match to Query 8415: 1232.619328 from(617.316940,2+) rtinseconds(1583) index(8351)
Title: Locus:1.1.1.1709.18
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

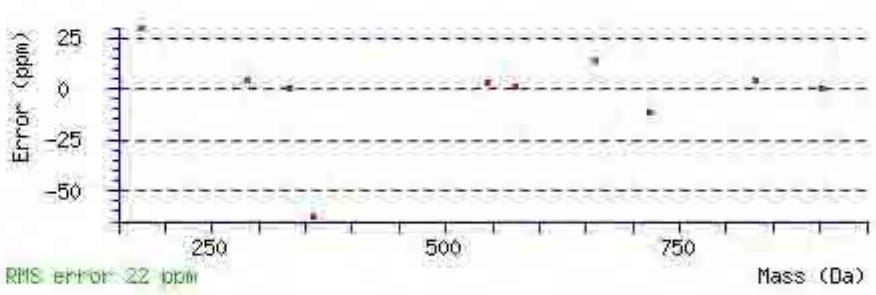
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1232.614944
Ions Score: 42 **Expect:** 0.0047
Matches : 10/112 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							12
2	205.097154	103.052215					F	1176.600764	588.804020	1159.574215	580.290746	1158.590199	579.798738	11
3	333.155732	167.081504	316.129183	158.568230			Q	1029.532350	515.269813	1012.505801	506.756538	1011.521785	506.264530	10
4	404.192846	202.600061	387.166297	194.086786			A	901.473772	451.240524	884.447223	442.727249	883.463207	442.235241	9
5	517.276910	259.142093	500.250361	250.628819			L	830.436658	415.721967	813.410109	407.208692	812.426093	406.716684	8
6	574.298374	287.652825	557.271825	279.139551			G	717.352594	359.179935	700.326045	350.666660	699.342029	350.174652	7
7	689.325317	345.166297	672.298768	336.653022	671.314752	336.161014	D	660.331130	330.669203	643.304581	322.155928	642.320565	321.663920	6
8	760.362431	380.684854	743.335882	372.171579	742.351866	371.679571	A	545.304187	273.155732	528.277638	264.642457	527.293622	264.150449	5
9	831.399545	416.203411	814.372996	407.690136	813.388980	407.198128	A	474.267073	237.637174	457.240524	229.123900	456.256508	228.631892	4
10	946.426488	473.716882	929.399939	465.203607	928.415923	464.711599	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
11	1059.510552	530.258914	1042.484003	521.745640	1041.499987	521.253631	I	288.203016	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GFQALGDAADIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1232.614944	0.004384	GFQALGDAADIR
16.7	1232.618973	0.000355	NIDGFLGPWAK
16.6	1232.618317	0.001011	CSEPVKGTGALR
12.4	1232.618286	0.001042	NMAALTEALQR
12.0	1232.618317	0.001011	GAGMLKTPSPSR
10.7	1232.629547	-0.010219	SRSICIGTQPR
10.5	1232.614944	0.004384	QGFPSSNDLLR
9.8	1232.630188	-0.010860	RSPNDFALWK
9.7	1232.618332	0.000996	CQLGDAGTVTLR
9.3	1232.628860	-0.009532	TLPLEFPAGEK

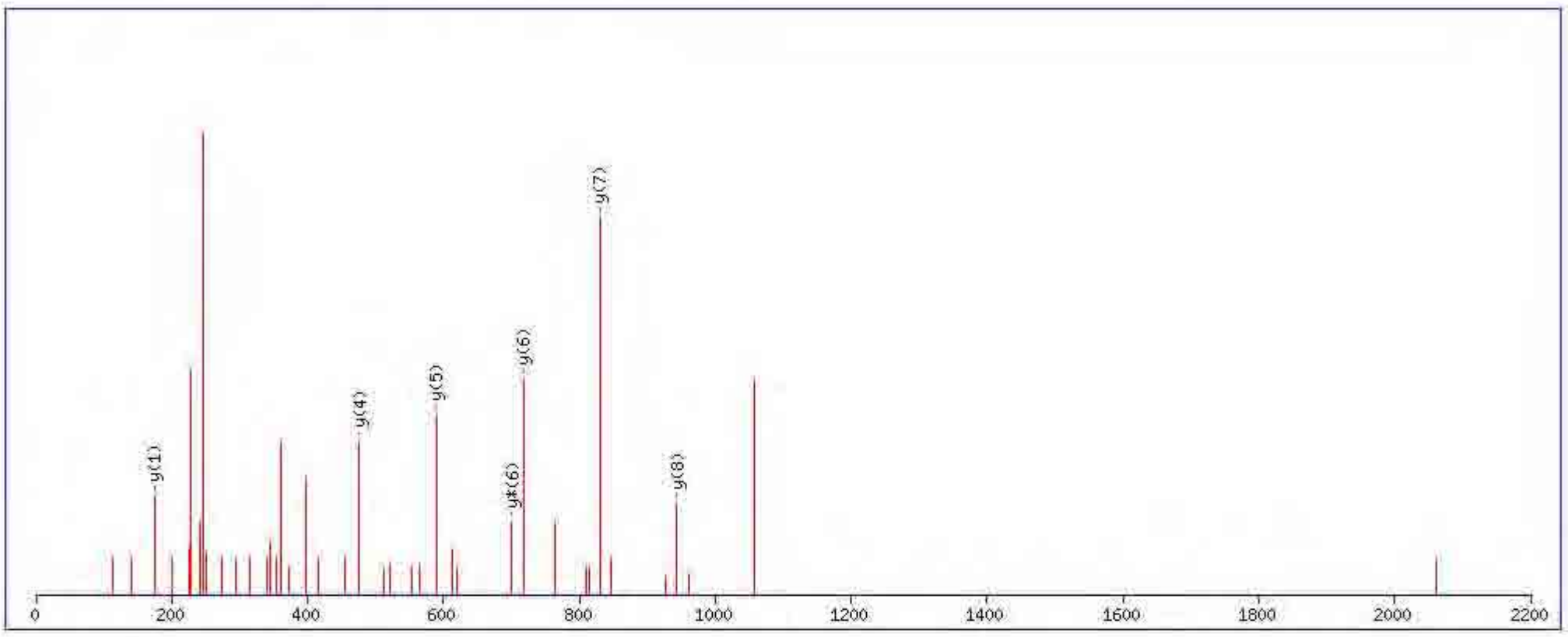
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPQLTSPR**
Found in **CAND1_HUMAN**, Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2

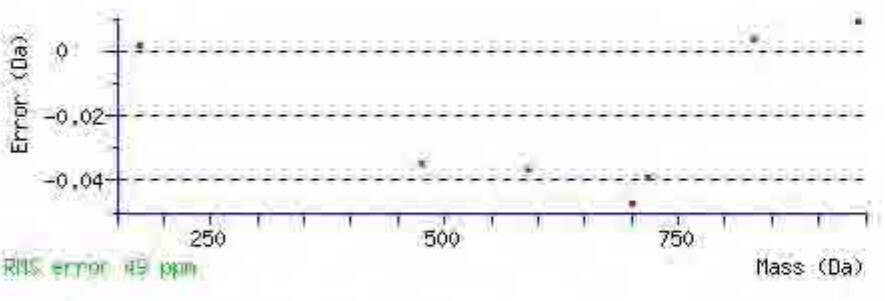
Match to Query 4509: 1055.605828 from(528.810190,2+) rtinseconds(1558) index(8062)
Title: Locus:1.1.1.1696.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

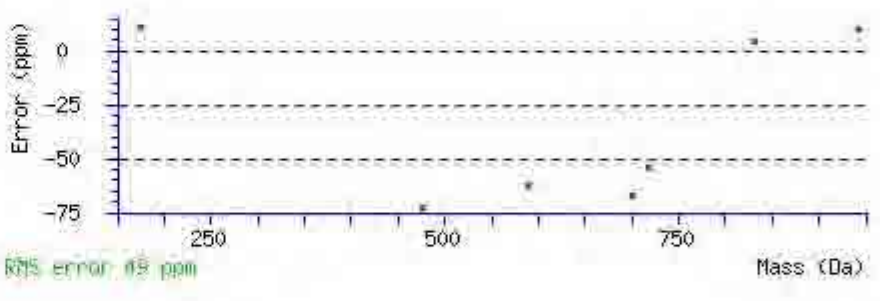
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597504
Variable modifications:
P3 : Oxidation (P)
P8 : Oxidation (P)
Ions Score: 52 **Expect:** 0.00081
Matches : 7/76 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*943.520723*	472.264000	926.494174	463.750725	925.510158	463.258717	8
3	340.223083	170.615179					P	*830.436659*	415.721968	813.410110	407.208693	812.426094	406.716685	7
4	468.281661	234.644468	451.255112	226.131194			Q	*717.388980*	359.198128	700.362431	350.684853	699.378415	350.192845	6
5	581.365725	291.186501	564.339176	282.673226			L	*589.330402*	295.168839	572.303853	286.655565	571.319837	286.163557	5
6	682.413404	341.710340	665.386855	333.197066	664.402839	332.705058	T	*476.246338*	238.626807	459.219789	230.113532	458.235773	229.621524	4
7	769.445432	385.226354	752.418883	376.713079	751.434867	376.221071	S	375.198659	188.102967	358.172110	179.589693	357.188094	179.097685	3
8	882.493111	441.750194	865.466562	433.236919	864.482546	432.744911	P	288.166631	144.586953	271.140082	136.073679			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLPQLTSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	1055.597504	0.008324	LLPQLTSPR
52.2	1055.597488	0.008340	PLIKVEEGR
36.2	1055.612762	-0.006934	LLIQPGPRF
35.9	1055.608704	-0.002876	ILLREAEGR
35.9	1055.612747	-0.006919	LLLPAATWR
35.9	1055.608704	-0.002876	LLLRAEGER
32.3	1055.597488	0.008340	LGPLALETAR
31.9	1055.597488	0.008340	LLKLDPADR
22.3	1055.612762	-0.006934	LLIQPGPRF
22.1	1055.604874	0.000954	ILLIKNMDP

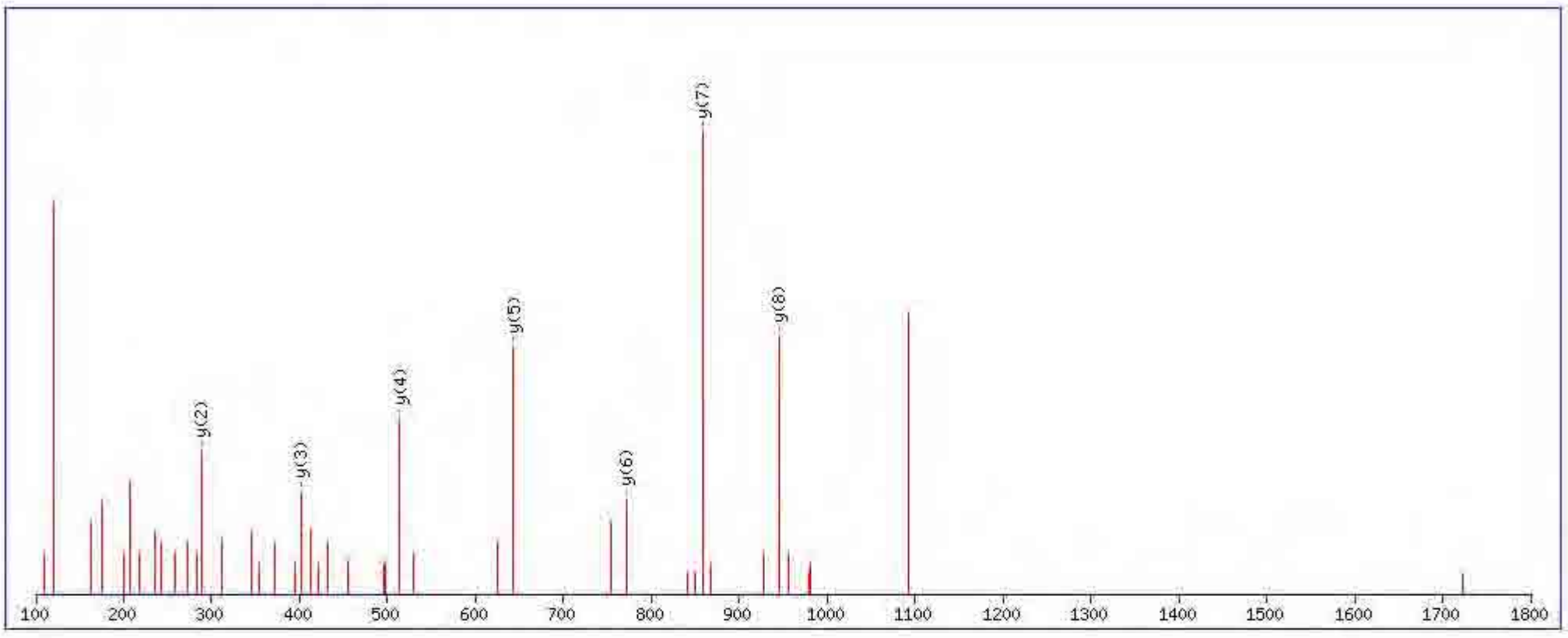
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSSQELILR**
Found in **TGM3_HUMAN**, Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4

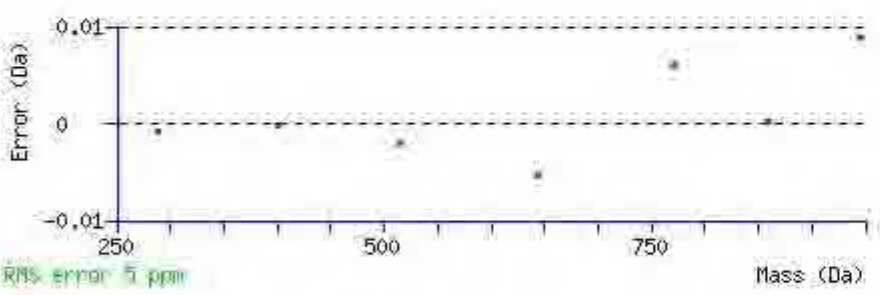
Match to Query 5186: 1091.603428 from(546.808990,2+) rtinseconds(1578) index(8306)
Title: Locus:1.1.1.1707.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

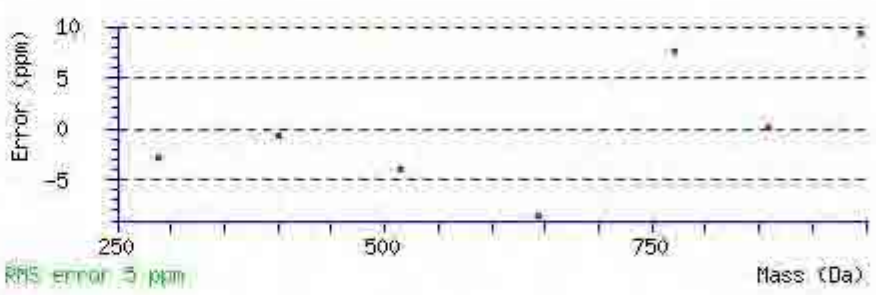
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1091.597488
Ions Score: 66 **Expect:** 2.9e-005
Matches : 7/80 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							9
2	235.107718	118.057497			217.097153	109.052214	S	*945.536371*	473.271824	928.509822	464.758549	927.525806	464.266541	8
3	322.139746	161.573511			304.129181	152.568229	S	*858.504343*	429.755810	841.477794	421.242535	840.493778	420.750527	7
4	450.198324	225.602800	433.171775	217.089526	432.187759	216.597518	Q	*771.472315*	386.239796	754.445766	377.726521	753.461750	377.234513	6
5	579.240917	290.124097	562.214368	281.610822	561.230352	281.118814	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	L	*514.371144*	257.689210	497.344595	249.175936			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	*401.287080*	201.147178	384.260531	192.633904			3
8	918.493109	459.750193	901.466560	451.236918	900.482544	450.744910	L	*288.203016*	144.605146	271.176467	136.091872			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of FSSQELILR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.8	1091.597488	0.005940	FSSQELILR
20.4	1091.597473	0.005955	YSAKPEILR
20.0	1091.608734	-0.005306	FSQSVQKIR
19.4	1091.597488	0.005940	FSLASADLLR
19.4	1091.608719	-0.005291	FSQKSNLIR
19.0	1091.612091	-0.008663	SMTSRILLR
18.0	1091.608734	-0.005306	PQLQPQLPR
16.5	1091.597504	0.005924	FSTLDIQLR
10.3	1091.608734	-0.005306	HLLTVQEPR
10.1	1091.612762	-0.009334	FSPRPLKFT

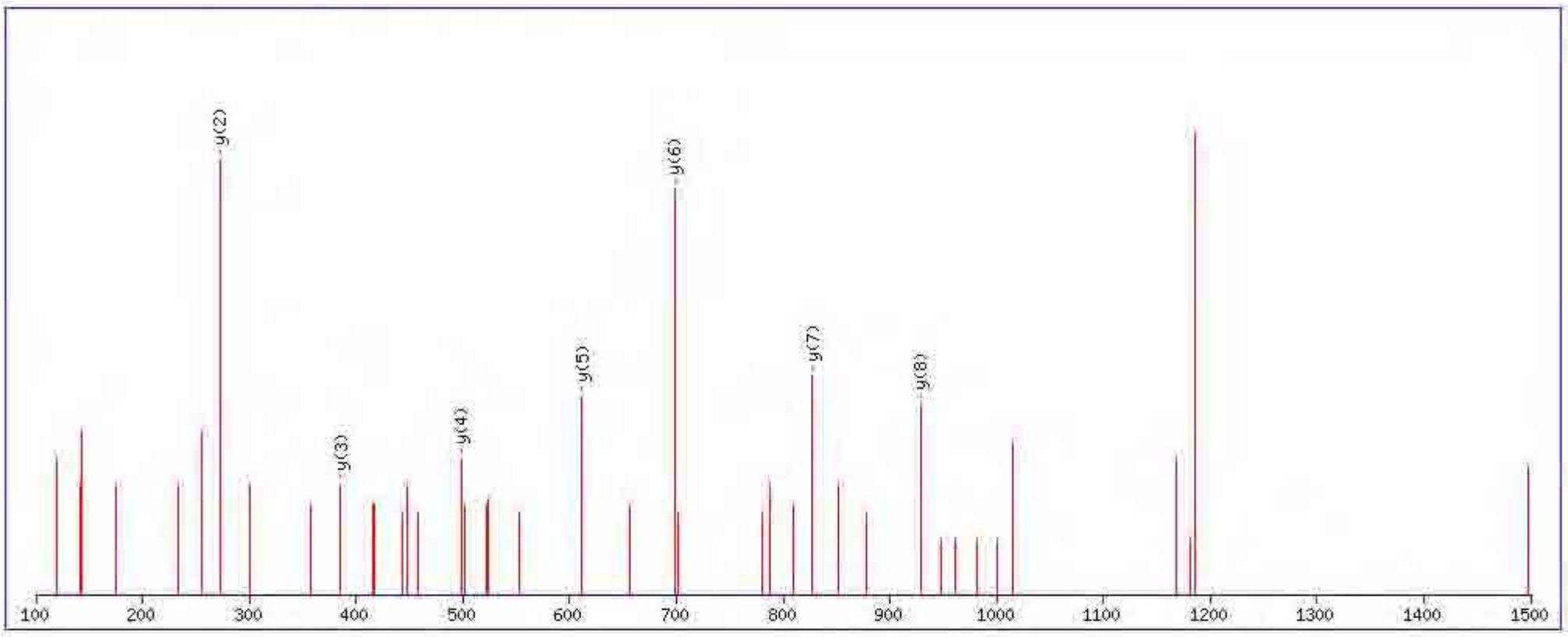
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

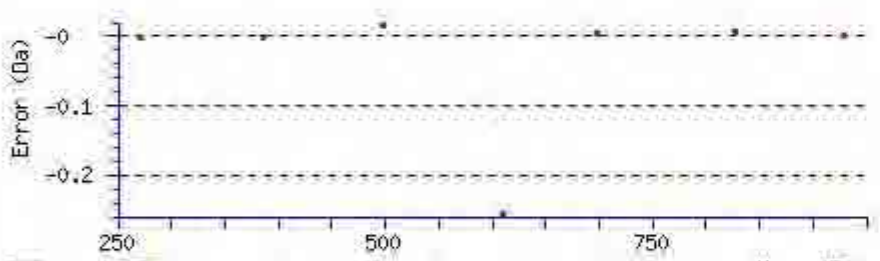
Match to Query 7361: 1184.674168 from(593.344360,2+) rtinseconds(1732) index(9934)
Title: Locus:1.1.1.1791.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

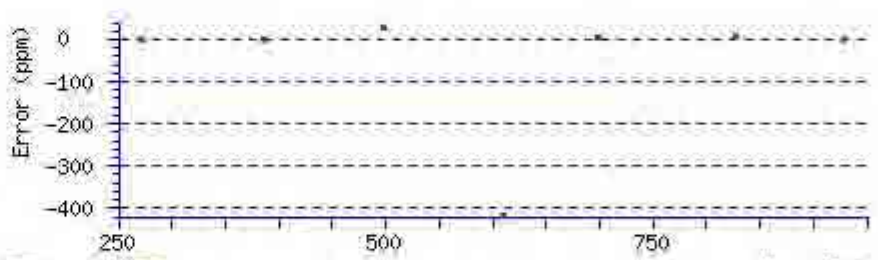
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 64 **Expect:** 4.6e-005
Matches : 7/86 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	1015.578236	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	*928.546208*	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	*827.498529*	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	*698.455936*	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	*611.423908*	306.215592	594.397359	297.702318			5
8	801.435260	401.221268	783.424695	392.215986	L	*498.339844*	249.673560	481.313295	241.160285			4
9	914.519324	457.763300	896.508759	448.758018	I	*385.255780*	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	*272.171716*	136.589496	255.145167	128.076221			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.6	1184.676468	-0.002300	GLSTESILIPR
19.0	1184.677795	-0.003627	PRHPEALLPR
18.2	1184.665237	0.008931	SSPIIIQLLSD
18.1	1184.676468	-0.002300	KEDLTTLLPR
11.4	1184.662552	0.011616	RGQTSASILPR
7.8	1184.676483	-0.002315	GPYVEISLISR
7.8	1184.676453	-0.002285	PAISELSSLLR
7.8	1184.676483	-0.002315	TPLLGLSPLSR
7.7	1184.680481	-0.006313	AAELSIKFLPP
7.5	1184.676468	-0.002300	APSILSVLKQN

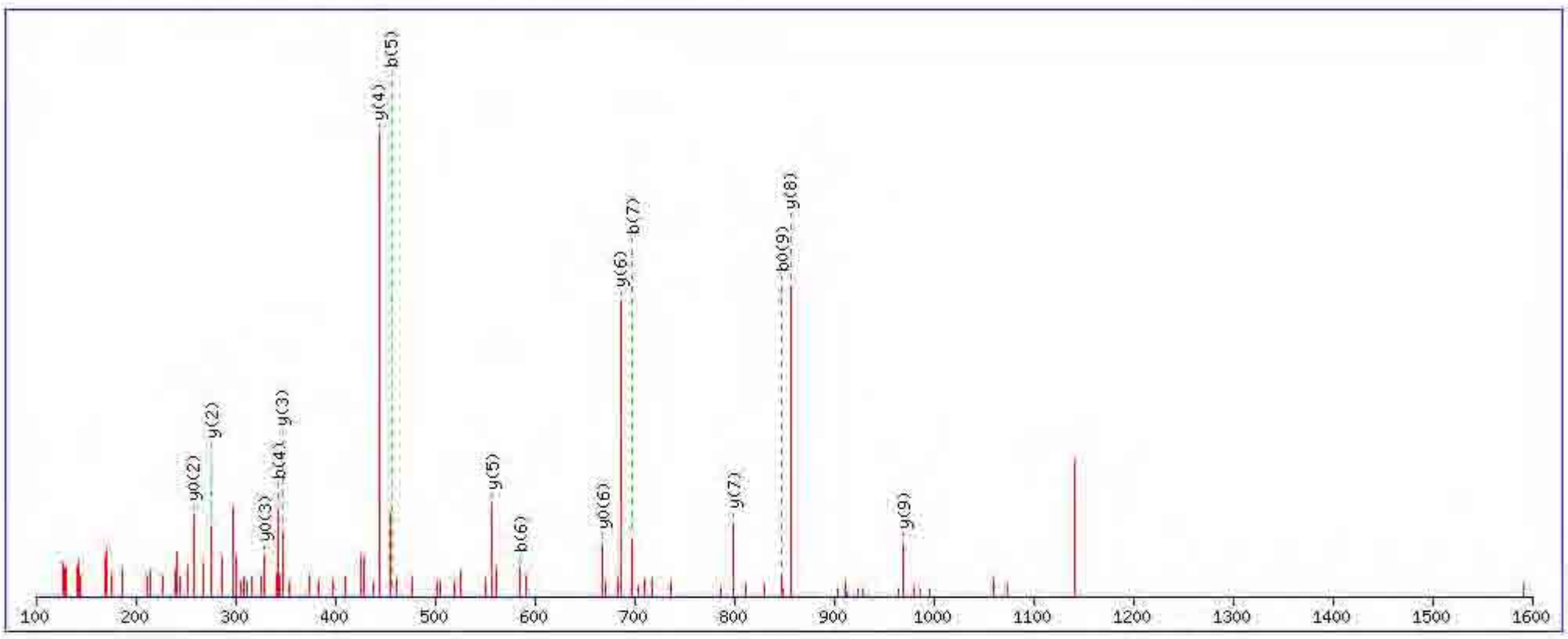
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDLGIEIPAEK**
Found in **KPYM_HUMAN**, Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4

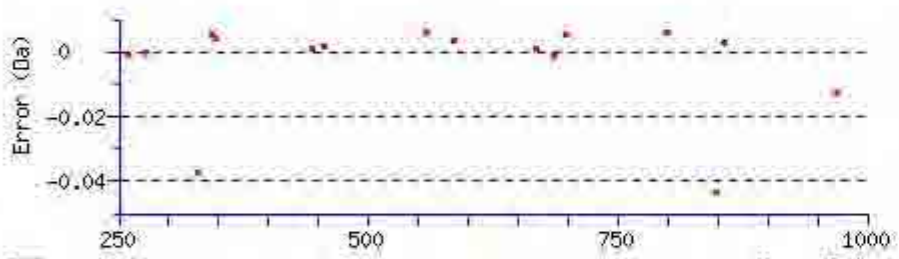
Match to Query 6155: 1140.607928 from(571.311240,2+) rtinseconds(1581) index(8327)
Title: Locus:1.1.1.1708.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

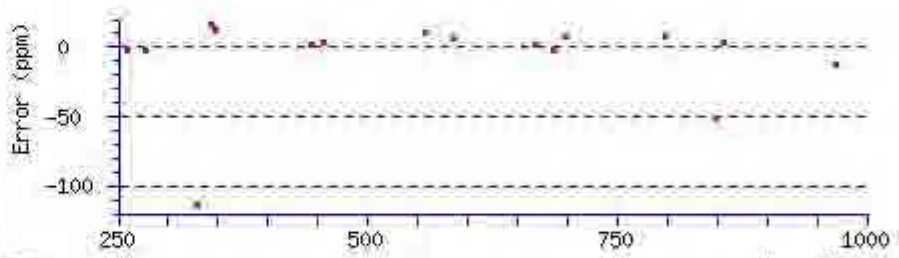
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1140.602631
Ions Score: 58 **Expect:** 0.00027
Matches : 16/96 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			G							11
2	173.055683	87.031479	155.045118	78.026197	D	1084.588467	542.797872	1067.561918	534.284597	1066.577902	533.792589	10
3	286.139747	143.573512	268.129182	134.568229	L	*969.561524*	485.284400	952.534975	476.771126	951.550959	476.279118	9
4	343.161211	172.084243	325.150646	163.078961	G	*856.477460*	428.742368	839.450911	420.229094	838.466895	419.737086	8
5	456.245275	228.626275	438.234710	219.620993	I	*799.455996*	400.231636	782.429447	391.718362	781.445431	391.226354	7
6	585.287868	293.147572	567.277303	284.142290	E	*686.371932*	343.689604	669.345383	335.176330	668.361367	334.684322	6
7	698.371932	349.689604	680.361367	340.684322	I	*557.329339*	279.168308	540.302790	270.655033	539.318774	270.163025	5
8	795.424696	398.215986	777.414131	389.210704	P	*444.245275*	222.626275	427.218726	214.113001	426.234710	213.620993	4
9	866.461810	433.734543	848.451245	424.729261	A	*347.192511*	174.099893	330.165962	165.586619	329.181946	165.094611	3
10	995.504403	498.255840	977.493838	489.250557	E	*276.155397*	138.581336	259.128848	130.068062	258.144832	129.576054	2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GDLGIEIPAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	1140.602631	0.005297	GDLGIEIPAEK
23.4	1140.603973	0.003955	RTWLEPAPR
13.2	1140.602600	0.005328	AAAELPLEAEK
12.5	1140.603973	0.003955	RTWLEPAPR
12.4	1140.613907	-0.005979	GPVSVELVGPR
11.9	1140.599945	0.007983	DPSRPKNATR
10.8	1140.613876	-0.005948	NDLLLEVGPR
10.6	1140.607346	0.000582	ALRPMPTAPR
10.0	1140.602631	0.005297	LQLTELQEPA
8.9	1140.602646	0.005282	TLKPTPEKDP

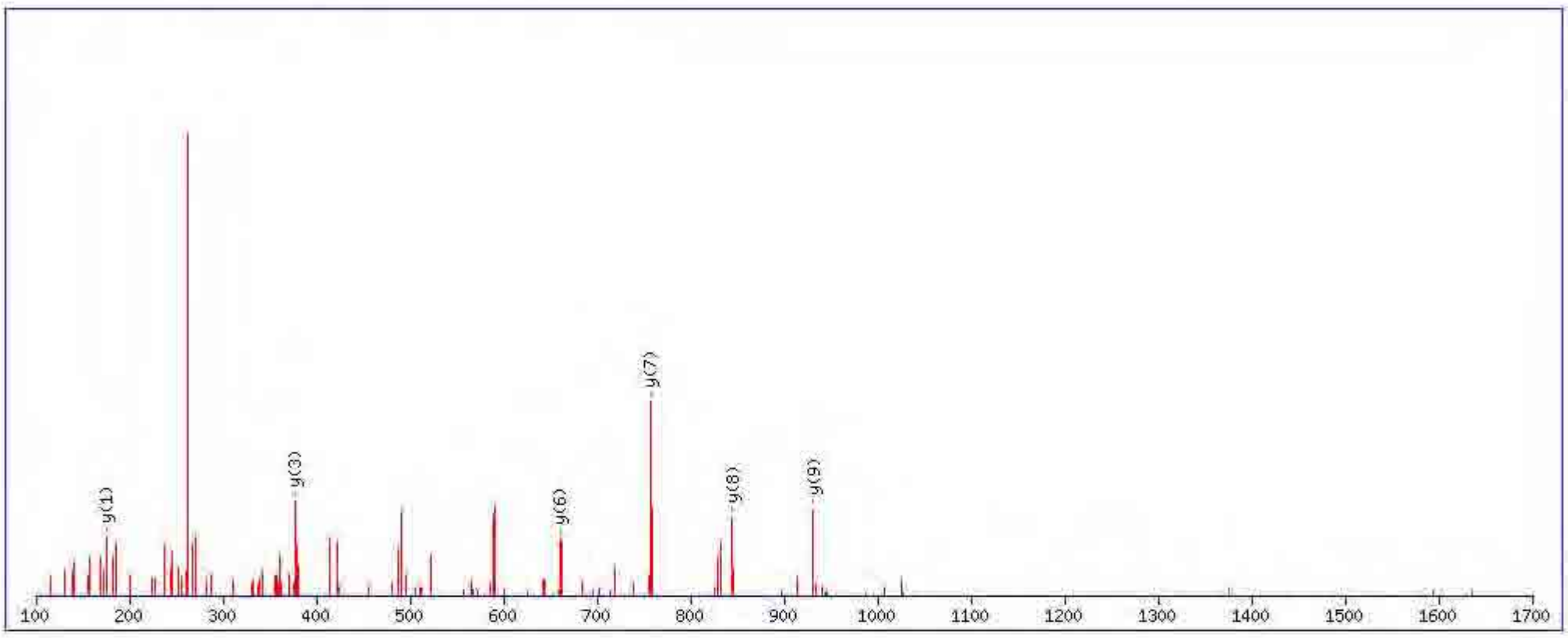
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSPVPAVCR**
Found in **RNH2A_HUMAN**, Ribonuclease H2 subunit A OS=Homo sapiens GN=RNASEH2A PE=1 SV=2

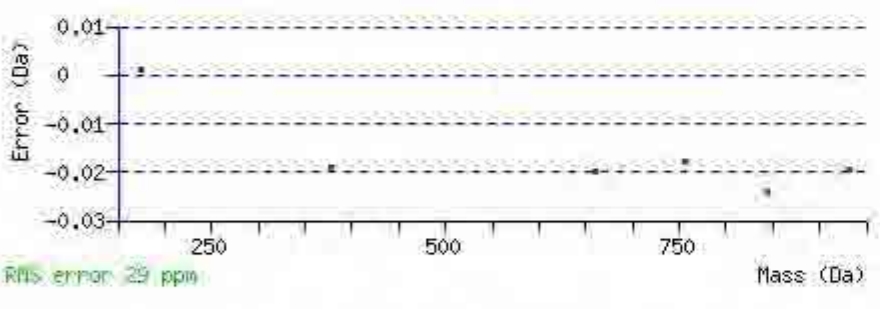
Match to Query 4299: 1043.533628 from(522.774090,2+) rtinseconds(910) index(2322)
Title: Locus:1.1.1.1329.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

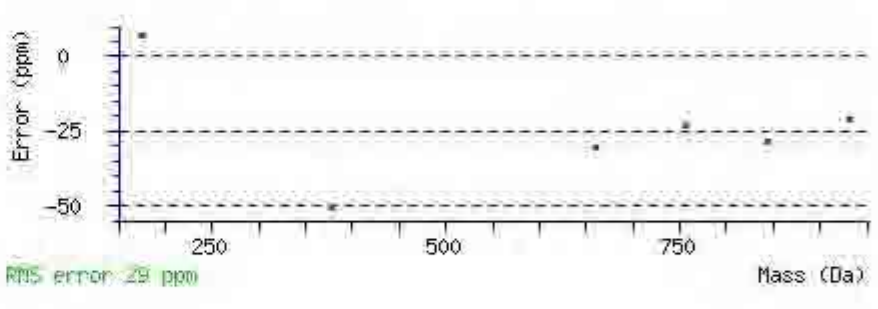
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1043.543365
Variable modifications:
P6 : Oxidation (P)
Ions Score: 46 **Expect:** 0.0067
Matches : 6/74 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	201.123368	101.065322	183.112803	92.060039	S	*931.466578*	466.236927	914.440029	457.723652	913.456013	457.231644	9
3	288.155396	144.581336	270.144831	135.576053	S	*844.434550*	422.720913	827.408001	414.207638	826.423985	413.715630	8
4	385.208160	193.107718	367.197595	184.102435	P	*757.402522*	379.204899	740.375973	370.691624			7
5	484.276574	242.641925	466.266009	233.636642	V	*660.349758*	330.678517	643.323209	322.165242			6
6	597.324253	299.165765	579.313688	290.160482	P	561.281344	281.144310	544.254795	272.631036			5
7	668.361367	334.684322	650.350802	325.679039	A	448.233665	224.620470	431.207116	216.107196			4
8	767.429781	384.218528	749.419216	375.213246	V	*377.196551*	189.101913	360.170002	180.588639			3
9	870.438966	435.723121	852.428401	426.717838	C	278.128137	139.567706	261.101588	131.054432			2
10					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSPVPAVCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	1043.543365	-0.009737	LSSPVPAVCR
32.5	1043.524734	0.008894	PKPLSPDSR
32.5	1043.524734	0.008894	PQPLSLDSR
30.7	1043.543365	-0.009737	LSSPVPAVCR
21.2	1043.535934	-0.002306	ESALREPSR
20.5	1043.524734	0.008894	DPPKTDLSR
19.9	1043.524734	0.008894	SSSTLPAPPR
19.5	1043.535965	-0.002337	PPRLATDSR
19.5	1043.524750	0.008878	QDVVLPDSR
19.5	1043.524734	0.008894	DPPKTDLSR

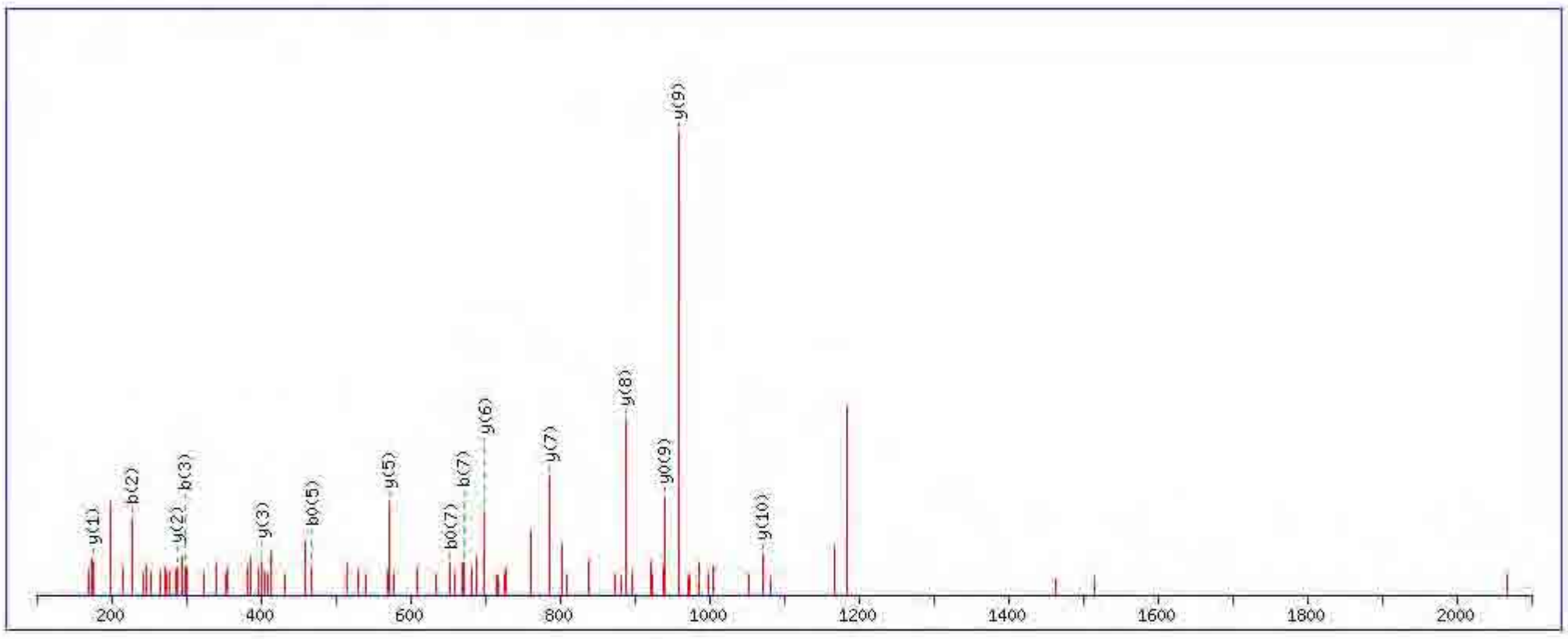
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIATSQGLLIR**
Found in **SEM3C_HUMAN**, Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=1 SV=2

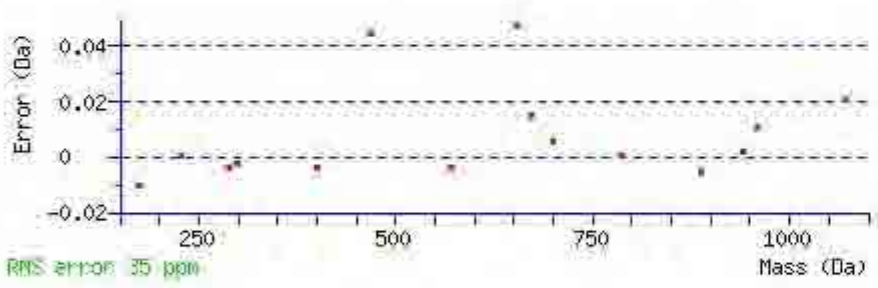
Match to Query 7312: 1183.732548 from(592.873550,2+) rtinseconds(1592) index(8444)
Title: Locus:1.1.1.1714.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

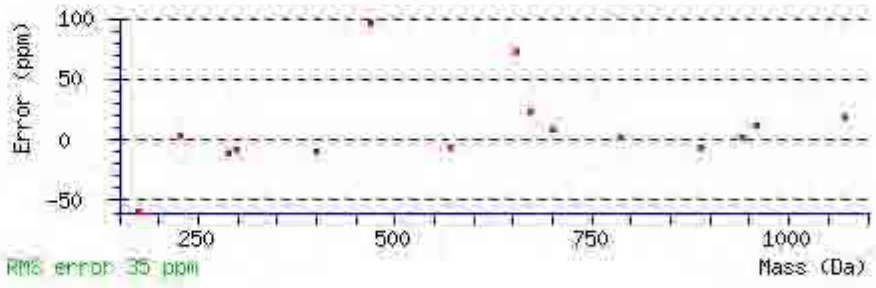
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1183.728836
Ions Score: 48 **Expect:** 0.00021
Matches : 15/92 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							11
2	227.175404	114.091340					I	*1071.652071*	536.329674	1054.625522	527.816399	1053.641506	527.324391	10
3	298.212518	149.609897					A	*958.568007*	479.787642	941.541458	471.274367	940.557442	470.782359	9
4	399.260197	200.133737			381.249632	191.128454	T	*887.530893*	444.269085	870.504344	435.755810	869.520328	435.263802	8
5	486.292225	243.649750			468.281660	234.644468	S	*786.483214*	393.745245	769.456665	385.231971	768.472649	384.739963	7
6	614.350803	307.679040	597.324254	299.165765	596.340238	298.673757	Q	*699.451186*	350.229231	682.424637	341.715957			6
7	*671.372267*	336.189772	654.345718	327.676497	653.361702	327.184489	G	*571.392608*	286.199942	554.366059	277.686668			5
8	784.456331	392.731804	767.429782	384.218529	766.445766	383.726521	L	514.371144	257.689210	497.344595	249.175936			4
9	897.540395	449.273836	880.513846	440.760561	879.529830	440.268553	L	*401.287080*	201.147178	384.260531	192.633903			3
10	1010.624459	505.815868	993.597910	497.302593	992.613894	496.810585	I	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IIATSQGLLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.1	1183.728836	0.003712	IIATSQGLLIR
8.3	1183.736221	-0.003673	LLMPAILLLR
7.4	1183.732864	-0.000316	LLPSPLFLIR
6.9	1183.728821	0.003727	LLASKLSLSPR
6.6	1183.740082	-0.007534	VVVLRASATLR
6.5	1183.732864	-0.000316	LLPSPLFLIR
6.5	1183.728836	0.003712	LPTIQKSLLR
6.3	1183.722305	0.010243	LLCVRALQLR
6.2	1183.728851	0.003697	LIRLTPTQVK
6.2	1183.728851	0.003697	LLRLTPTQVK

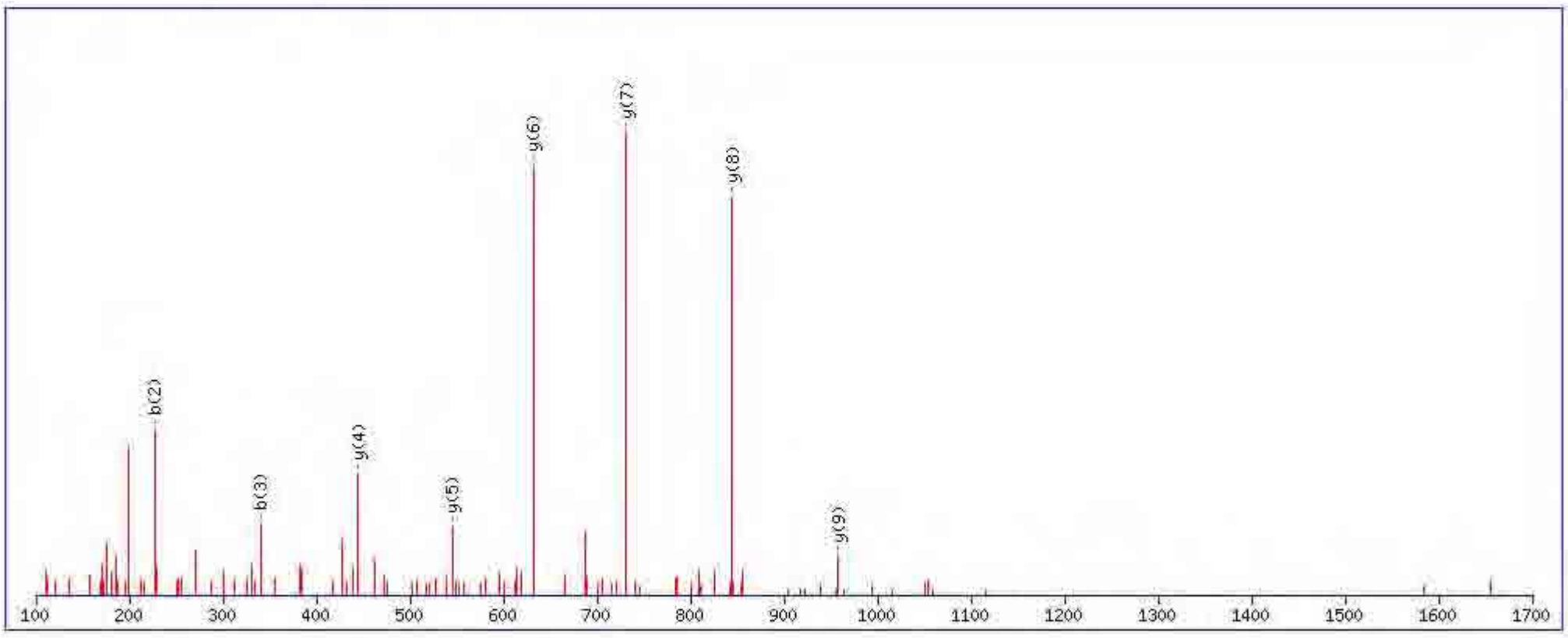
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

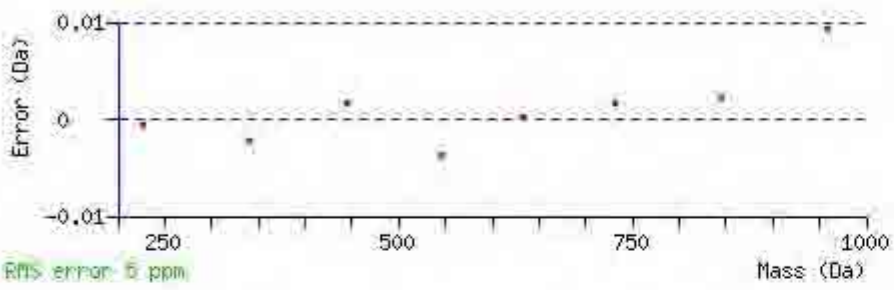
Match to Query 4776: 1069.649408 from(535.831980,2+) rtinseconds(1396) index(6383)
Title: Locus:1.1.1.1606.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

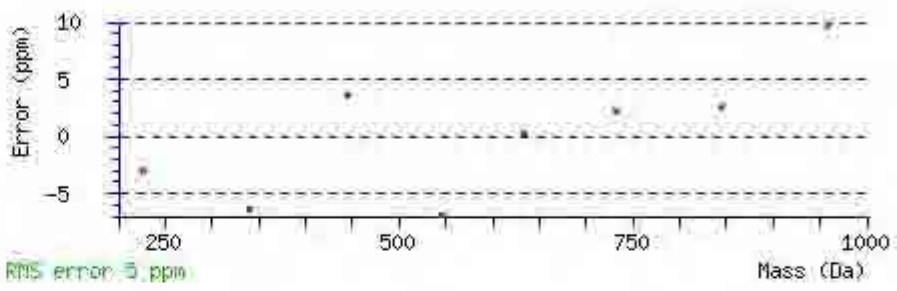
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 58 **Expect:** 5.7e-005
Matches : 8/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	844.488694	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	731.404630	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	632.336216	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	444.256509	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	1069.649536	-0.000128	LLIVSTPTAR
28.0	1069.649521	-0.000113	PLLSVKELR
26.4	1069.649506	-0.000098	LLLDALREK
23.8	1069.653564	-0.004156	LLLWVSVVAA
23.0	1069.639633	0.009775	LLWPTRLR
17.0	1069.649521	-0.000113	LLIIRSAPAT
16.1	1069.649521	-0.000113	IIIQLLSDR
16.1	1069.649536	-0.000128	LILLDQTVR
16.1	1069.649506	-0.000098	LILLSENLR
16.1	1069.649521	-0.000113	LLLAAVSLDR

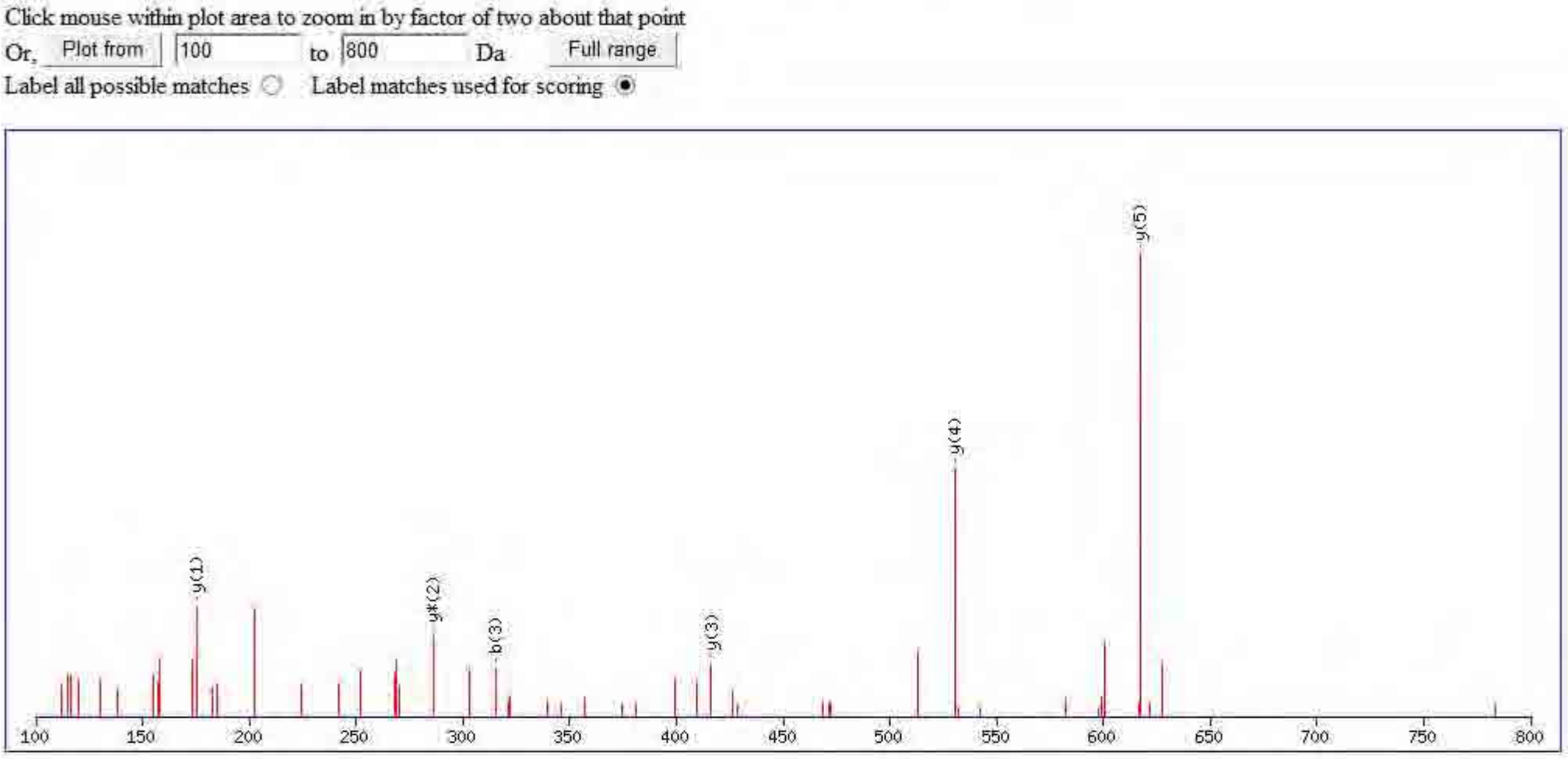
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISNIQR**
Found in **RIC1_HUMAN**, Protein RIC1 homolog OS=Homo sapiens GN=KIAA1432 PE=1 SV=2

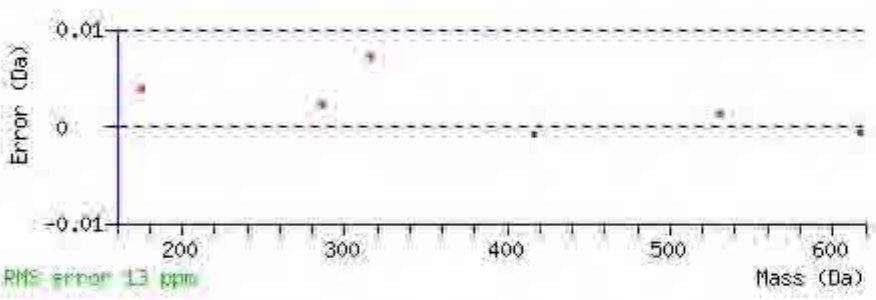
Match to Query 168: 729.412688 from(365.713620,2+) rtinseconds(395) index(287)
Title: Locus:1.1.1.1040.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

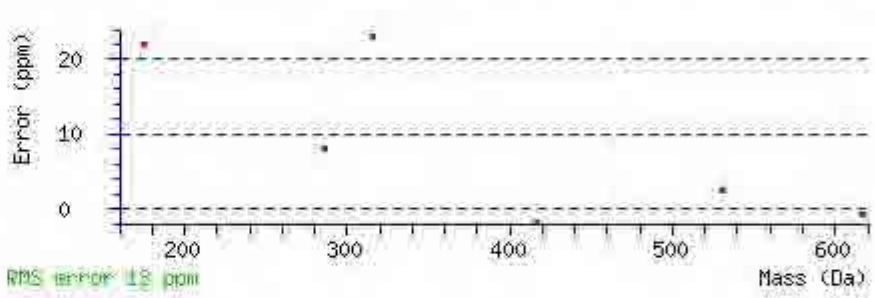
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 729.413315
Ions Score: 41 **Expect:** 0.015
Matches : 6/46 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							6
2	201.123368	101.065322			183.112803	92.060039	S	*617.336549*	309.171913	600.310000	300.658638	599.325984	300.166630	5
3	**315.166295**	158.086785	298.139746	149.573511	297.155730	149.081503	N	*530.304521*	265.655899	513.277972	257.142624			4
4	428.250359	214.628818	411.223810	206.115543	410.239794	205.623535	I	*416.261594*	208.634435	399.235045	200.121160			3
5	556.308937	278.658107	539.282388	270.144832	538.298372	269.652824	Q	303.177530	152.092403	286.150981	143.579128			2
6							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ISNIQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	729.413315	-0.000627	ISNIQR
40.9	729.413315	-0.000627	LSNIQR
40.9	729.413315	-0.000627	LSNLQR
40.9	729.413315	-0.000627	PSNIKR
40.9	729.413315	-0.000627	PSNLKR
35.6	729.413315	-0.000627	ISNQIR
35.6	729.413315	-0.000627	LSNAGLR
35.6	729.413315	-0.000627	LSNGLAR
35.6	729.413315	-0.000627	LSNQLR
23.6	729.413315	-0.000627	PSNLRK

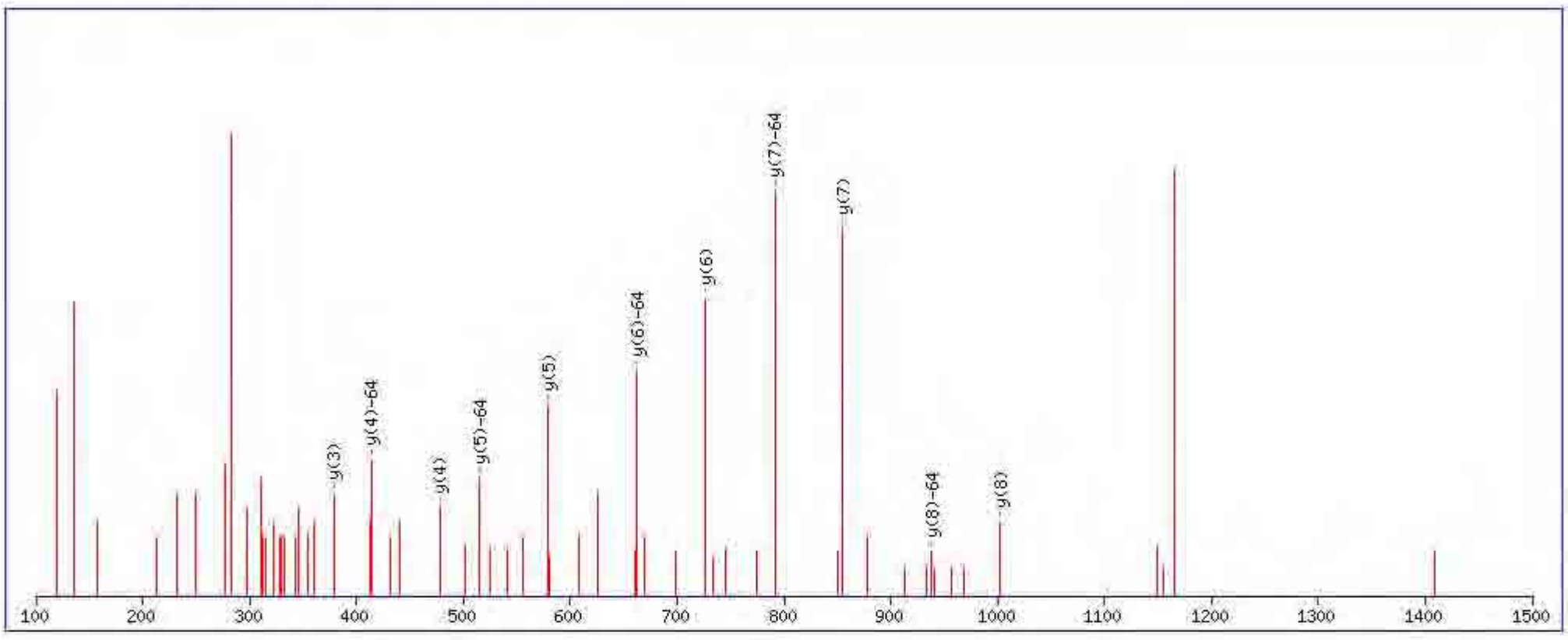
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFEFTVMGR**
Found in **TSP4_HUMAN**, Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2

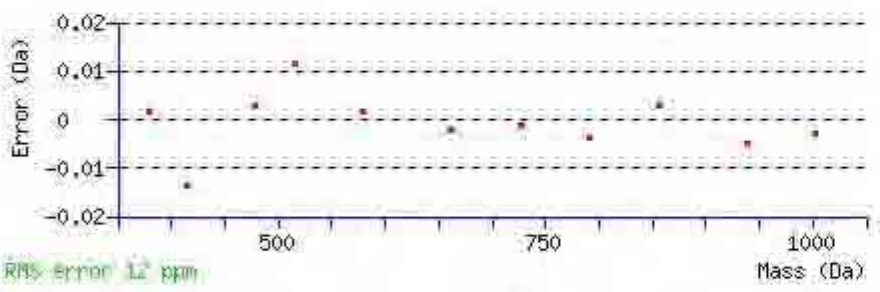
Match to Query 6719: 1164.528168 from(583.271360,2+) rtinseconds(1660) index(9103)
Title: Locus:1.1.1.1752.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

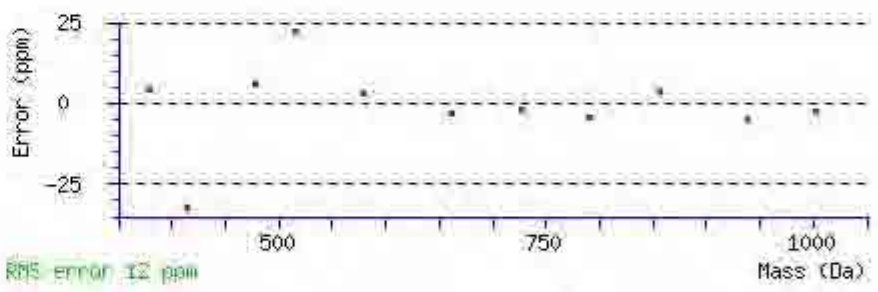
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1164.527390
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 38 **Expect:** 0.0026
Matches : 11/108 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	311.139019	156.073148			F	*1002.471330*	501.739303	985.444781	493.226029	984.460765	492.734021	8
3	440.181612	220.594444	422.171047	211.589162	E	*855.402916*	428.205096	838.376367	419.691822	837.392351	419.199814	7
4	587.250026	294.128651	569.239461	285.123369	F	*726.360323*	363.683800	709.333774	355.170525	708.349758	354.678517	6
5	688.297705	344.652491	670.287140	335.647208	T	*579.291909*	290.149593	562.265360	281.636318	561.281344	281.144310	5
6	787.366119	394.186698	769.355554	385.181415	V	*478.244230*	239.625753	461.217681	231.112479			4
7	934.401519	467.704398	916.390954	458.699115	M	*379.175816*	190.091546	362.149267	181.578272			3
8	991.422983	496.215130	973.412418	487.209847	G	232.140416	116.573846	215.113867	108.060572			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YFEFTVMGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.1	1164.527390	0.000778	YFEFTVMGR
9.9	1164.534576	-0.006408	RFAEMNPPR
6.8	1164.523361	0.004807	VEQMFQDPR
3.4	1164.535233	-0.007065	YFWHVREE
3.0	1164.537979	-0.009811	VLNSTGVCCGGR
3.0	1164.529907	-0.001739	EQGVTFPSGDI
2.9	1164.526733	0.001435	LNMDPMTVGR
0.6	1164.533234	-0.005066	MAQDLSEKDL

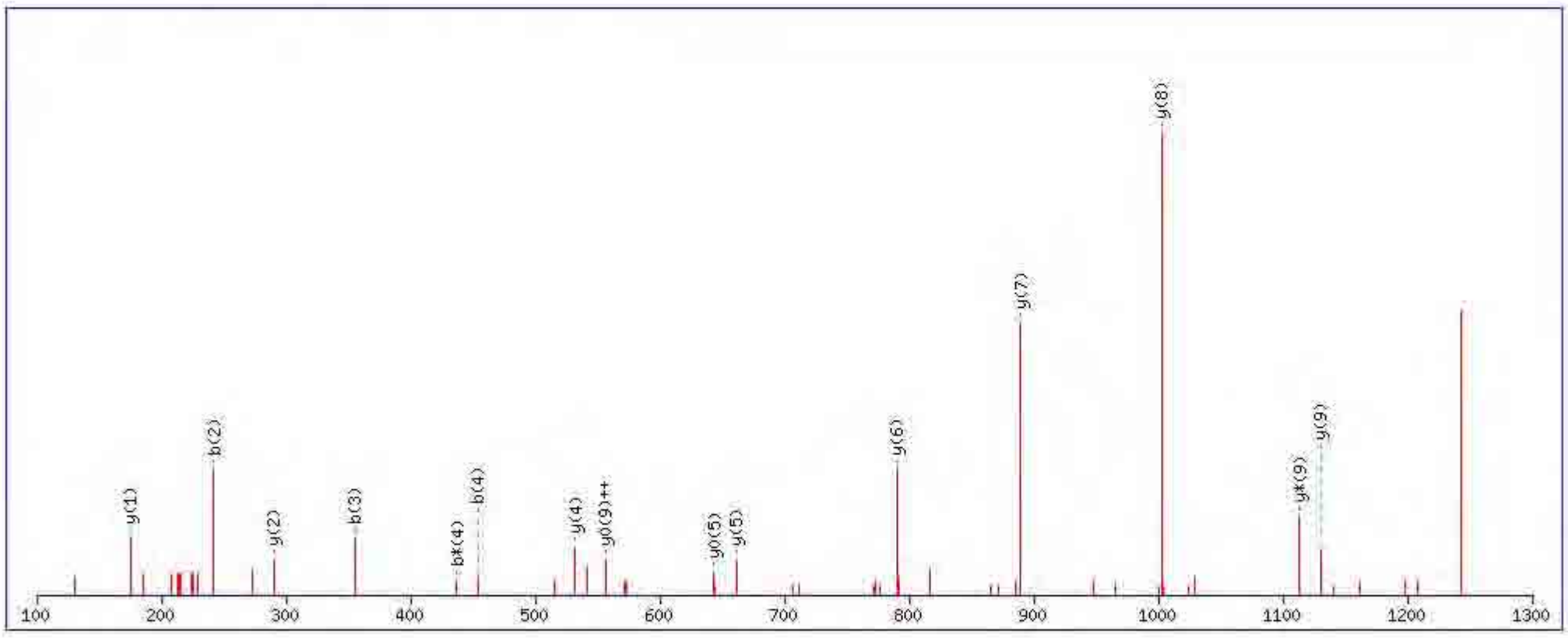
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQLVEEELDR**
Found in **TPM1_HUMAN**, Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2

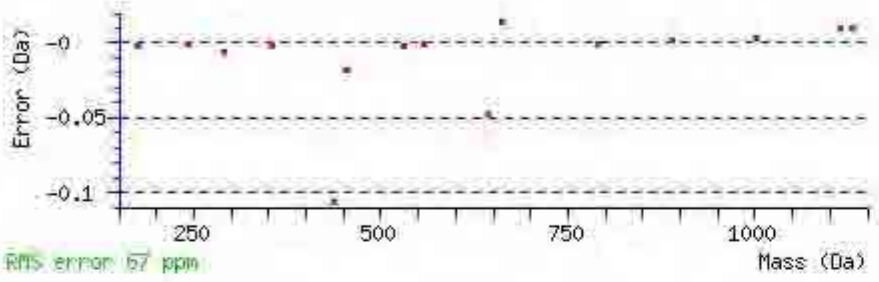
Match to Query 8624: 1242.654828 from(622.334690,2+) rtinseconds(1566) index(8165)
Title: Locus:1.1.1.1700.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

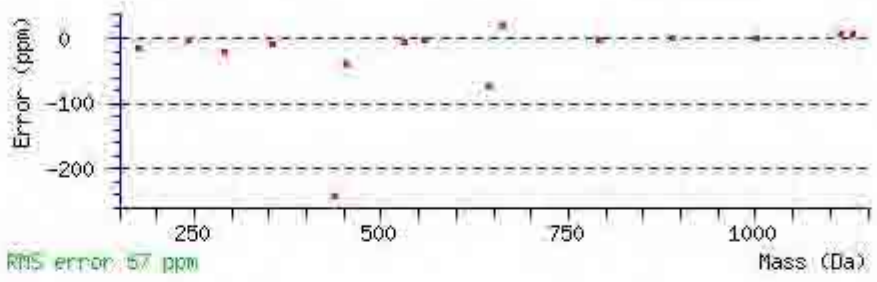
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1242.645554
Ions Score: 67 **Expect:** 7.7e-005
Matches : 15/96 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							10
2	**242.149918**	121.578597	225.123369	113.065323			Q	*1130.568794*	565.788035	1113.542245	557.274761	1112.558229	556.782753	9
3	**355.233982**	178.120629	338.207433	169.607355			L	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	8
4	**454.302396**	227.654836	437.275847	219.141562			V	*889.426152*	445.216714	872.399603	436.703440	871.415587	436.211432	7
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	E	*790.357738*	395.682507	773.331189	387.169233	772.347173	386.677225	6
6	712.387582	356.697429	695.361033	348.184155	694.377017	347.692147	E	*661.315145*	331.161211	644.288596	322.647936	643.304580	322.155928	5
7	841.430175	421.218726	824.403626	412.705451	823.419610	412.213443	E	*532.272552*	266.639914	515.246003	258.126640	514.261987	257.634632	4
8	954.514239	477.760758	937.487690	469.247483	936.503674	468.755475	L	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	1069.541182	535.274229	1052.514633	526.760955	1051.530617	526.268947	D	*290.145895*	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQLVEEELDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.0	1242.645554	0.009274	IQLVEEELDR
22.0	1242.646912	0.007916	KPLDIPDHHR
18.1	1242.656784	-0.001956	IVKQNEELDR
17.3	1242.656799	-0.001971	IGALLQSSGPER
16.1	1242.664200	-0.009372	GAIPVMIPAQSK
16.1	1242.664200	-0.009372	GAIPVMIPAQSK
16.1	1242.660858	-0.006030	QIPVHPVPDPL
16.1	1242.660858	-0.006030	QIPVHPVPDPL
16.1	1242.660858	-0.006030	QIPVHPVPDPL
16.1	1242.665543	-0.010715	QPLVLHHPRM

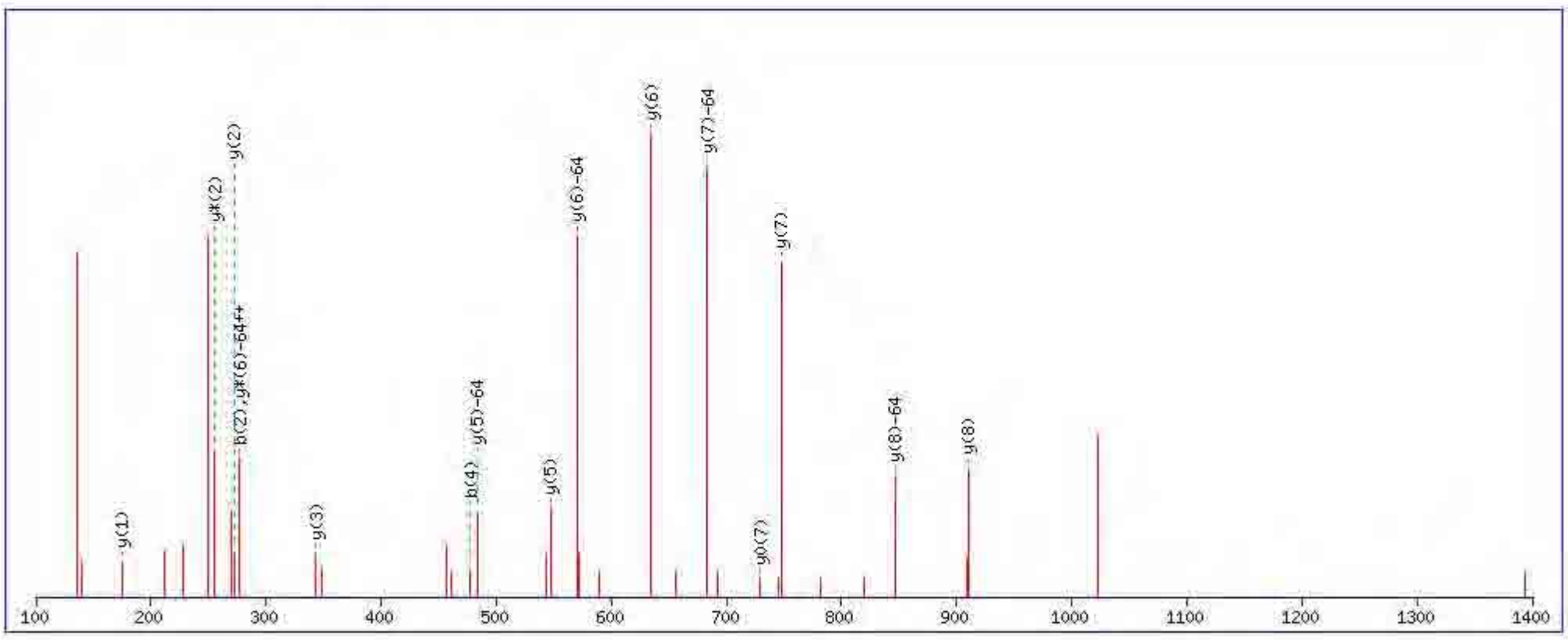
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYISGMAPR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

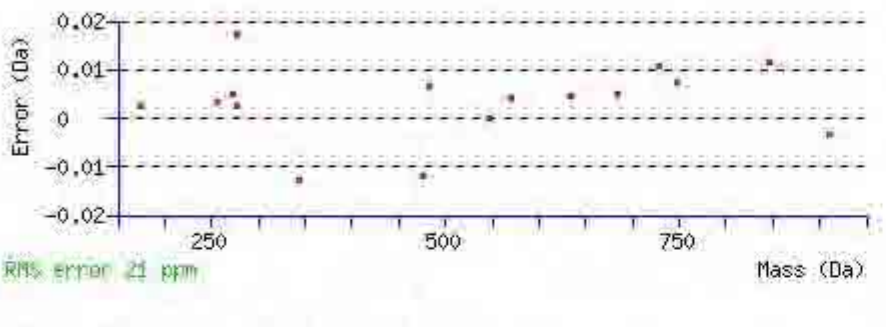
Match to Query 3925: 1022.525288 from(512.269920,2+) rtinseconds(948) index(2685)
Title: Locus:1.1.1.1351.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

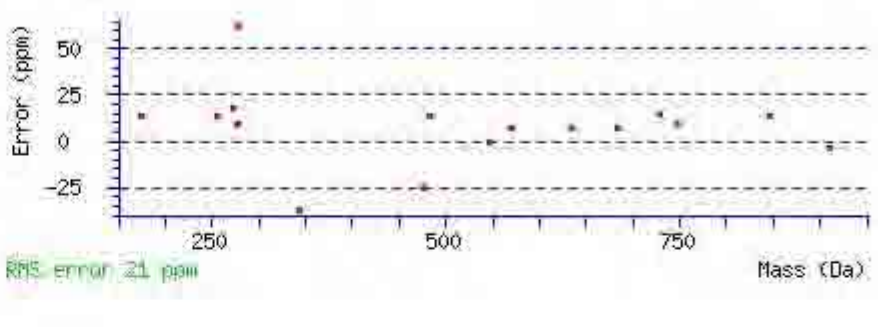
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1022.521881
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 42 **Expect:** 0.0087
Matches : 16/102 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	277.154669	139.080973			Y	*910.445115*	455.726196	893.418566	447.212921	892.434550	446.720913	8
3	390.238733	195.623005			I	*747.381786*	374.194531	730.355237	365.681257	729.371221	365.189249	7
4	477.270761	239.139019	459.260196	230.133736	S	*634.297722*	317.652499	617.271173	309.139225	616.287157	308.647217	6
5	534.292225	267.649751	516.281660	258.644468	G	*547.265694*	274.136485	530.239145	265.623211			5
6	681.327625	341.167451	663.317060	332.162168	M	490.244230	245.625753	473.217681	237.112478			4
7	752.364739	376.686008	734.354174	367.680725	A	*343.208830*	172.108053	326.182281	163.594778			3
8	849.417503	425.212390	831.406938	416.207107	P	*272.171716*	136.589496	255.145167	128.076221			2
9					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IYISGMAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1022.521881	0.003407	IYISGMAPR
21.1	1022.528427	-0.003139	IKVPSFSET
15.1	1022.521881	0.003407	IYISGMAPR
10.1	1022.528397	-0.003109	LYLDKEDK
10.1	1022.529755	-0.004467	LYPPPQHR
6.9	1022.521912	0.003376	PYGMAVVVR
5.6	1022.528412	-0.003124	IYSLSSQPI
2.1	1022.521881	0.003407	EFLPMKAR
1.5	1022.518539	0.006749	PNPIFFTR
1.4	1022.518524	0.006764	FFGESLPAR

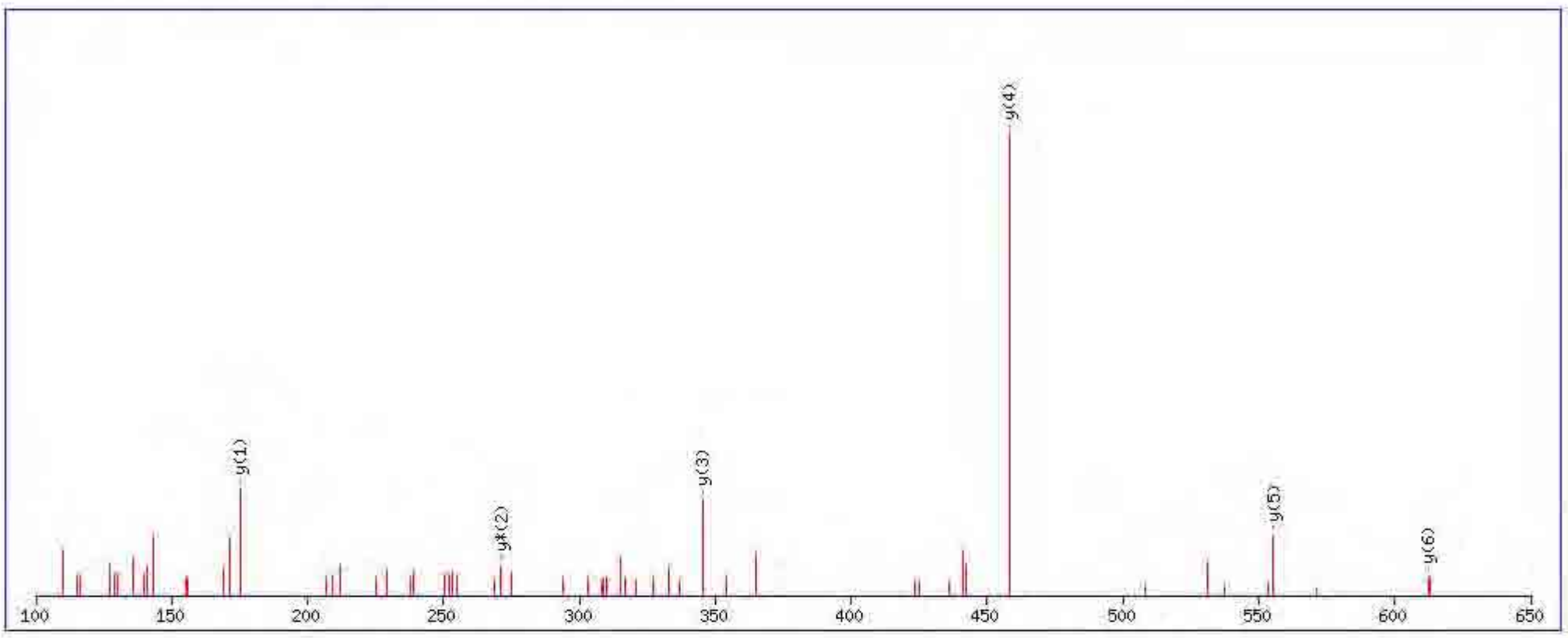
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGPPGPR**
Found in **CAC1A_HUMAN**, Voltage-dependent P/Q-type calcium channel subunit alpha-1A OS=Homo sapiens GN=CACNA1A PE=1 SV=2

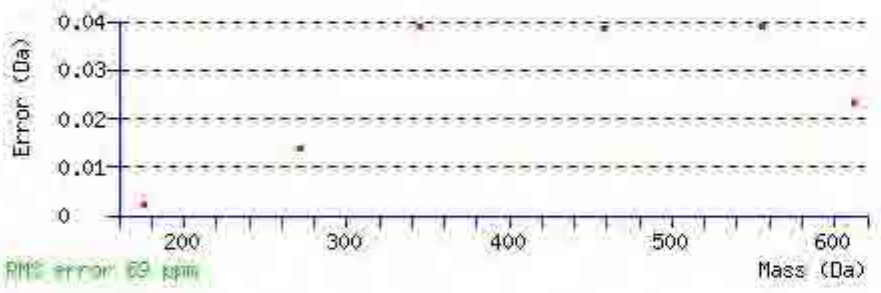
Match to Query 224: 740.350048 from(371.182300,2+) rtinseconds(559) index(630)
Title: Locus:1.1.1.1134.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_3.mgf

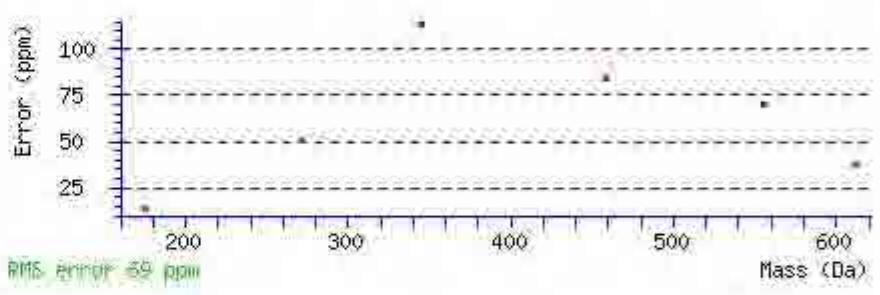
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 740.345322
Variable modifications:
P4 : Oxidation (P)
P6 : Oxidation (P)
Ions Score: 55 **Expect:** 0.00035
Matches : 6/48 fragment ions using 6 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.049869	65.528572	112.039304	56.523290	E					7
2	187.071333	94.039305	169.060768	85.034022	G	*612.310002*	306.658639	595.283453	298.145365	6
3	284.124097	142.565687	266.113532	133.560404	P	*555.288538*	278.147907	538.261989	269.634633	5
4	397.171776	199.089526	379.161211	190.084243	P	*458.235774*	229.621525	441.209225	221.108250	4
5	454.193240	227.600258	436.182675	218.594975	G	*345.188095*	173.097685	328.161546	164.584411	3
6	567.240919	284.124098	549.230354	275.118815	P	288.166631	144.586953	271.140082	136.073679	2
7					R	*175.118952*	88.063114	158.092403	79.549840	1





NCBI **BLAST** search of EGPPGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.9	740.345322	0.004726	EGPPGPR
35.5	740.345322	0.004726	EGPGPPR
32.1	740.345322	0.004726	EGPPGPR
31.7	740.345322	0.004726	GEPPPGR
31.4	740.345322	0.004726	EPGPPGR
31.2	740.345306	0.004742	EGPGEPR
31.2	740.345306	0.004742	EGPPDAR
20.5	740.345337	0.004711	GPPPGPR
20.5	740.345322	0.004726	PEGPGPR
20.5	740.345322	0.004726	PGEPGPR

Sibling 2 – technical replicate # 4

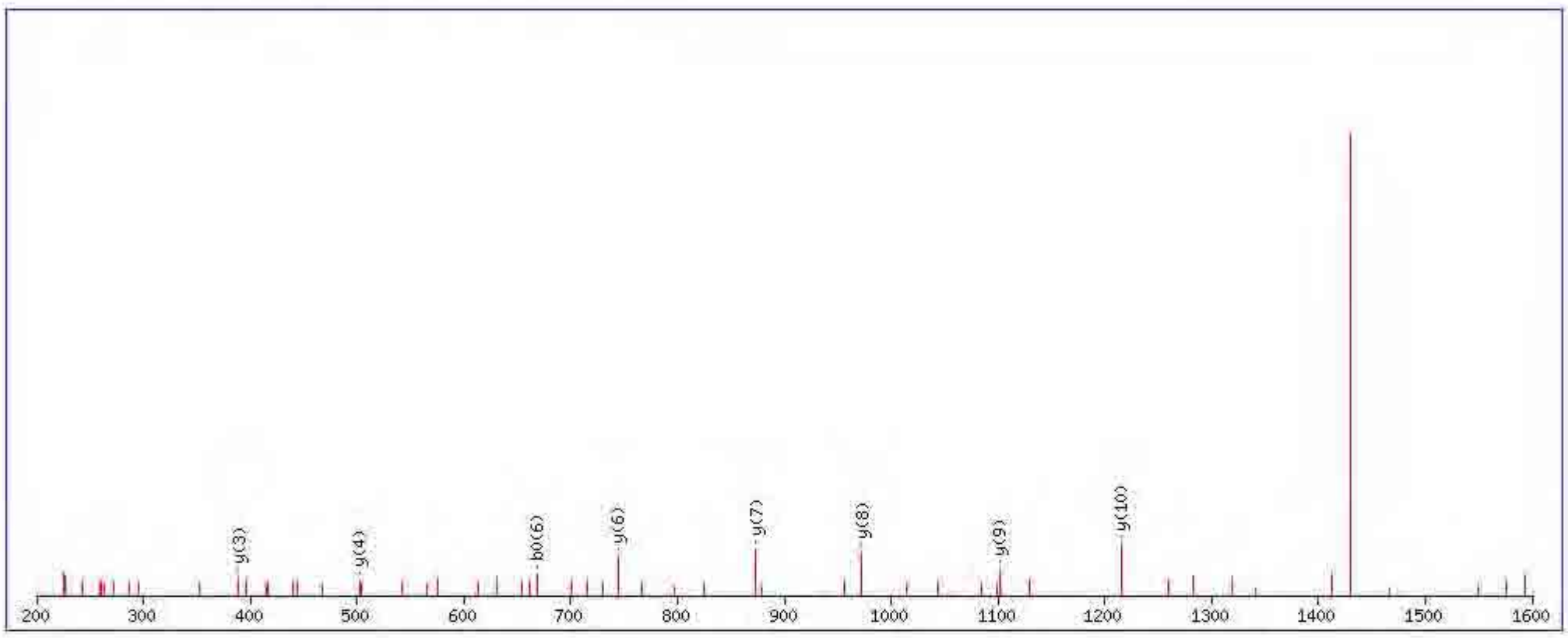
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TINEVENQILTR**
Found in **ACTN1_HUMAN**, Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2

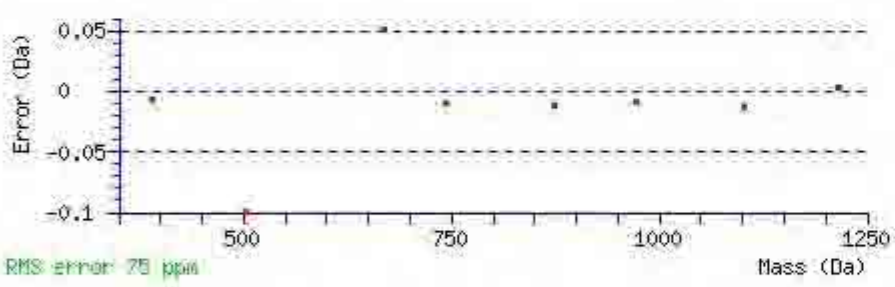
Match to Query 11242: 1428.755788 from(715.385170,2+) rtinseconds(1616) index(8730)
Title: Locus:1.1.1.1650.20
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

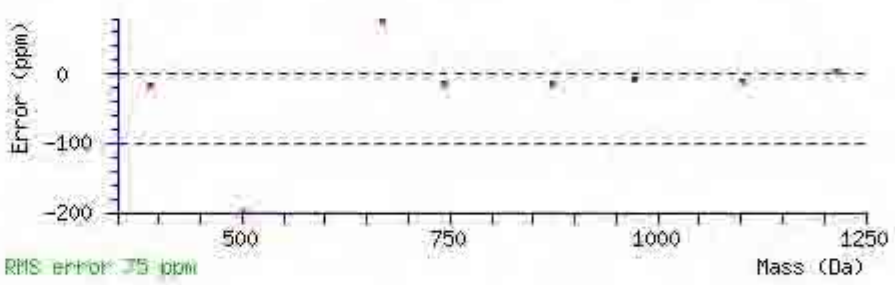
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1428.757233
Ions Score: 52 **Expect:** 8e-005
Matches : 8/126 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	215.139019	108.073147			197.128454	99.067865	I	1328.716855	664.862065	1311.690306	656.348791	1310.706290	655.856783	11
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	N	*1215.632791*	608.320034	1198.606242	599.806759	1197.622226	599.314751	10
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	E	*1101.589864*	551.298570	1084.563315	542.785295	1083.579299	542.293287	9
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	V	*972.547271*	486.777273	955.520722	478.263999	954.536706	477.771991	8
6	686.335546	343.671411	669.308997	335.158137	668.324981	334.666129	E	*873.478857*	437.243067	856.452308	428.729792	855.468292	428.237784	7
7	800.378473	400.692875	783.351924	392.179600	782.367908	391.687592	N	*744.436264*	372.721770	727.409715	364.208495	726.425699	363.716487	6
8	928.437051	464.722164	911.410502	456.208889	910.426486	455.716881	Q	630.393337	315.700307	613.366788	307.187032	612.382772	306.695024	5
9	1041.521115	521.264196	1024.494566	512.750921	1023.510550	512.258913	I	*502.334759*	251.671017	485.308210	243.157743	484.324194	242.665735	4
10	1154.605179	577.806227	1137.578630	569.292953	1136.594614	568.800945	L	*389.250695*	195.128985	372.224146	186.615711	371.240130	186.123703	3
11	1255.652858	628.330067	1238.626309	619.816793	1237.642293	619.324784	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TINEVENQILTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	1428.757233	-0.001445	TINEVENQILTR
7.6	1428.746002	0.009786	DSLAAEIVTPEIR
6.0	1428.757233	-0.001445	LTNPEDIRTNIK
5.6	1428.746017	0.009771	ISQDLEGVPPSKK
5.2	1428.746033	0.009755	TVVSADLLIDDRP
4.5	1428.757233	-0.001445	LTGTPESIEQAKR
4.2	1428.745972	0.009816	TLENKNNLLEIE
3.6	1428.746017	0.009771	DKPVTDQQLIEK
3.5	1428.764633	-0.008845	INVMEEPVIITR
3.5	1428.746002	0.009786	LNETQQLTPEIK

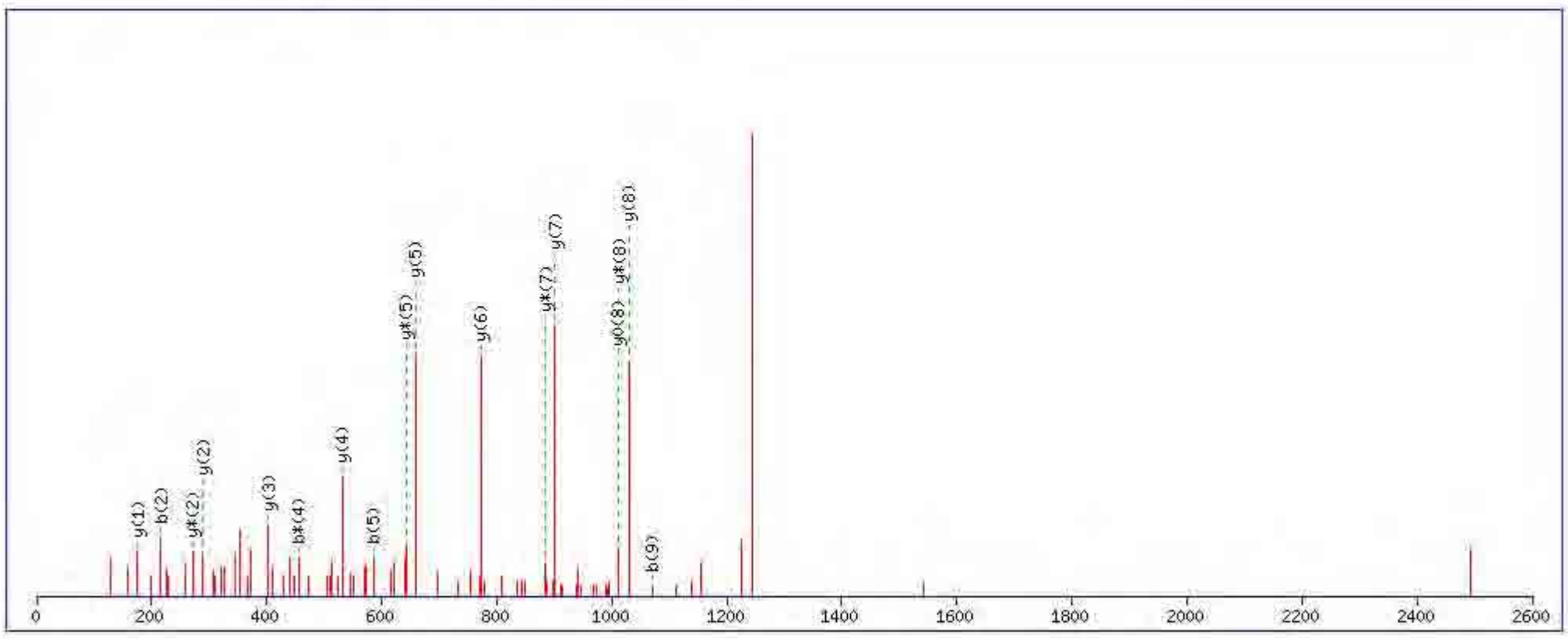
Mascot Search Results

Peptide View

MS/MS Fragmentation of TNQELQEINR
Found in ANXA2_HUMAN, Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

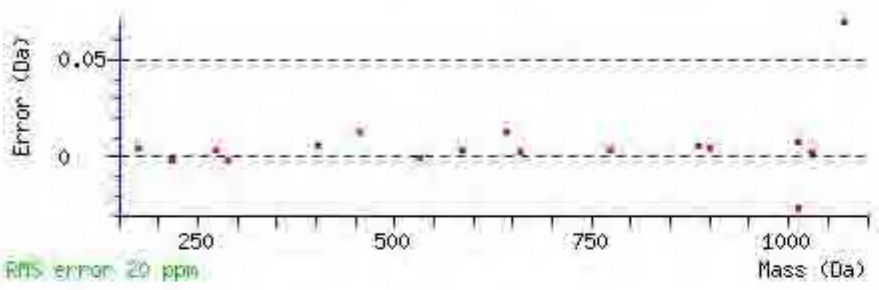
Match to Query 8504: 1243.620328 from(622.817440,2+) rtinseconds(918) index(2514)
Title: Locus:1.1.1.1266.13
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

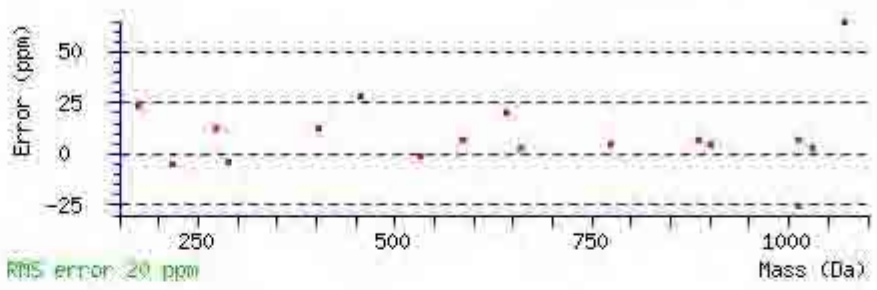
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1243.615646
Ions Score: 72 **Expect:** 1.6e-005
Matches : 17/100 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							10
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	N	1143.575276	572.291276	1126.548727	563.778002	1125.564711	563.285994	9
3	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	*1029.532349*	515.269813	1012.505800	506.756538	1011.521784	506.264530	8
4	473.199053	237.103164	456.172504	228.589890	455.188488	228.097882	E	*901.473771*	451.240524	884.447222	442.727249	883.463206	442.235241	7
5	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	L	*772.431178*	386.719227	755.404629	378.205953	754.420613	377.713945	6
6	714.341695	357.674486	697.315146	349.161211	696.331130	348.669203	Q	*659.347114*	330.177195	642.320565	321.663921	641.336549	321.171913	5
7	843.384288	422.195782	826.357739	413.682508	825.373723	413.190500	E	*531.288536*	266.147906	514.261987	257.634632	513.277971	257.142624	4
8	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	I	*402.245943*	201.626609	385.219394	193.113335			3
9	1070.511279	535.759278	1053.484730	527.246003	1052.500714	526.753995	N	*289.161879*	145.084577	272.135330	136.571303			2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TNQELQEINR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.7	1243.615646	0.004682	TNQELQEINR
19.6	1243.630905	-0.010577	HYSPTKELNR
15.6	1243.630905	-0.010577	KESQPAIWNR
15.2	1243.626892	-0.006564	QTDGEQAARIR
14.8	1243.608444	0.011884	QSLKDSPYYK
14.8	1243.615662	0.004666	KEEAAGVSGPAGR
13.9	1243.615662	0.004666	AKGSEGEQGPLR
11.8	1243.615677	0.004651	GKTGQPGLEGER
11.4	1243.626892	-0.006564	QRSSSLPPSNR
10.9	1243.628418	-0.008090	ACHPPPWLAPR

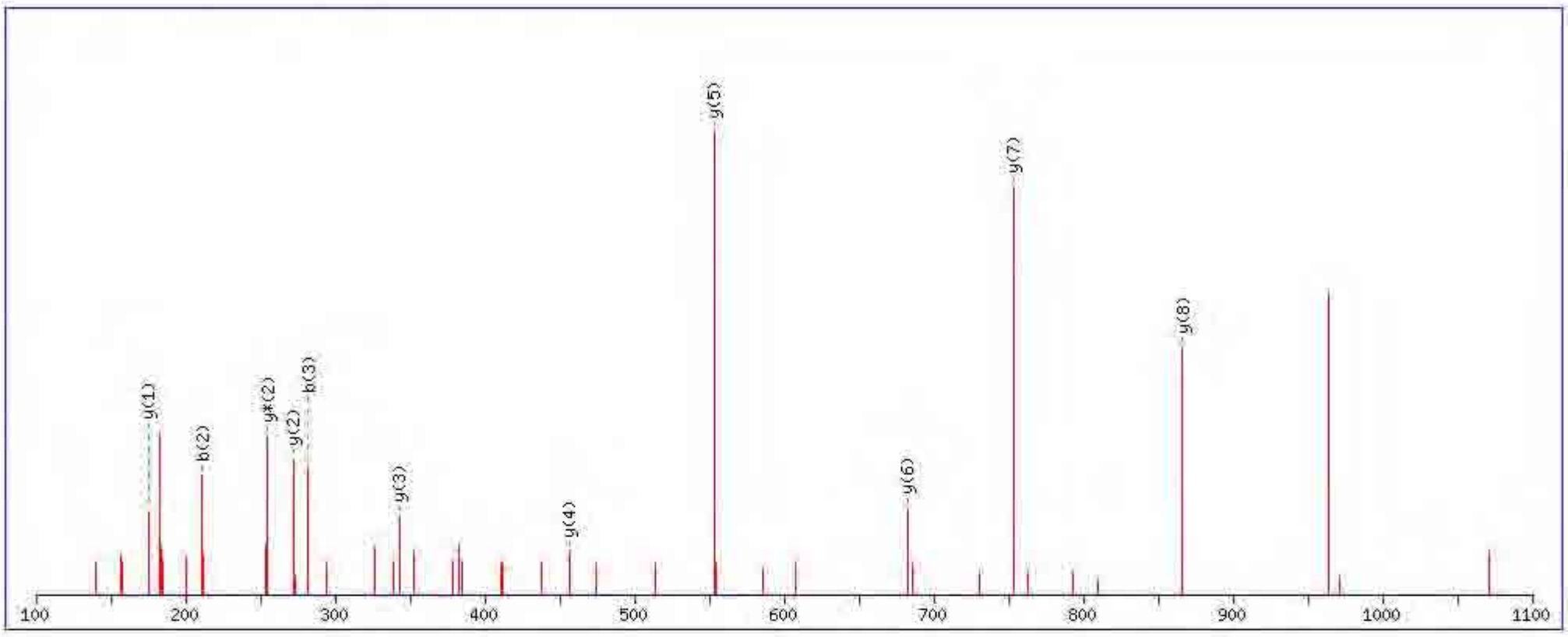
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLAEPLAPR**
Found in **LFNG_HUMAN**, Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2

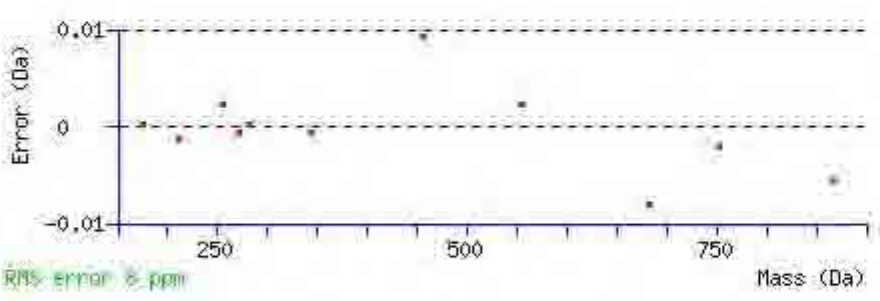
Match to Query 3071: 962.555268 from(482.284910,2+) rtinseconds(1163) index(4381)
Title: Locus:1.1.1.1404.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

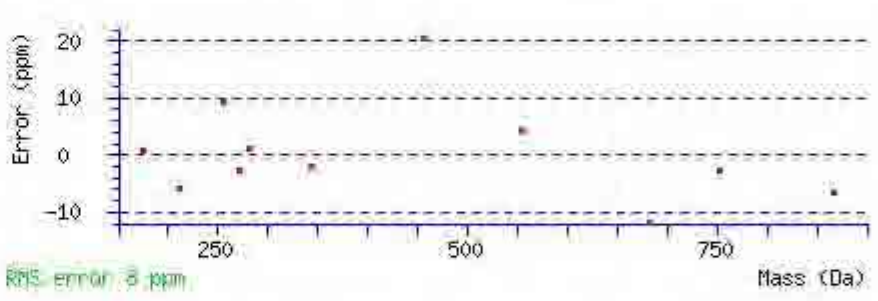
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 962.554886
Ions Score: 62 **Expect:** 3.5e-005
Matches : 11/64 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.060040	49.533658			P							9
2	211.144104	106.075690			L	866.509429	433.758353	849.482880	425.245078	848.498864	424.753070	8
3	282.181218	141.594247			A	753.425365	377.216321	736.398816	368.703046	735.414800	368.211038	7
4	411.223811	206.115544	393.213246	197.110261	E	682.388251	341.697764	665.361702	333.184489	664.377686	332.692481	6
5	508.276575	254.641926	490.266010	245.636643	P	553.345658	277.176467	536.319109	268.663193			5
6	621.360639	311.183958	603.350074	302.178675	L	456.292894	228.650085	439.266345	220.136811			4
7	692.397753	346.702515	674.387188	337.697232	A	343.208830	172.108053	326.182281	163.594779			3
8	789.450517	395.228897	771.439952	386.223614	P	272.171716	136.589496	255.145167	128.076222			2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PLAEPLAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.0	962.554886	0.000382	PLAEPLAPR
35.4	962.554901	0.000367	PLALPSPPR
25.3	962.554901	0.000367	PLALPSPPR
23.6	962.554901	0.000367	PPLSLPPAR
22.4	962.554916	0.000352	PPALTPVPR
13.8	962.554901	0.000367	PLALPSPPR
12.7	962.554916	0.000352	PPALTPVPR
11.9	962.547028	0.008240	VMKELSLK
11.5	962.554901	0.000367	PPLSLPPAR
10.7	962.554886	0.000382	PAEILPPAR

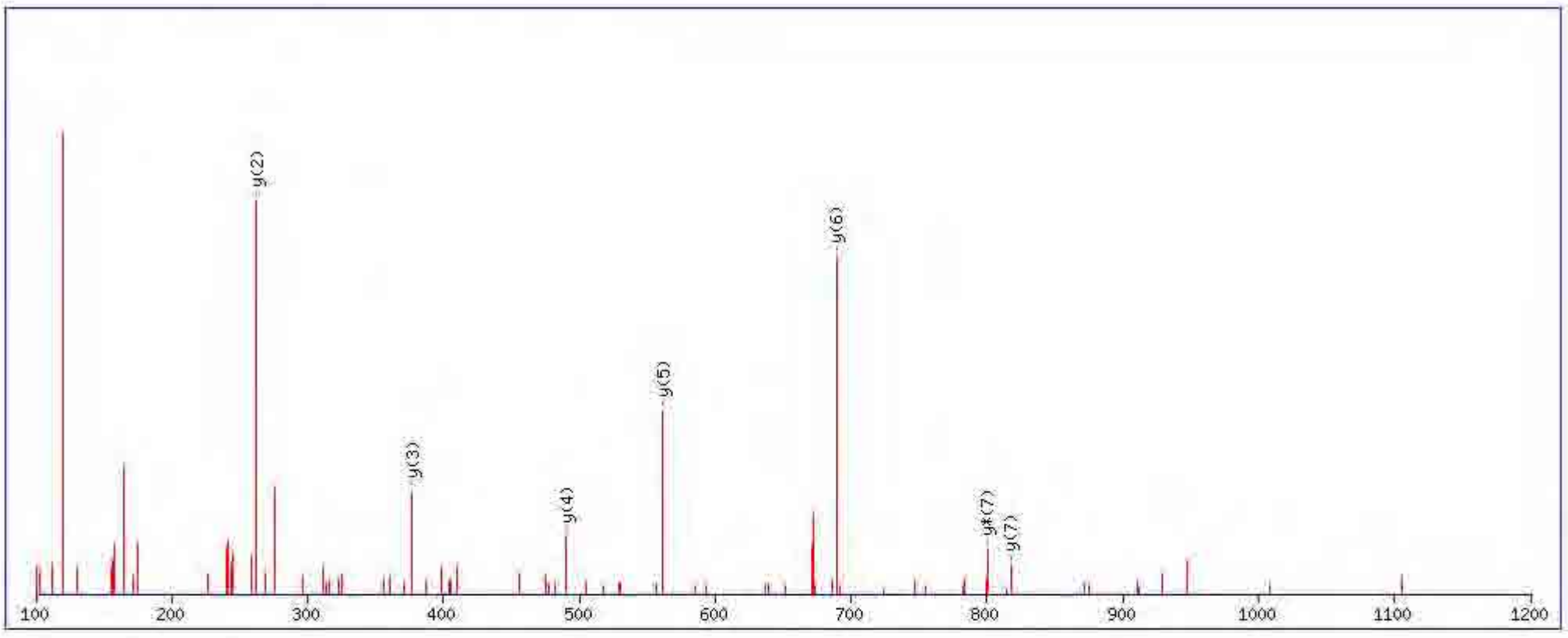
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQQAIDSR**
Found in **CASPE_HUMAN**, Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2

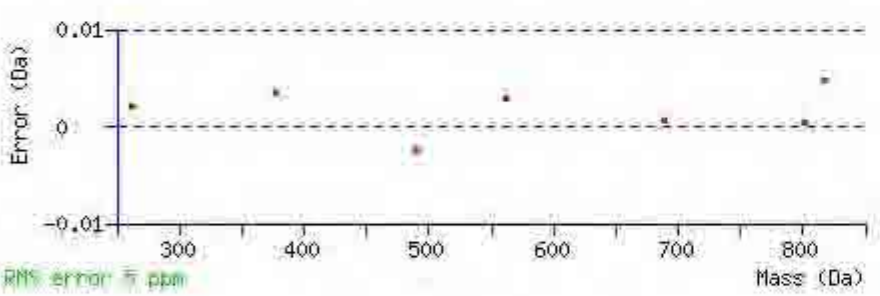
Match to Query 3077: 963.481608 from(482.748080,2+) rtinseconds(730) index(1361)
Title: Locus:1.1.1.1163.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

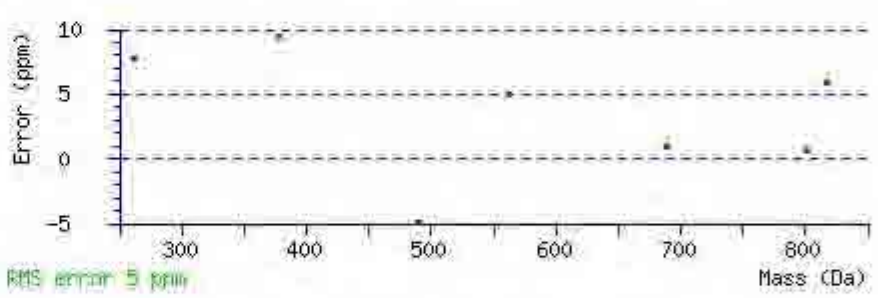
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 963.477386
Ions Score: 59 **Expect:** 0.00021
Matches : 7/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							8
2	276.134268	138.570772	259.107719	130.057497			Q	*817.416257*	409.211767	800.389708	400.698492	799.405692	400.206484	7
3	404.192846	202.600061	387.166297	194.086786			Q	*689.357679*	345.182478	672.331130	336.669203	671.347114	336.177195	6
4	475.229960	238.118618	458.203411	229.605343			A	*561.299101*	281.153189	544.272552	272.639914	543.288536	272.147906	5
5	588.314024	294.660650	571.287475	286.147376			I	*490.261987*	245.634631	473.235438	237.121357	472.251422	236.629349	4
6	703.340967	352.174122	686.314418	343.660847	685.330402	343.168839	D	*377.177923*	189.092599	360.151374	180.579325	359.167358	180.087317	3
7	790.372995	395.690136	773.346446	387.176861	772.362430	386.684853	S	*262.150980*	131.579128	245.124431	123.065853	244.140415	122.573845	2
8							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FQQAIDSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	963.477386	0.004222	FQQAIDSR
26.8	963.477402	0.004206	FQQTARPT
26.5	963.480743	0.000865	MKQEIGSR
24.8	963.484787	-0.003179	MKQAGFPLG
21.5	963.480759	0.000849	MQLTNVSR
20.9	963.488617	-0.007009	FQQERTR
15.5	963.477402	0.004206	FQTVPNSR
13.8	963.477386	0.004222	FQIGQESR
13.8	963.488617	-0.007009	FQSPSRSR
12.6	963.487274	-0.005666	STSQELAKT

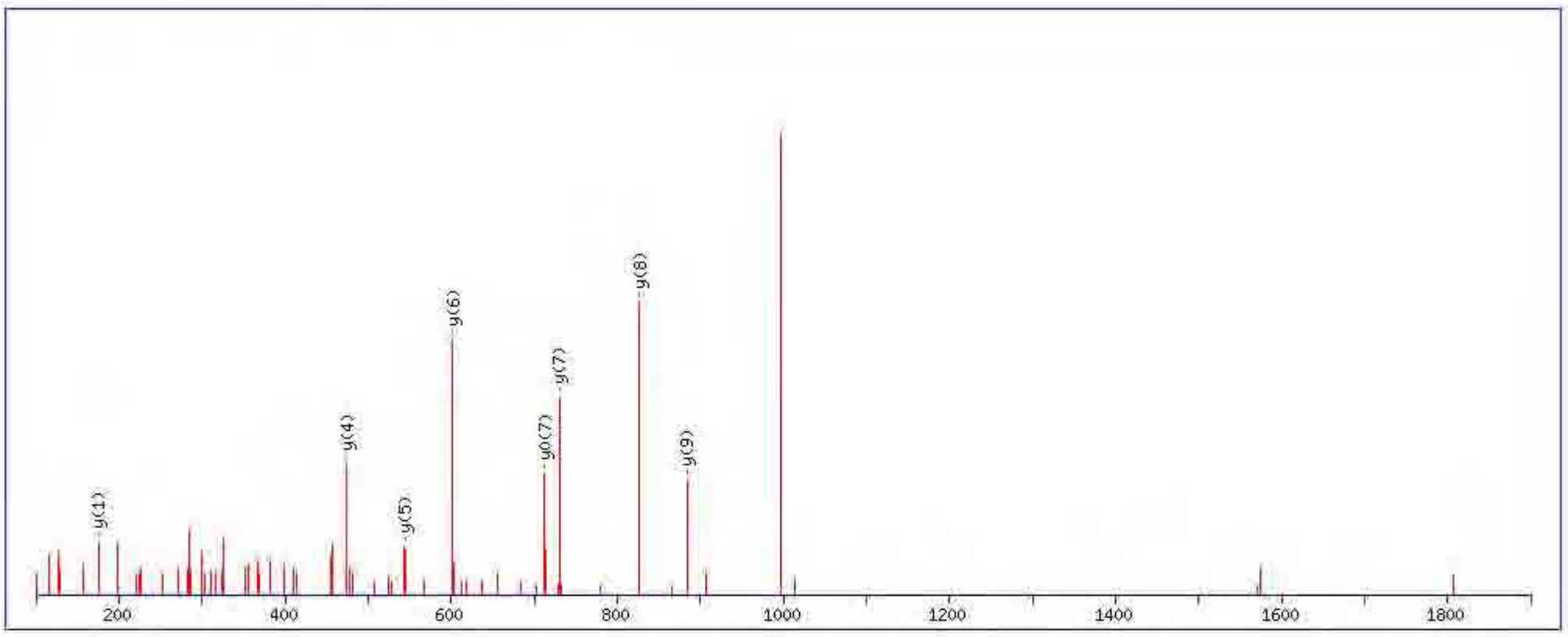
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGPKGAPGER**
Found in **CO9A3_HUMAN**, Collagen alpha-3(IX) chain OS=Homo sapiens GN=COL9A3 PE=2 SV=2

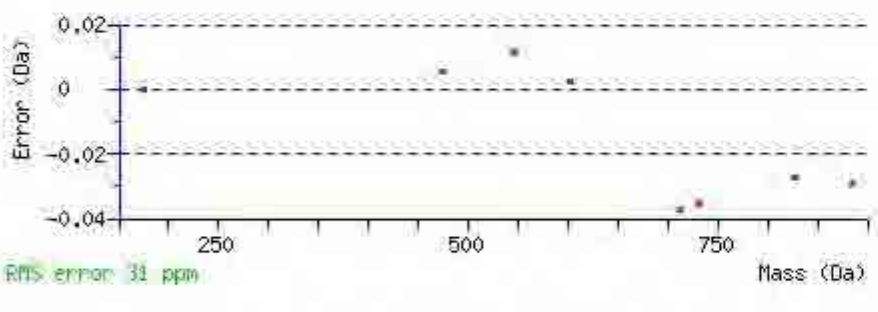
Match to Query 3573: 996.506048 from(499.260300,2+) rtinseconds(592) index(771)
Title: Locus:1.1.1.1088.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

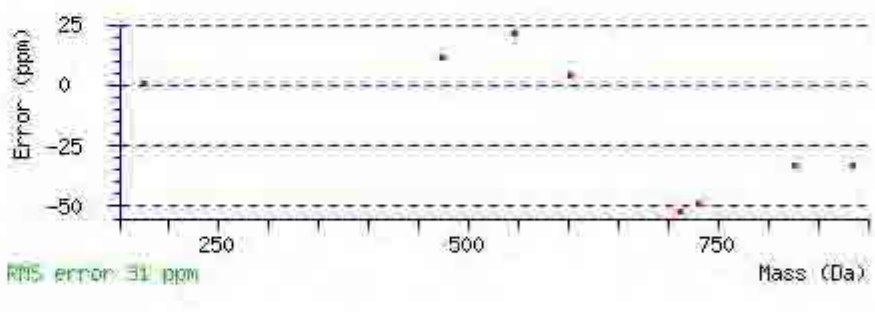
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 996.498856
Variable modifications:
P1 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 47 **Expect:** 0.0035
Matches : 8/84 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116					P							10
2	171.076419	86.041847					G	*884.458457*	442.732867	867.431908	434.219592	866.447892	433.727584	9
3	268.129183	134.568229					P	*827.436993*	414.222135	810.410444	405.708860	809.426428	405.216852	8
4	396.224146	198.615711	379.197597	190.102436			K	*730.384229*	365.695753	713.357680	357.182478	712.373664	356.690470	7
5	453.245610	227.126443	436.219061	218.613168			G	*602.289266*	301.648271	585.262717	293.134997	584.278701	292.642989	6
6	524.282724	262.645000	507.256175	254.131726			A	*545.267802*	273.137539	528.241253	264.624265	527.257237	264.132257	5
7	637.330403	319.168840	620.303854	310.655565			P	*474.230688*	237.618982	457.204139	229.105708	456.220123	228.613700	4
8	694.351867	347.679572	677.325318	339.166297			G	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
9	823.394460	412.200868	806.367911	403.687594	805.383895	403.195586	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
10							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of PGPKGAPGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	996.498856	0.007192	PGPKGAPGER
23.5	996.498871	0.007177	PGPSGPPGKR
21.8	996.498856	0.007192	PGPAGPKGER
20.7	996.498856	0.007192	PGPKGAPGER
20.5	996.512756	-0.006708	VAPKEPVEE
19.0	996.514114	-0.008066	PGPWGQALR
18.9	996.498871	0.007177	LGPPQGGSPR
18.2	996.498871	0.007177	PGQPGLPGSR
17.7	996.498856	0.007192	PGPQAGAGAGAK
15.8	996.512772	-0.006724	LGPELSPSPT

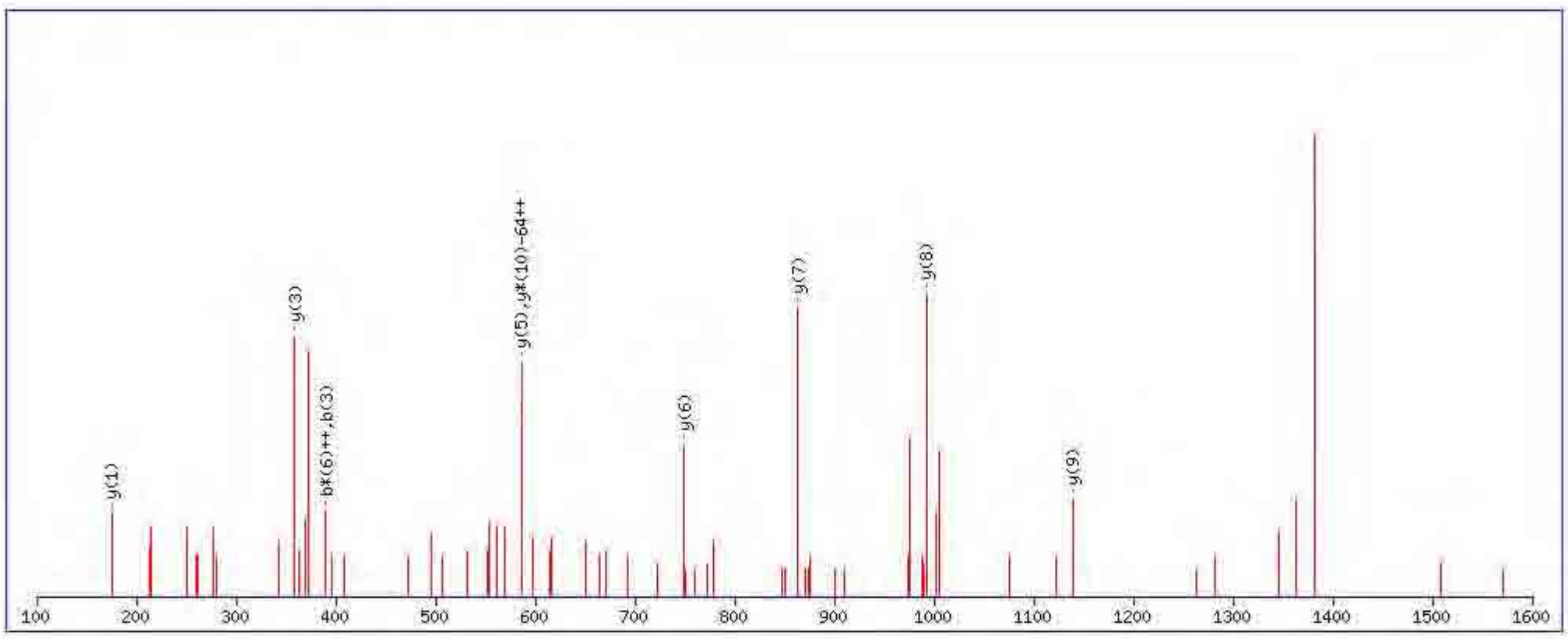
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIMENYNIALR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

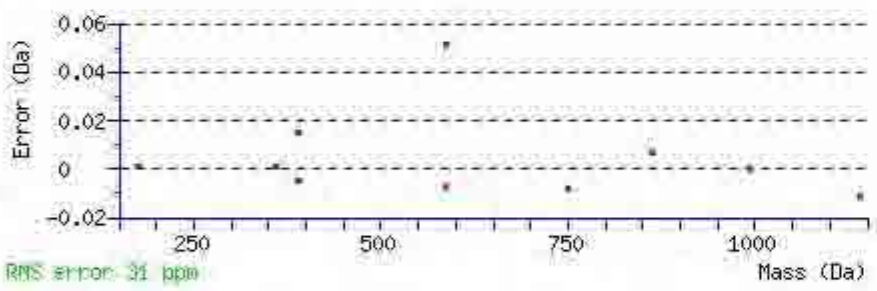
Match to Query 10606: 1380.684228 from(691.349390,2+) rtinseconds(1478) index(7349)
Title: Locus:1.1.1.1576.25
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

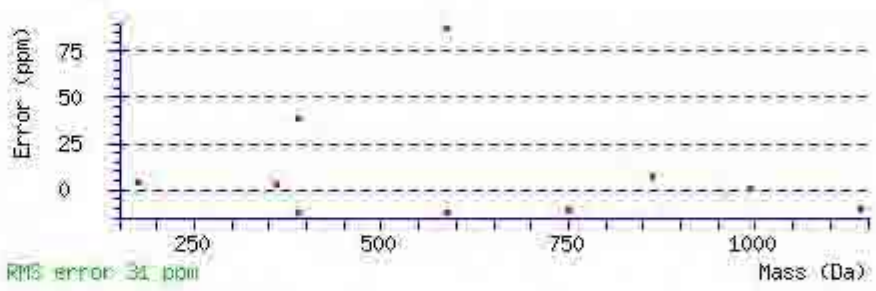
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1380.670700
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 53 **Expect:** 0.00031
Matches : 10/154 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	I	1252.635434	626.821355	1235.608885	618.308081	1234.624869	617.816073	10
3	390.169333	195.588304			372.158768	186.583022	M	*1139.551370*	570.279323	1122.524821	561.766049	1121.540805	561.274040	9
4	519.211926	260.109601			501.201361	251.104319	E	*992.515970*	496.761623	975.489421	488.248348	974.505405	487.756340	8
5	633.254853	317.131065	616.228304	308.617790	615.244288	308.125782	N	*863.473377*	432.240326	846.446828	423.727052			7
6	796.318182	398.662729	779.291633	390.149454	778.307617	389.657446	Y	*749.430450*	375.218863	732.403901	366.705588			6
7	910.361109	455.684192	893.334560	447.170918	892.350544	446.678910	N	*586.367121*	293.687199	569.340572	285.173924			5
8	1023.445173	512.226224	1006.418624	503.712950	1005.434608	503.220942	I	472.324194	236.665735	455.297645	228.152460			4
9	1094.482287	547.744782	1077.455738	539.231507	1076.471722	538.739499	A	*359.240130*	180.123703	342.213581	171.610428			3
10	1207.566351	604.286813	1190.539802	595.773539	1189.555786	595.281531	L	288.203016	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIMENYNIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.9	1380.670700	0.013528	EIMENYNIALR
14.6	1380.688492	-0.004264	YIPENVSSSTLR
14.0	1380.695877	-0.011649	EIMEYSVLLPR
8.4	1380.681961	0.002267	EDLMPSRPPSPR
7.5	1380.681976	0.002252	FQKVADMATNTR
7.0	1380.670715	0.013513	LEEFLSAMQSAR
6.2	1380.685989	-0.001761	KNYPPVCEIFR
5.8	1380.681961	0.002267	ETFLRCIEASGR
5.2	1380.686020	-0.001792	LEVVSHMAGPWGV
5.0	1380.697220	-0.012992	LHHMEVEFAIR

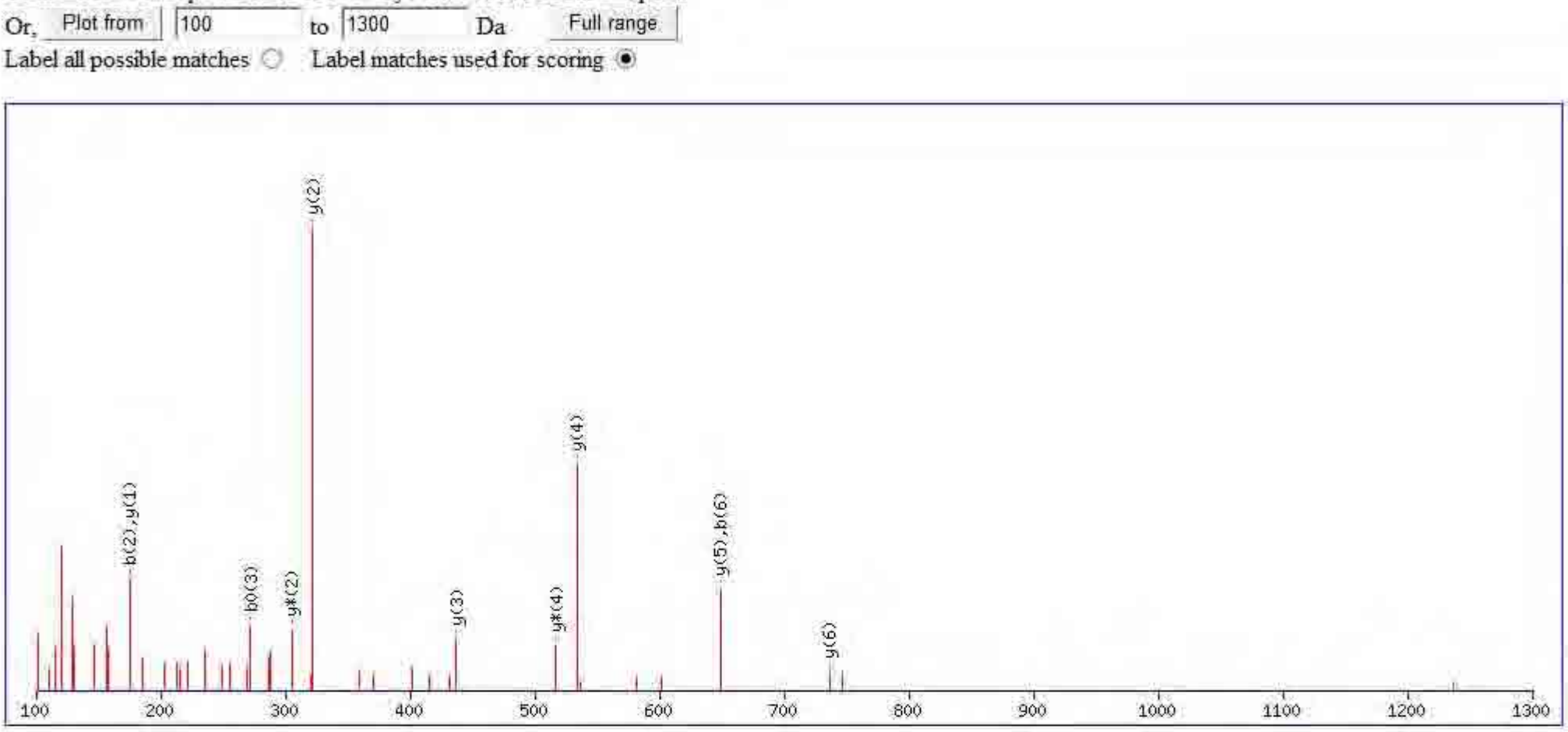
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSDPDFR**
Found in **DSC3_HUMAN**, Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3

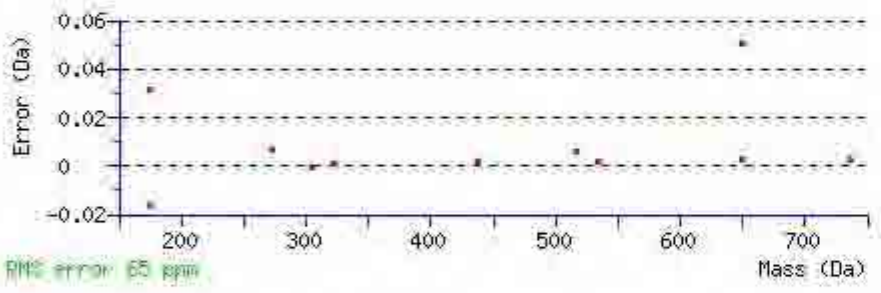
Match to Query 843: 822.356148 from(412.185350,2+) rtinseconds(610) index(821)
Title: Locus:1.1.1.1098.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

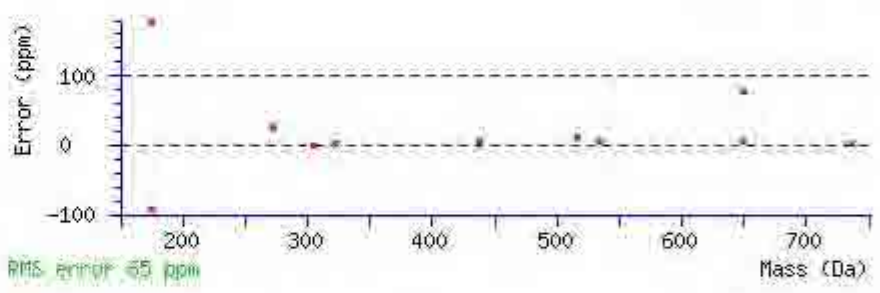
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 822.350800
Ions Score: 50 **Expect:** 0.0011
Matches : 11/56 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	175.071332	88.039304	157.060767	79.034021	S	736.326044	368.666660	719.299495	360.153386	718.315479	359.661378	6
3	290.098275	145.552776	272.087710	136.547493	D	649.294016	325.150646	632.267467	316.637372	631.283451	316.145364	5
4	387.151039	194.079158	369.140474	185.073875	P	534.267073	267.637175	517.240524	259.123900	516.256508	258.631892	4
5	502.177982	251.592629	484.167417	242.587347	D	437.214309	219.110793	420.187760	210.597518	419.203744	210.105510	3
6	649.246396	325.126836	631.235831	316.121554	F	322.187366	161.597321	305.160817	153.084047			2
7					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SSDPDFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.7	822.350800	0.005348	SSDPDFR
23.0	822.350800	0.005348	SAPDFDR
15.3	822.354156	0.001992	SAVEMDR
11.4	822.354172	0.001976	DSSPVMR
11.4	822.350784	0.005364	AAEFDDR
11.4	822.362030	-0.005882	RDFDDR
11.1	822.350800	0.005348	SFPSDDR
10.0	822.354156	0.001992	PESTAMR
9.3	822.354141	0.002007	KEEMDR
9.3	822.350784	0.005364	QEEFDR

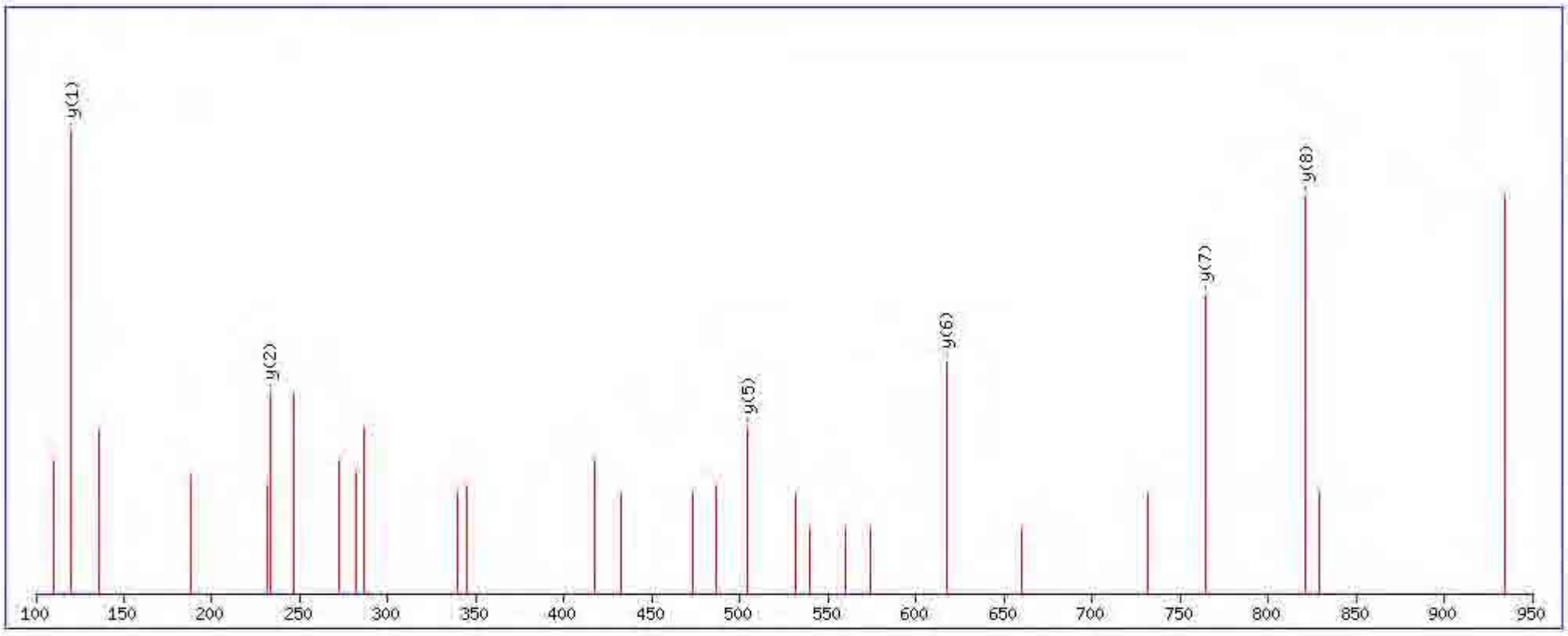
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGFLAEALT**
Found in **EPHAA_HUMAN**, Ephrin type-A receptor 10 OS=Homo sapiens GN=EPHA10 PE=2 SV=1

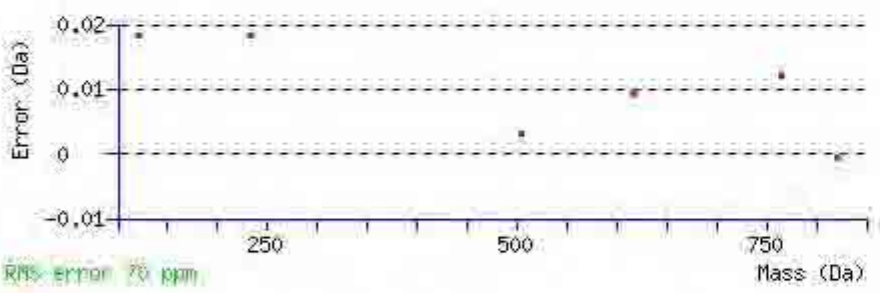
Match to Query 2674: 933.520448 from(467.767500,2+) rtinseconds(1527) index(7885)
Title: Locus:1.1.1.1603.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

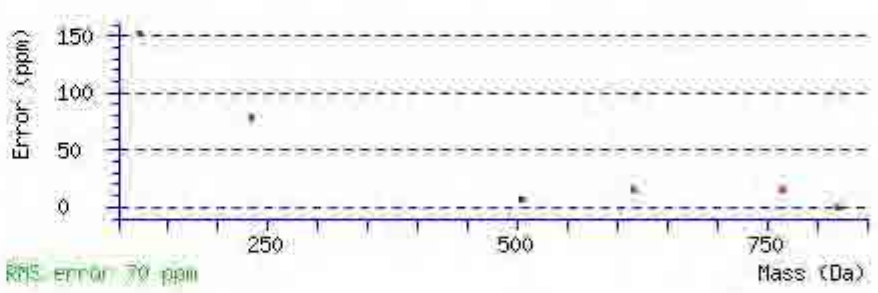
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 933.517120
Ions Score: 54 **Expect:** 0.00045
Matches : 6/54 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L					9
2	171.112804	86.060040			G	*821.440347*	411.223812	803.429782	402.218529	8
3	318.181218	159.594247			F	*764.418883*	382.713080	746.408318	373.707797	7
4	431.265282	216.136279			L	*617.350469*	309.178873	599.339904	300.173590	6
5	502.302396	251.654836			A	*504.266405*	252.636840	486.255840	243.631558	5
6	631.344989	316.176133	613.334424	307.170850	E	433.229291	217.118283	415.218726	208.113001	4
7	702.382103	351.694690	684.371538	342.689407	A	304.186698	152.596987	286.176133	143.591704	3
8	815.466167	408.236722	797.455602	399.231439	L	*233.149584*	117.078430	215.139019	108.073148	2
9					T	*120.065520*	60.536398	102.054955	51.531116	1





NCBI **BLAST** search of LGFLAEALT
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	933.517120	0.003328	LGFLAEALT
22.4	933.517120	0.003328	IGFIEEVK
22.1	933.517151	0.003297	LGFTPSVTI
22.0	933.528351	-0.007903	IGFIDKNK
16.8	933.528351	-0.007903	IFNKSVNI
11.1	933.517151	0.003297	IGSVVVYPT
11.1	933.528381	-0.007933	IGVKFNVGT
10.8	933.528366	-0.007918	IGFEGVKGK
10.8	933.517151	0.003297	IFGVLAVDT
10.8	933.513107	0.007341	LGSSVTDKK

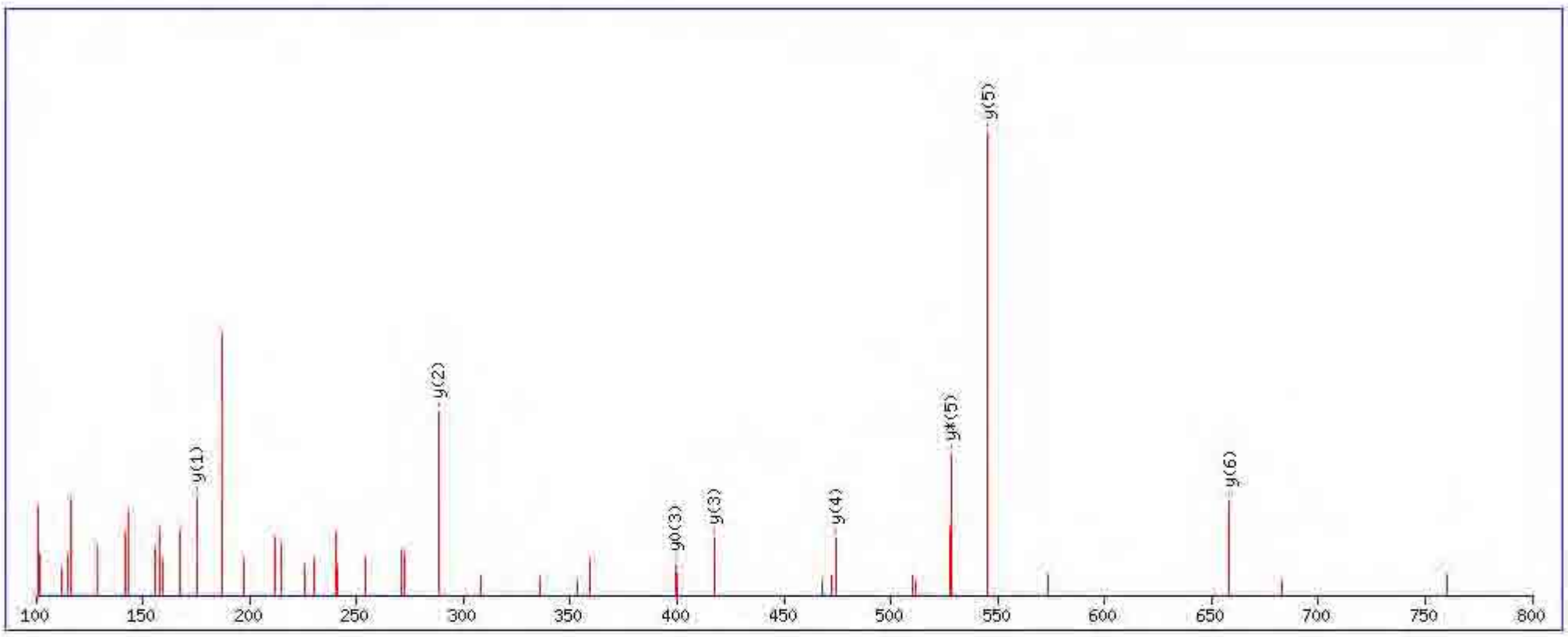
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLAGEIR**
Found in **ERC2_HUMAN**, ERC protein 2 OS=Homo sapiens GN=ERC2 PE=1 SV=3

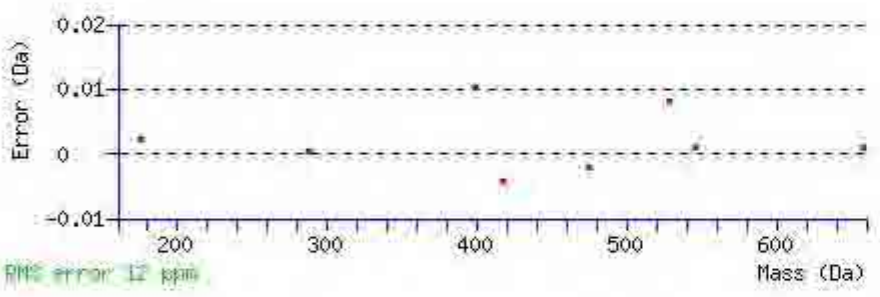
Match to Query 349: 758.428568 from(380.221560,2+) rtinseconds(774) index(1538)
Title: Locus:1.1.1.1187.2
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

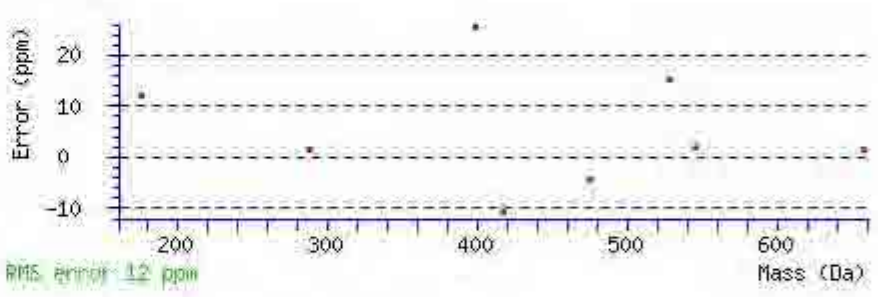
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 758.428635
Ions Score: 54 **Expect:** 0.00088
Matches : 8/56 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							7
2	215.139019	108.073147	197.128454	99.067865	L	*658.388251*	329.697764	641.361702	321.184489	640.377686	320.692481	6
3	286.176133	143.591704	268.165568	134.586422	A	*545.304187*	273.155732	528.277638	264.642457	527.293622	264.150449	5
4	343.197597	172.102436	325.187032	163.097154	G	*474.267073*	237.637174	457.240524	229.123900	456.256508	228.631892	4
5	472.240190	236.623733	454.229625	227.618450	E	*417.245609*	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	585.324254	293.165765	567.313689	284.160483	I	*288.203016*	144.605146	271.176467	136.091872			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TLAGEIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.6	758.428635	-0.000067	TLAGEIR
37.4	758.428635	-0.000067	TIQEIR
37.4	758.428635	-0.000067	TLQELR
37.4	758.428635	-0.000067	TPKELR
34.5	758.428635	-0.000067	TLAEGLR
23.7	758.428635	-0.000067	TIEKPR
23.7	758.428635	-0.000067	TIEQLR
23.7	758.428635	-0.000067	TLEQLR
23.7	758.428635	-0.000067	TPEKIR
23.7	758.428635	-0.000067	TPEKLR

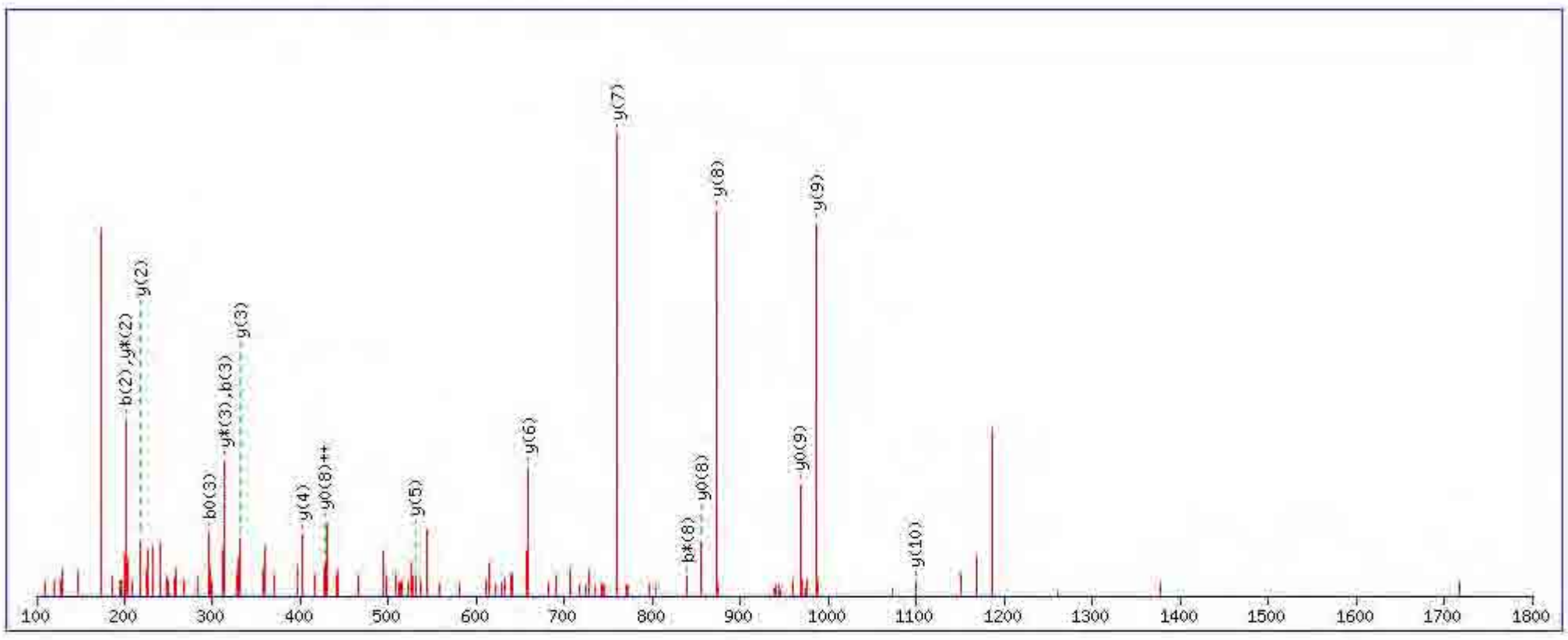
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILLTEQALAK**
Found in **LACRT_HUMAN**, Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1

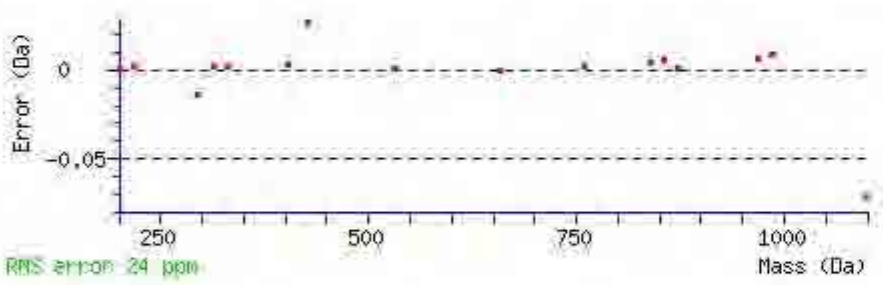
Match to Query 7310: 1185.705848 from(593.860200,2+) rtinseconds(1603) index(8616)
Title: Locus:1.1.1.1643.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

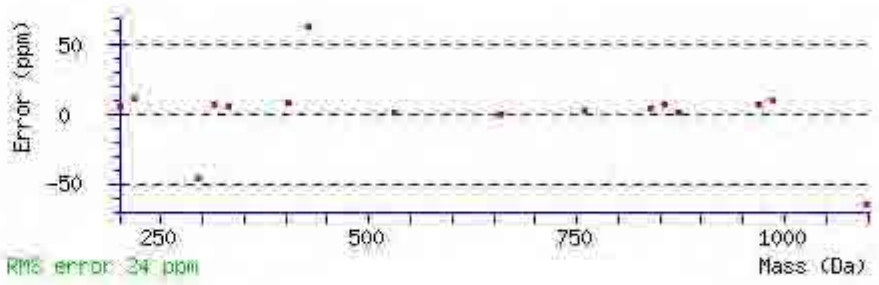
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1185.696854
Ions Score: 68 **Expect:** 6.8e-006
Matches : 18/98 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	201.123368	101.065322			183.112803	92.060039	I	*1099.672138*	550.339707	1082.645589	541.826433	1081.661573	541.334425	10
3	314.207432	157.607354			296.196867	148.602071	L	*986.588074*	493.797675	969.561525	485.284401	968.577509	484.792393	9
4	427.291496	214.149386			409.280931	205.144104	L	*873.504010*	437.255643	856.477461	428.742369	855.493445	428.250361	8
5	528.339175	264.673226			510.328610	255.667943	T	*760.419946*	380.713611	743.393397	372.200337	742.409381	371.708329	7
6	657.381768	329.194522			639.371203	320.189240	E	*659.372267*	330.189772	642.345718	321.676497	641.361702	321.184489	6
7	785.440346	393.223811	768.413797	384.710537	767.429781	384.218529	Q	*530.329674*	265.668475	513.303125	257.155201			5
8	856.477460	428.742368	839.450911	420.229094	838.466895	419.737086	A	*402.271096*	201.639186	385.244547	193.125912			4
9	969.561524	485.284400	952.534975	476.771126	951.550959	476.279118	L	*331.233982*	166.120629	314.207433	157.607355			3
10	1040.598638	520.802957	1023.572089	512.289683	1022.588073	511.797675	A	*218.149918*	109.578597	201.123369	101.065323			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SILLTEQALAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.9	1185.696854	0.008994	SILLTEQALAK
26.6	1185.698212	0.007636	LSILTPRHHL
25.0	1185.696869	0.008979	TVLTELQAKIA
19.2	1185.708099	-0.002251	SIIPRGSLSLK
18.7	1185.696854	0.008994	SILILQEKDK
16.8	1185.708084	-0.002236	ISLLNLTERK
15.6	1185.700882	0.004966	ISLLLIESWL
15.2	1185.698212	0.007636	TVLNPAFLRR
14.5	1185.712128	-0.006280	SIWLSGLLGIK
14.5	1185.708084	-0.002236	ISASALLKQQK

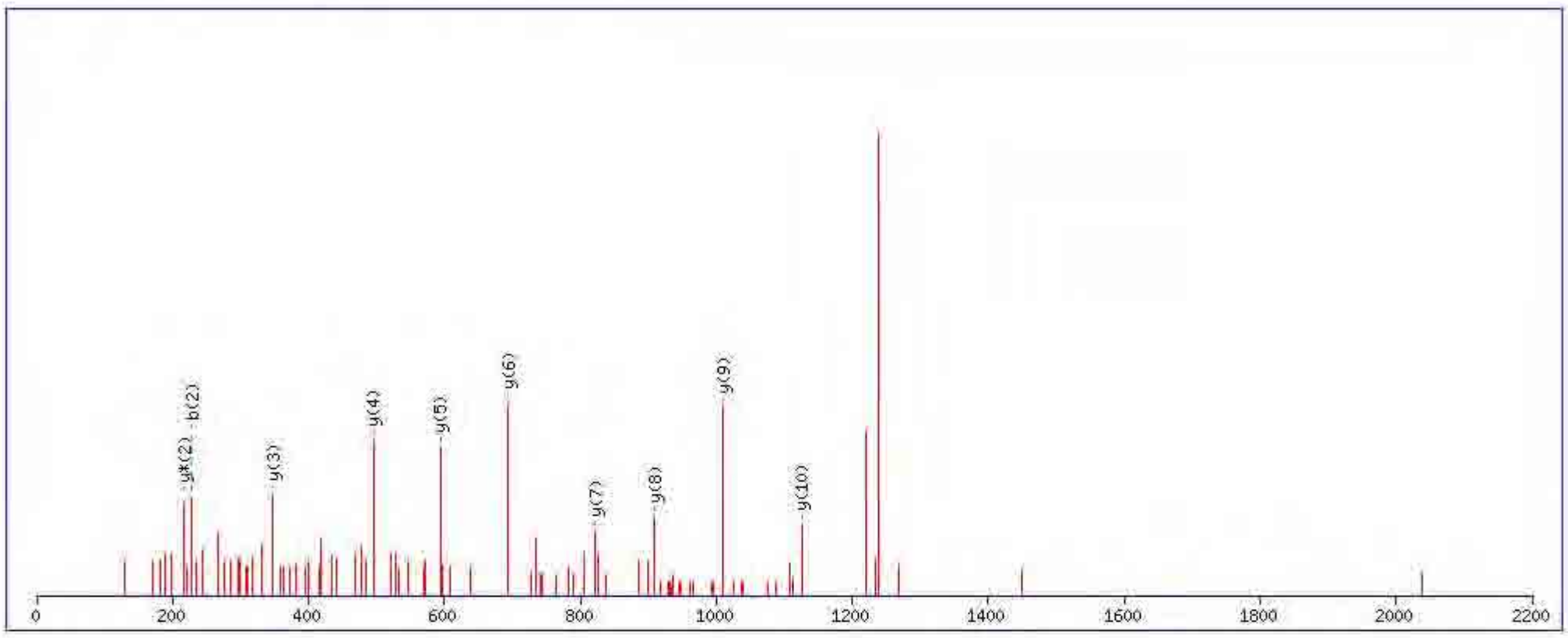
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTSEVVFNSK**
Found in **LEG7_HUMAN**, Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2

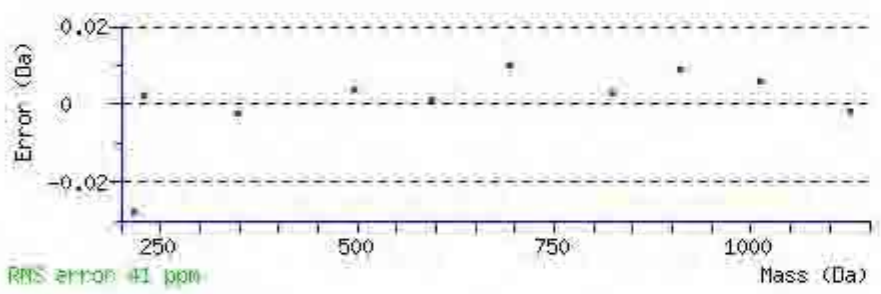
Match to Query 8412: 1237.629188 from(619.821870,2+) rtinseconds(1395) index(6507)
Title: Locus:1.1.1.1531.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

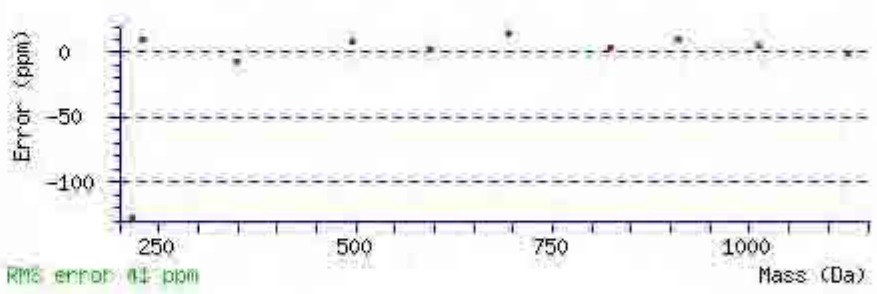
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1237.619034
Ions Score: 75 **Expect:** 3.7e-006
Matches : 10/100 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	229.118283	115.062779			211.107718	106.057497	D	*1125.542244*	563.274760	1108.515695	554.761486	1107.531679	554.269477	10
3	330.165962	165.586619			312.155397	156.581336	T	*1010.515301*	505.761288	993.488752	497.248014	992.504736	496.756006	9
4	417.197990	209.102633			399.187425	200.097350	S	*909.467622*	455.237449	892.441073	446.724174	891.457057	446.232166	8
5	546.240583	273.623930			528.230018	264.618647	E	*822.435594*	411.721435	805.409045	403.208160	804.425029	402.716152	7
6	645.308997	323.158137			627.298432	314.152854	V	*693.393001*	347.200138	676.366452	338.686864	675.382436	338.194856	6
7	744.377411	372.692343			726.366846	363.687061	V	*594.324587*	297.665932	577.298038	289.152657	576.314022	288.660649	5
8	891.445825	446.226550			873.435260	437.221268	F	*495.256173*	248.131724	478.229624	239.618450	477.245608	239.126442	4
9	1005.488752	503.248014	988.462203	494.734739	987.478187	494.242731	N	*348.187759*	174.597517	331.161210	166.084243	330.177194	165.592235	3
10	1092.520780	546.764028	1075.494231	538.250753	1074.510215	537.758745	S	234.144832	117.576054	217.118283	109.062779	216.134267	108.570771	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDTSEVVFNSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.5	1237.619034	0.010154	LDTSEVVFNSK
16.5	1237.634293	-0.005105	SFIFVDPREL
14.3	1237.622406	0.006782	LCLSTPSSSTVK
9.8	1237.619049	0.010139	IDVPPTANTPTP
8.9	1237.637650	-0.008462	LVKYCQSGLDI
8.5	1237.630249	-0.001061	QERLSPEVAPP
5.5	1237.619049	0.010139	IDVPPTANTPTP
5.5	1237.619049	0.010139	IDVPPTANTPTP
5.5	1237.634293	-0.005105	LDFVVRYETP
5.5	1237.619019	0.010169	LKPEGAPEPEGV

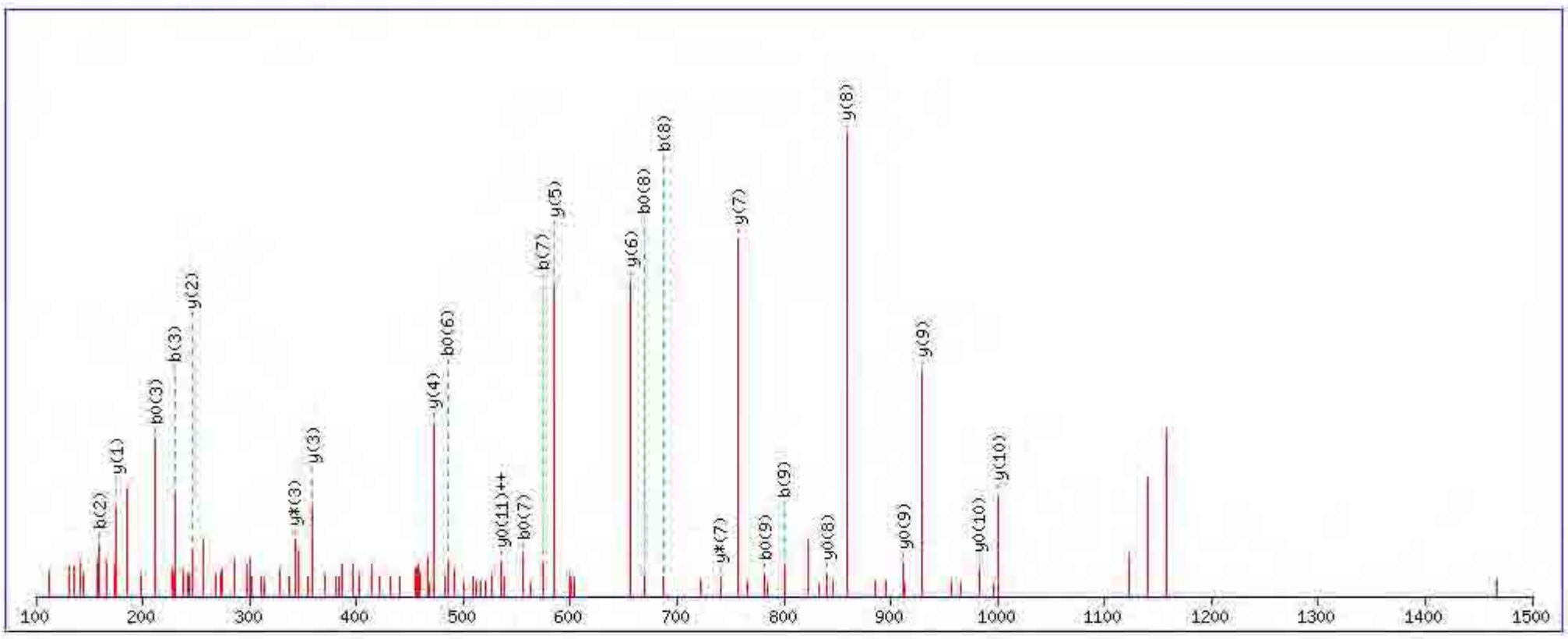
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAATTAILIAR**
Found in **GDN_HUMAN**, Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1

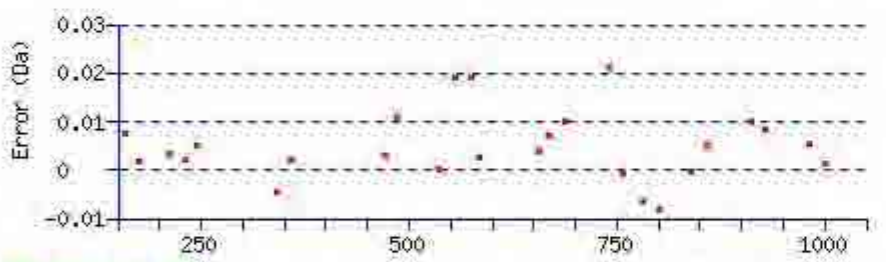
Match to Query 6585: 1157.680668 from(579.847610,2+) rtinseconds(1440) index(6961)
Title: Locus:1.1.1.1556.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

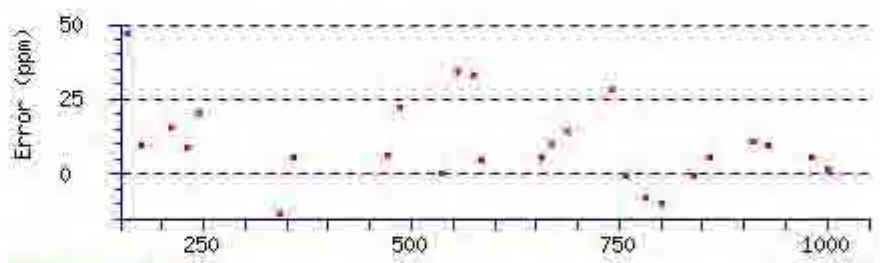
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1157.676788
Ions Score: 89 Expect: 5.8e-008
Matches : 26/96 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							12
2	159.076418	80.041847	141.065853	71.036564	S	1087.646986	544.327131	1070.620437	535.813857	1069.636421	535.321849	11
3	230.113532	115.560404	212.102967	106.555121	A	1000.614958	500.811117	983.588409	492.297843	982.604393	491.805835	10
4	301.150646	151.078961	283.140081	142.073679	A	929.577844	465.292560	912.551295	456.779286	911.567279	456.287278	9
5	402.198325	201.602801	384.187760	192.597518	T	858.540730	429.774003	841.514181	421.260729	840.530165	420.768721	8
6	503.246004	252.126640	485.235439	243.121358	T	757.493051	379.250164	740.466502	370.736889	739.482486	370.244881	7
7	574.283118	287.645197	556.272553	278.639915	A	656.445372	328.726324	639.418823	320.213050			6
8	687.367182	344.187229	669.356617	335.181947	I	585.408258	293.207767	568.381709	284.694493			5
9	800.451246	400.729261	782.440681	391.723979	L	472.324194	236.665735	455.297645	228.152461			4
10	913.535310	457.271293	895.524745	448.266011	I	359.240130	180.123703	342.213581	171.610429			3
11	984.572424	492.789850	966.561859	483.784568	A	246.156066	123.581671	229.129517	115.068397			2
12					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ASAATTAILIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.4	1157.676788	0.003880	ASAATTAILIAR
17.9	1157.676804	0.003864	TSIGILAAAVSR
14.4	1157.684189	-0.003521	LMDLTLLLAR
12.4	1157.669601	0.011067	APFIELLPVK
10.6	1157.680817	-0.000149	GTAALPYPLKK
8.6	1157.676804	0.003864	VTNSTLAAIIR
8.4	1157.680832	-0.000164	FPVKPADLKK
8.4	1157.676788	0.003880	LKETLAQLSR
7.2	1157.669617	0.011051	EFPTVPLVKL
6.6	1157.688034	-0.007366	LTLALSGTRAR

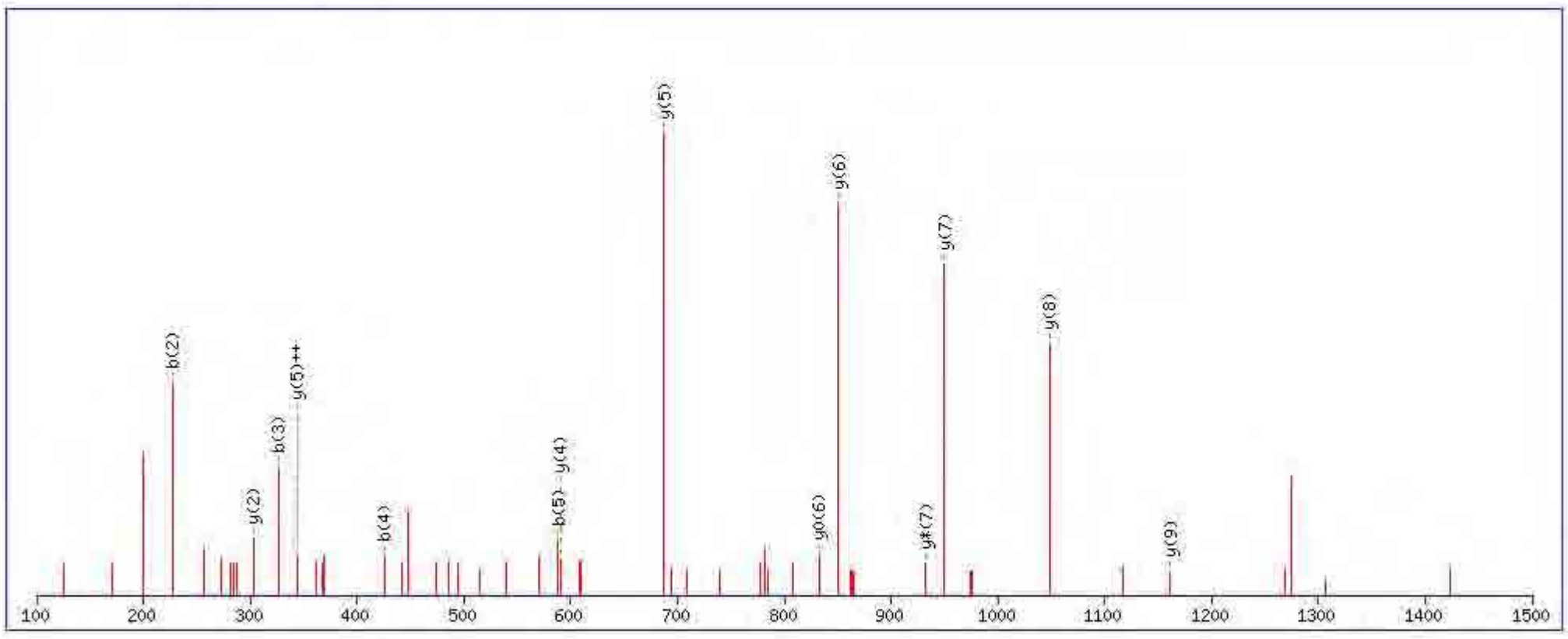
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLVVYPWTQR**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

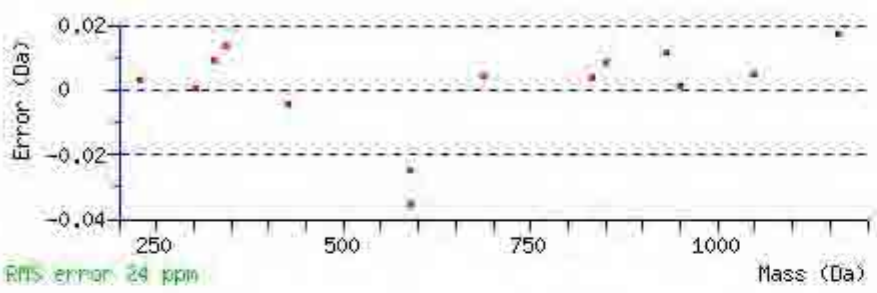
Match to Query 8972: 1273.727508 from(637.871030,2+) rtinseconds(2022) index(13326)
Title: Locus:1.1.1.1870.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

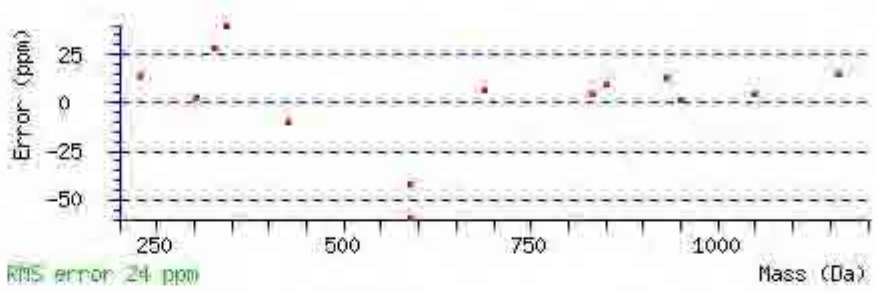
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1273.718292
Ions Score: 36 **Expect:** 0.0054
Matches : 14/74 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							10
2	227.175404	114.091340					L	*1161.641507*	581.324392	1144.614958	572.811117	1143.630942	572.319109	9
3	326.243818	163.625547					V	*1048.557443*	524.782360	1031.530894	516.269085	1030.546878	515.777077	8
4	425.312232	213.159754					V	*949.489029*	475.248153	932.462480	466.734878	931.478464	466.242870	7
5	588.375561	294.691419					Y	*850.420615*	425.713946	833.394066	417.200671	832.410050	416.708663	6
6	685.428325	343.217801					P	*687.357286*	344.182281	670.330737	335.669007	669.346721	335.176999	5
7	871.507638	436.257457					W	*590.304522*	295.655899	573.277973	287.142625	572.293957	286.650617	4
8	972.555317	486.781297			954.544752	477.776014	T	404.225209	202.616243	387.198660	194.102968	386.214644	193.610960	3
9	1100.613895	550.810586	1083.587346	542.297311	1082.603330	541.805303	Q	*303.177530*	152.092403	286.150981	143.579129			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLVVYPWTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	1273.718292	0.009216	LLVVYPWTQR
11.1	1273.739410	-0.011902	LLSLFLRGSAPT
10.4	1273.739395	-0.011887	ILLQIYEVQR
10.0	1273.739426	-0.011918	IIVTDLPFGKR
10.0	1273.739395	-0.011887	IPVLYEQLKR
9.4	1273.728180	-0.000672	IIGIPSPSSLFK
9.1	1273.731522	-0.004014	LLPLSMEAKIK
8.8	1273.716949	0.010559	IIVELVEFISP
8.8	1273.728180	-0.000672	ILVQYGADLLAV
8.8	1273.728195	-0.000687	LIVTQTPPYVK

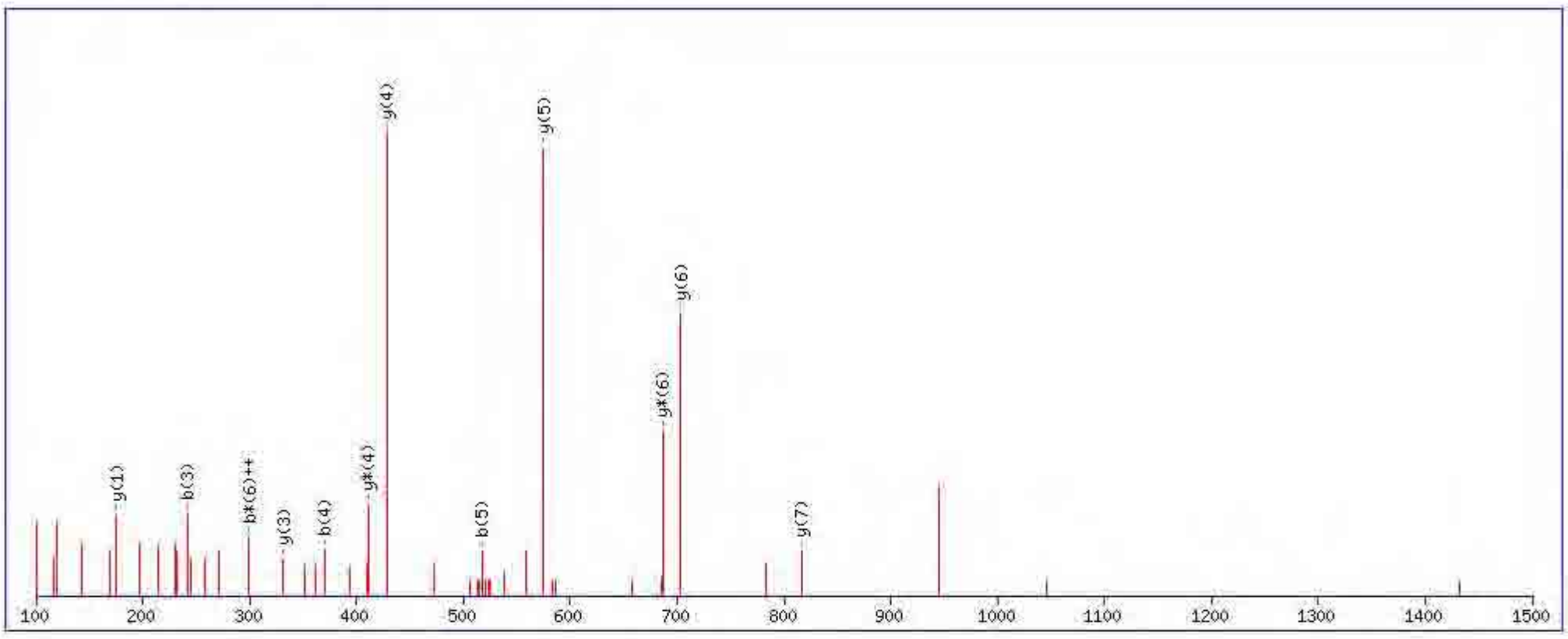
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **H2A1A_HUMAN**, Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3

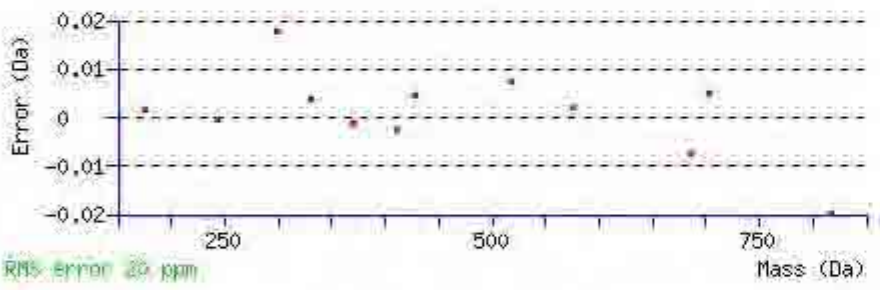
Match to Query 2796: 943.526468 from(472.770510,2+) rtinseconds(1498) index(7596)
Title: Locus:1.1.1.1587.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

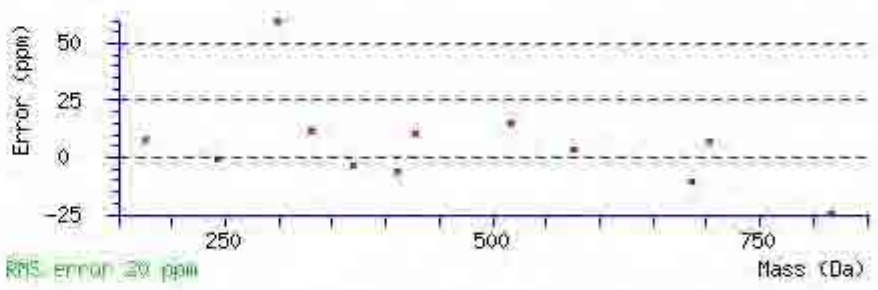
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 943.523956
Ions Score: 55 **Expect:** 0.00063
Matches : 12/58 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	873.494114	437.250695	856.467565	428.737421	8
3	242.149918	121.578597			L	*816.472650*	408.739963	799.446101	400.226689	7
4	370.208496	185.607886	353.181947	177.094612	Q	*703.388586*	352.197931	686.362037	343.684657	6
5	517.276910	259.142093	500.250361	250.628819	F	*575.330008*	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	*428.261594*	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	*331.208830*	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	232.140416	116.573846	215.113867	108.060571	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of AGLQFPVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.6	943.523956	0.002512	AGLQFPVGR
33.6	943.527298	-0.000830	QIQACLLR
33.6	943.519897	0.006571	QLKAQNSR
33.6	943.535172	-0.008704	QPKPFRR
26.9	943.533829	-0.007361	KIGEVSSPK
24.9	943.533813	-0.007345	KLGEEQLK
23.6	943.533813	-0.007345	QIKEAIDK
23.6	943.533813	-0.007345	QLKEVAEK
21.5	943.533844	-0.007376	LKGEGVTPK
19.5	943.527313	-0.000845	GLAKGMPVR

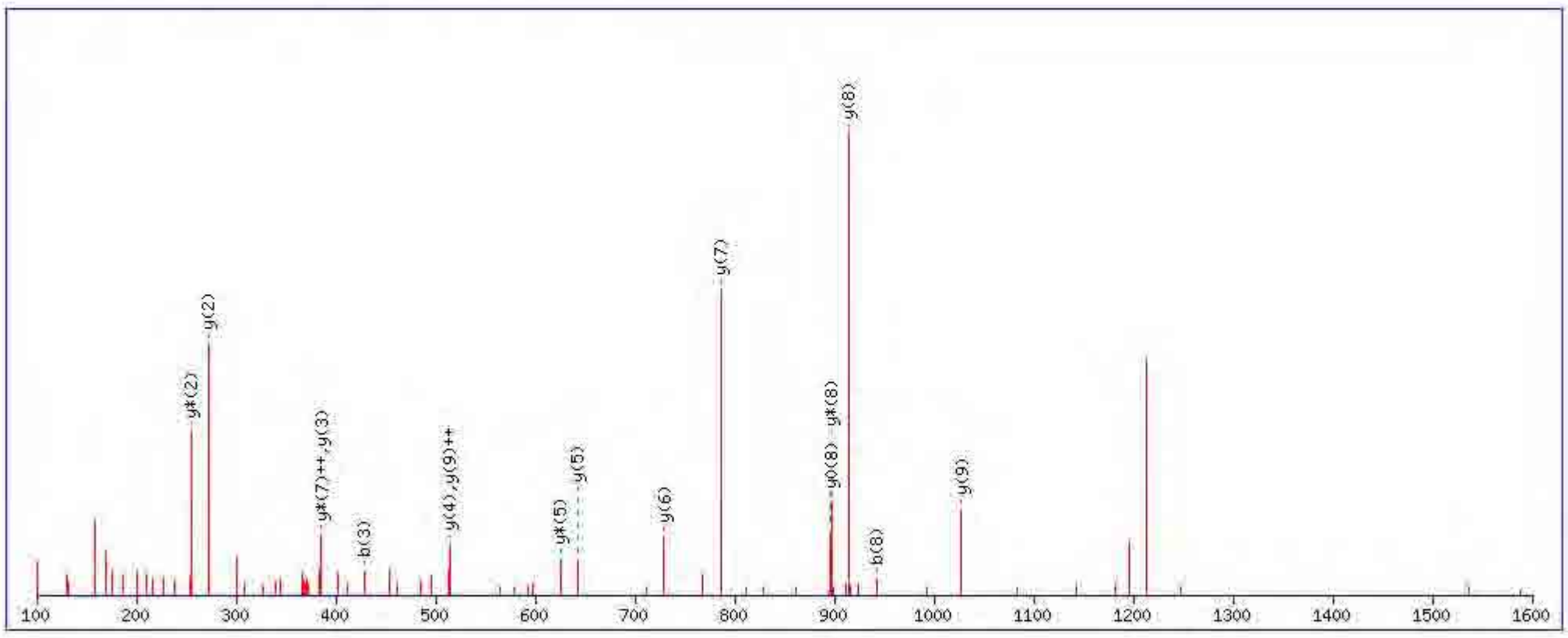
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

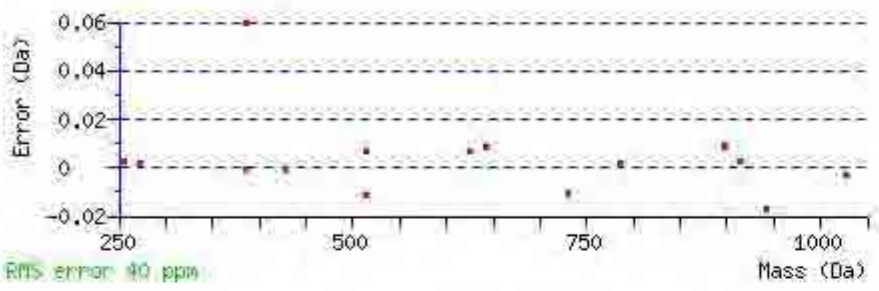
Match to Query 7914: 1212.635168 from(607.324860,2+) rtinseconds(1374) index(6303)
Title: Locus:1.1.1.1520.15
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

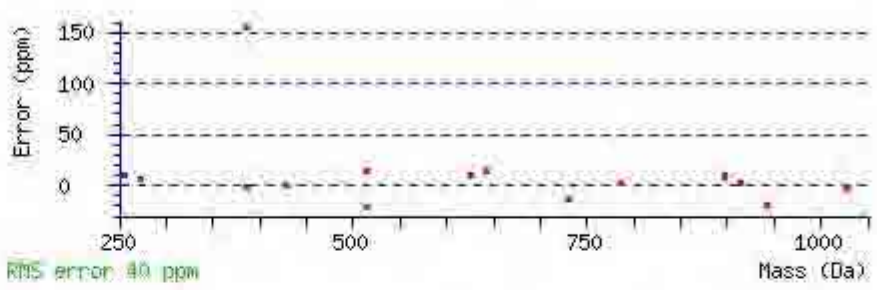
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1212.625107
Ions Score: 67 **Expect:** 4.4e-005
Matches : 16/90 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							10
2	300.170653	150.588965					L	*1027.553085*	514.280181	1010.526536	505.766906	1009.542520	505.274898	9
3	**428.229231**	214.618254	411.202682	206.104979			Q	*914.469021*	457.738148	897.442472	449.224874	896.458456	448.732866	8
4	485.250695	243.128986	468.224146	234.615711			G	*786.410443*	393.708860	769.383894	385.195585	768.399878	384.703577	7
5	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	S	*729.388979*	365.198128	712.362430	356.684853	711.378414	356.192845	6
6	700.341301	350.674289	683.314752	342.161014	682.330736	341.669006	Q	*642.356951*	321.682114	625.330402	313.168839	624.346386	312.676831	5
7	829.383894	415.195585	812.357345	406.682311	811.373329	406.190303	E	*514.298373*	257.652825	497.271824	249.139550	496.287808	248.647542	4
8	**942.467958**	471.737617	925.441409	463.224343	924.457393	462.732335	L	*385.255780*	193.131528	368.229231	184.618253			3
9	1039.520722	520.263999	1022.494173	511.750724	1021.510157	511.258716	P	*272.171716*	136.589496	255.145167	128.076221			2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WLQGSQELPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.6	1212.625107	0.010061	WLQGSQELPR
26.7	1212.646225	-0.011057	GELKATAPASPR
18.9	1212.646225	-0.011057	GELKATAPASPR
16.8	1212.646240	-0.011072	EGQGIKTDIPR
15.8	1212.636353	-0.001185	GTIRYHTPPR
13.7	1212.646240	-0.011072	VSPQEALPGRK
11.9	1212.640366	-0.005198	WIKHHPGEPL
11.6	1212.625107	0.010061	QWGSPEKLPR
11.4	1212.635010	0.000158	TSEAPILTPPR
11.3	1212.628479	0.006689	ALDPPMRLPR

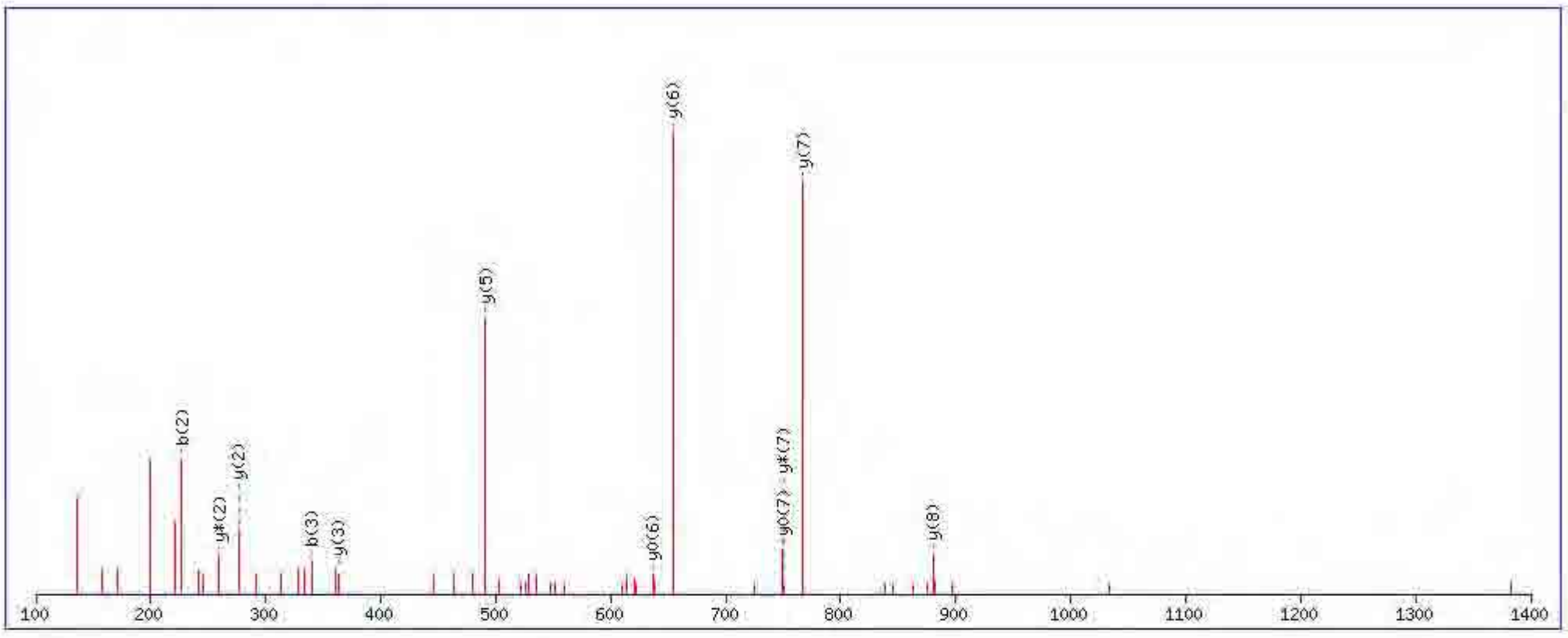
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYGASTR**
Found in **KV113_HUMAN**, Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1

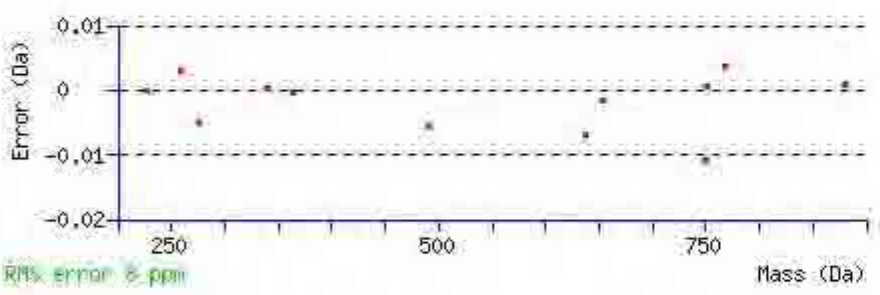
Match to Query 3514: 992.570728 from(497.292640,2+) rtinseconds(1319) index(5732)
Title: Locus:1.1.1.1490.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

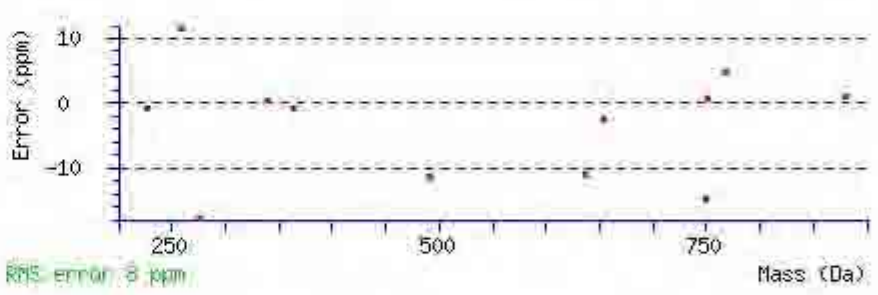
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 992.565460
Ions Score: 40 **Expect:** 0.0077
Matches : 12/66 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*880.488694*	440.747985	863.462145	432.234711	862.478129	431.742703	8
3	340.259468	170.633372			I	*767.404630*	384.205953	750.378081	375.692679	749.394065	375.200671	7
4	503.322797	252.165036			Y	*654.320566*	327.663921	637.294017	319.150647	636.310001	318.658639	6
5	560.344261	280.675769			G	*491.257237*	246.132256	474.230688	237.618982	473.246672	237.126974	5
6	631.381375	316.194326			A	434.235773	217.621524	417.209224	209.108250	416.225208	208.616242	4
7	718.413403	359.710340	700.402838	350.705057	S	*363.198659*	182.102967	346.172110	173.589693	345.188094	173.097685	3
8	819.461082	410.234179	801.450517	401.228897	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
9					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYGASTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	992.565460	0.005268	LLIYGASTR
31.5	992.565460	0.005268	LLIYGATSR
22.6	992.576706	-0.005978	LLLRHGADV
17.7	992.569504	0.001224	IILNAVFGF
17.7	992.566803	0.003925	ILPHWRR
17.7	992.565475	0.005253	ILPSVSHKP
17.7	992.565460	0.005268	LIINSSPHL
17.7	992.565460	0.005268	LILGPHESK
17.7	992.576706	-0.005978	LLIGDIHGR
17.7	992.565460	0.005268	LLLDPASHK

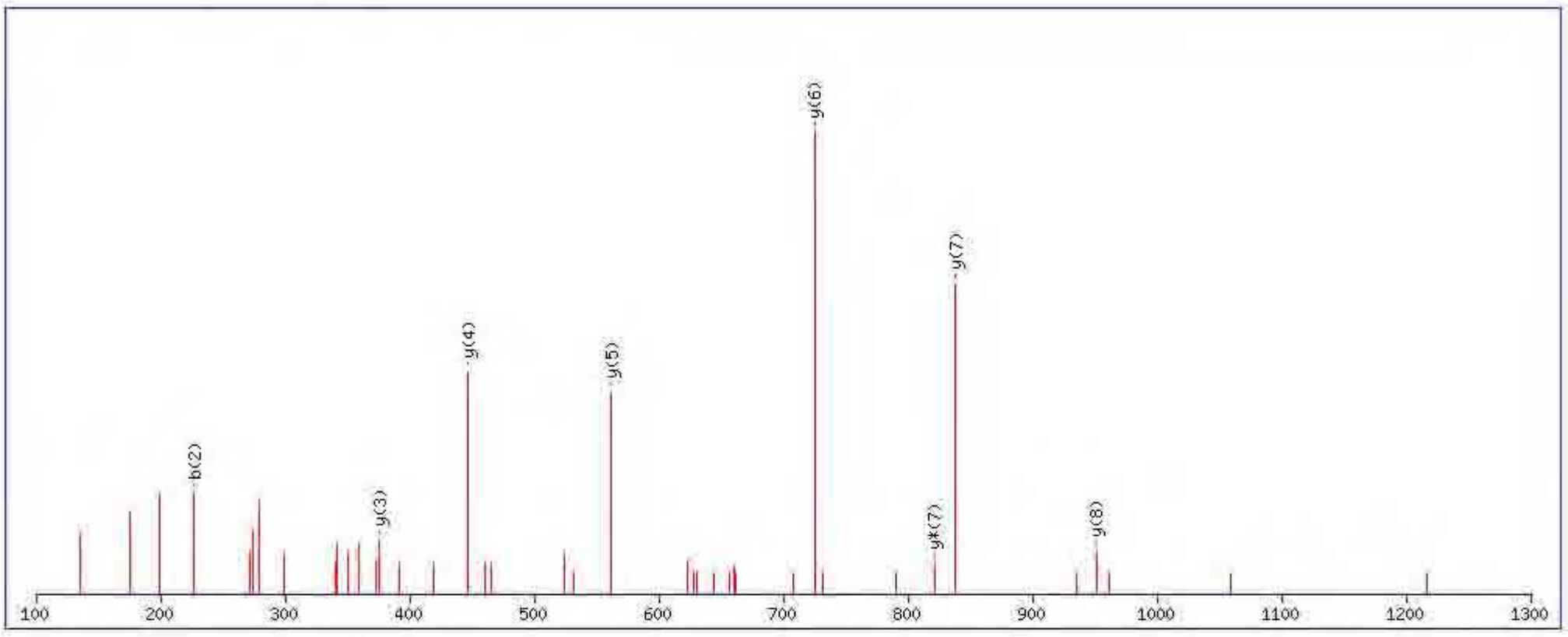
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **KV309_HUMAN**, Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1

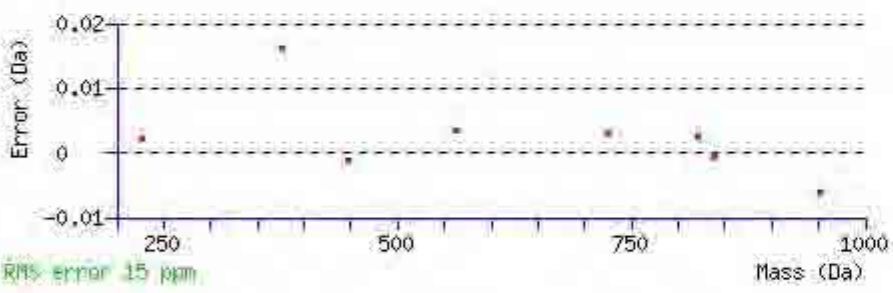
Match to Query 4668: 1063.573888 from(532.794220,2+) rtinseconds(1350) index(6069)
Title: Locus:1.1.1.1507.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

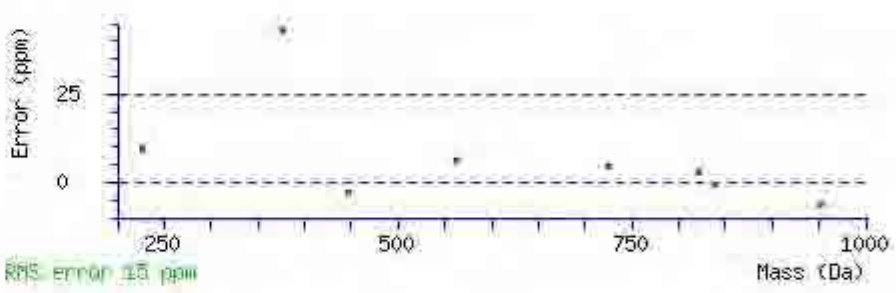
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1063.566177
Ions Score: 50 **Expect:** 0.0013
Matches : 8/70 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	227.175404	114.091340					L	*951.489421*	476.248348	934.462872	467.735074	933.478856	467.243066	8
3	340.259468	170.633372					I	*838.405357*	419.706316	821.378808	411.193042	820.394792	410.701034	7
4	503.322797	252.165036					Y	*725.321293*	363.164285	708.294744	354.651010	707.310728	354.159002	6
5	618.349740	309.678508			600.339175	300.673226	D	*562.257964*	281.632620	545.231415	273.119345	544.247399	272.627337	5
6	689.386854	345.197065			671.376289	336.191782	A	*447.231021*	224.119148	430.204472	215.605874	429.220456	215.113866	4
7	776.418882	388.713079			758.408317	379.707796	S	*376.193907*	188.600591	359.167358	180.087317	358.183342	179.595309	3
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	289.161879	145.084577	272.135330	136.571303			2
9							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDASNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1063.566177	0.007711	LLIYDASNR
25.1	1063.573593	0.000295	LLPNFGKML
25.0	1063.566193	0.007695	ELPPATPSPR
18.5	1063.577438	-0.003550	PPPPALRPR
18.1	1063.581451	-0.007563	ILTNWYVR
17.2	1063.577438	-0.003550	PPPPALRPR
16.9	1063.566193	0.007695	PEPPEKPVR
16.9	1063.581467	-0.007579	PLPIPWGPR
16.9	1063.577438	-0.003550	PLPRPAPPR
16.8	1063.566223	0.007665	LLPPGPPPGR

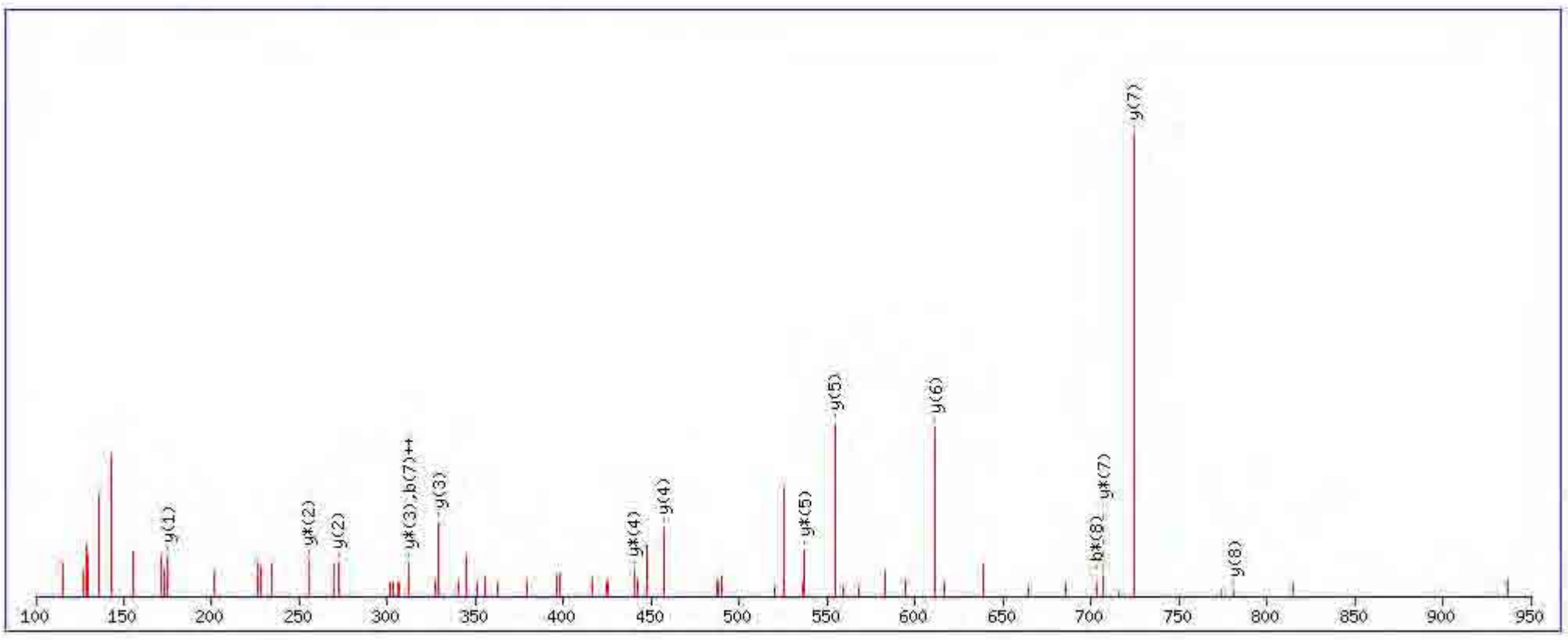
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PGLGPQGPR**
Found in **IPPK_HUMAN**, Inositol-pentakisphosphate 2-kinase OS=Homo sapiens GN=IPPK PE=1 SV=1

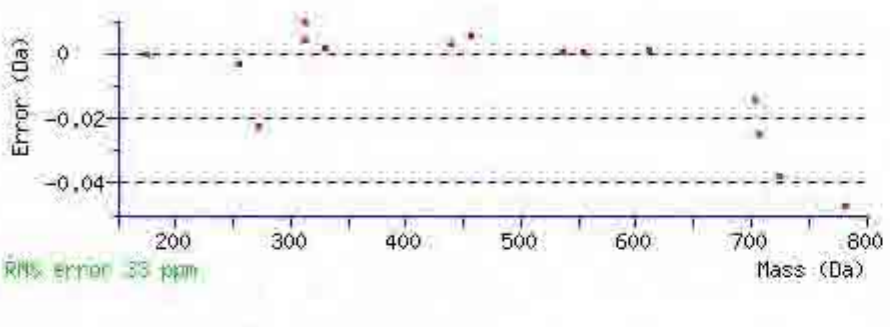
Match to Query 2071: 893.477768 from(447.746160,2+) rtinseconds(710) index(1289)
Title: Locus:1.1.1.1152.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

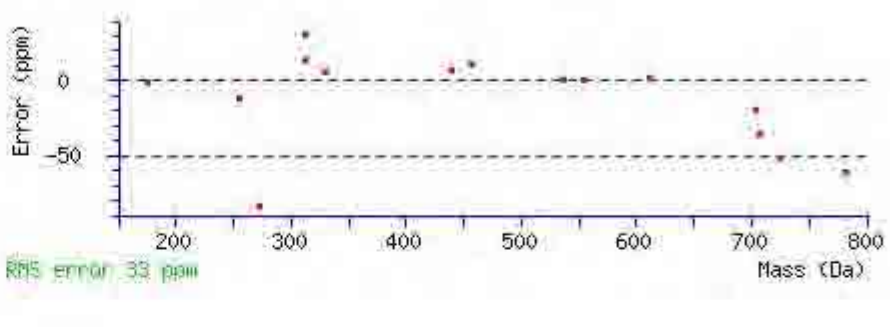
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 893.471924
Variable modifications:
P1 : Oxidation (P)
Ions Score: 47 **Expect:** 0.0025
Matches : 15/54 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.054955	57.531116			P					9
2	171.076419	86.041847			G	*781.431514*	391.219395	764.404965	382.706121	8
3	284.160483	142.583879			L	*724.410050*	362.708663	707.383501	354.195389	7
4	341.181947	171.094611			G	*611.325986*	306.166631	594.299437	297.653357	6
5	438.234711	219.620994			P	*554.304522*	277.655899	537.277973	269.142625	5
6	566.293289	283.650283	549.266740	275.137008	Q	*457.251758*	229.129517	440.225209	220.616243	4
7	623.314753	312.161015	606.288204	303.647740	G	*329.193180*	165.100228	312.166631	156.586953	3
8	720.367517	360.687397	703.340968	352.174122	P	*272.171716*	136.589496	255.145167	128.076221	2
9					R	*175.118952*	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of PGLGPQGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	893.471924	0.005844	PGLGPQGPR
41.4	893.471924	0.005844	GLPGPQGPR
41.4	893.471924	0.005844	GPPGPKGPR
28.3	893.471924	0.005844	GPPGKPGPR
16.3	893.471924	0.005844	PGPGPGRPK
16.1	893.471924	0.005844	GLPGPQGPR
16.1	893.471924	0.005844	GPPGPKGPR
15.3	893.471924	0.005844	GLPGPPGQR
15.3	893.471924	0.005844	GLPGPRGPQ
15.3	893.471924	0.005844	GPPGPPGKR

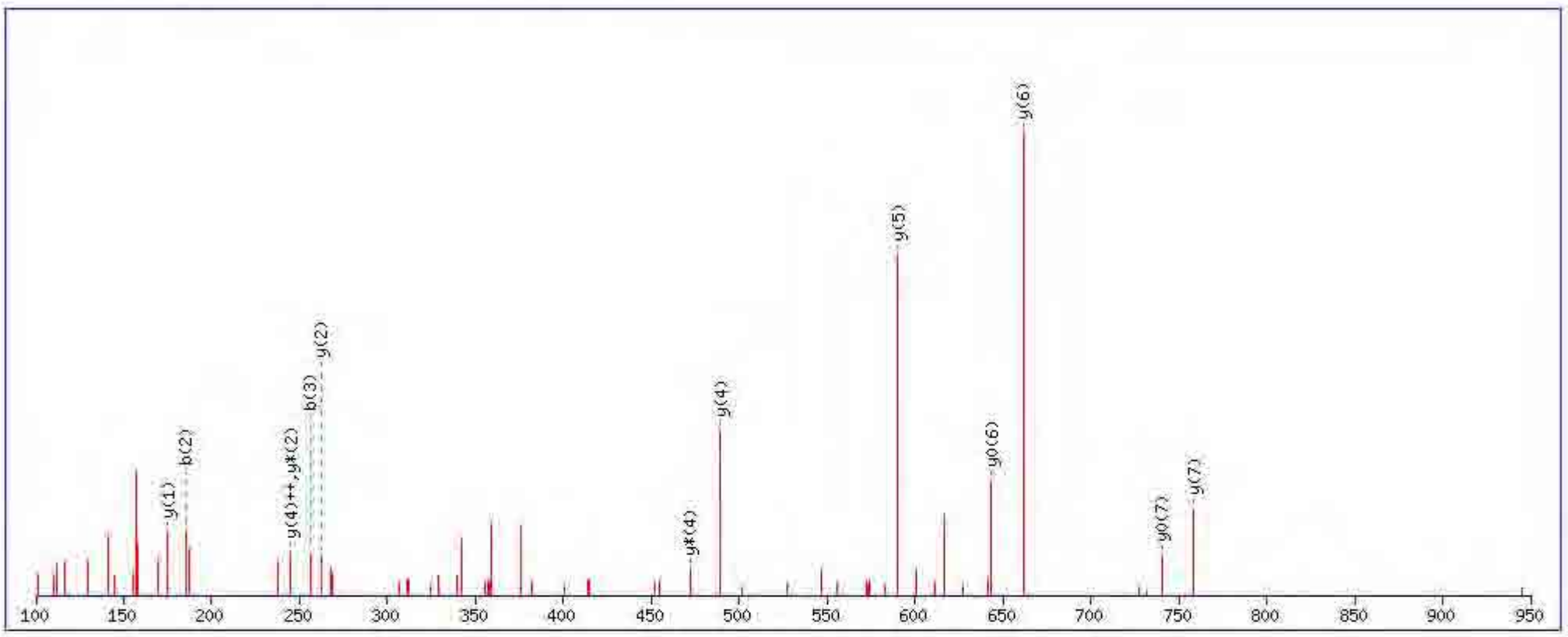
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPATVQSR**
Found in **K1C23_HUMAN**, Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2

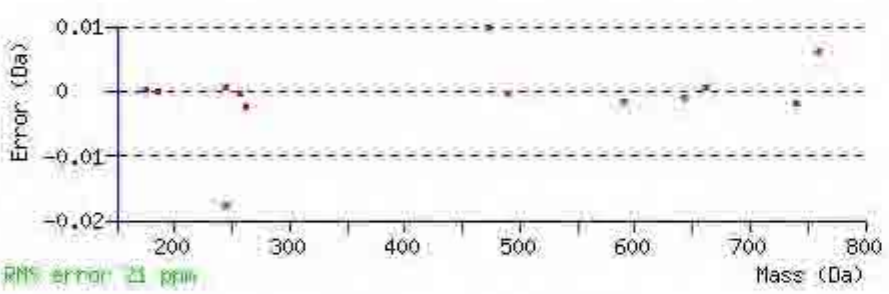
Match to Query 1254: 844.444008 from(423.229280,2+) rtinseconds(437) index(337)
Title: Locus:1.1.1.1004.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

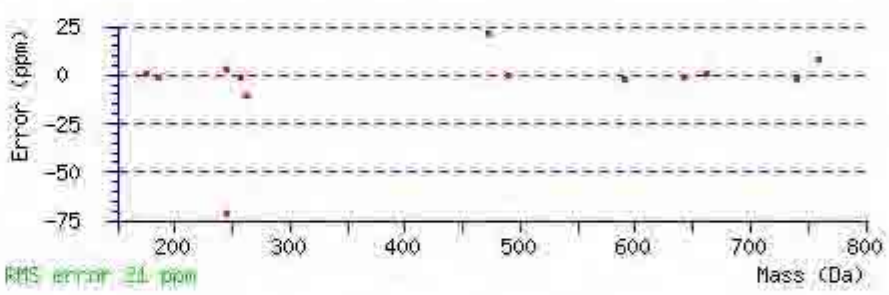
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 844.440277
Ions Score: 46 **Expect:** 0.006
Matches : 13/72 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	185.092068	93.049672			167.081503	84.044389	P	758.415529	379.711403	741.388980	371.198128	740.404964	370.706120	7
3	256.129182	128.568229			238.118617	119.562947	A	661.362765	331.185021	644.336216	322.671746	643.352200	322.179738	6
4	357.176861	179.092068			339.166296	170.086786	T	590.325651	295.666464	573.299102	287.153189	572.315086	286.661181	5
5	456.245275	228.626275			438.234710	219.620993	V	489.277972	245.142624	472.251423	236.629350	471.267407	236.137342	4
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	Q	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
7	671.335881	336.171579	654.309332	327.658304	653.325316	327.166296	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SPATVQSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.8	844.440277	0.003731	SPATVQSR
38.1	844.440277	0.003731	SVIGPNSR
30.9	844.440262	0.003746	SPATADKR
20.3	844.440262	0.003746	SPSSKRPS
18.1	844.440262	0.003746	SPASSLQR
18.0	844.451492	-0.007484	PAARATSR
17.6	844.440277	0.003731	SPSGTVAAR
15.6	844.451477	-0.007469	AIRENSR
15.6	844.451508	-0.007500	SPGSVRSR
15.6	844.440262	0.003746	SPGTEKAR

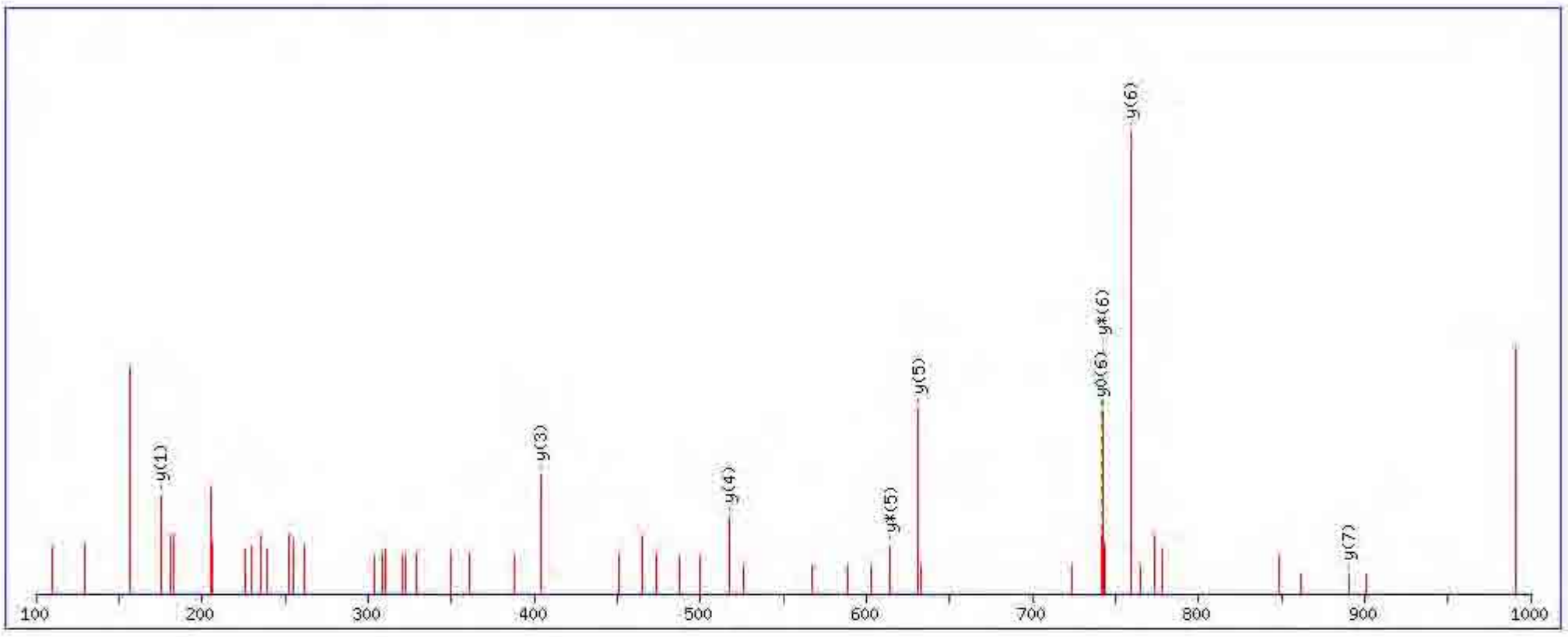
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMQNLNDR**
Found in **K1C10_HUMAN**, Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

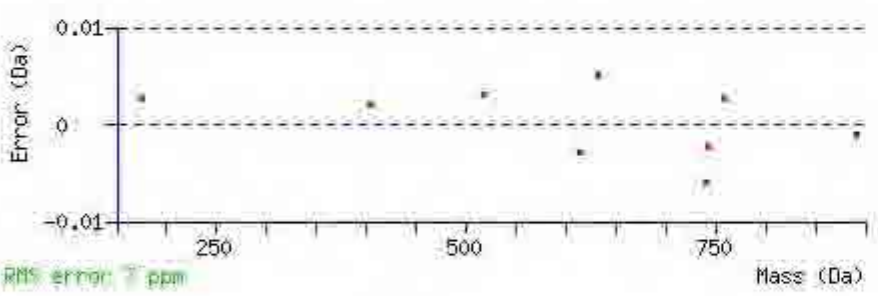
Match to Query 3459: 990.462648 from(496.238600,2+) rtinseconds(605) index(812)
Title: Locus:1.1.1.1095.6
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

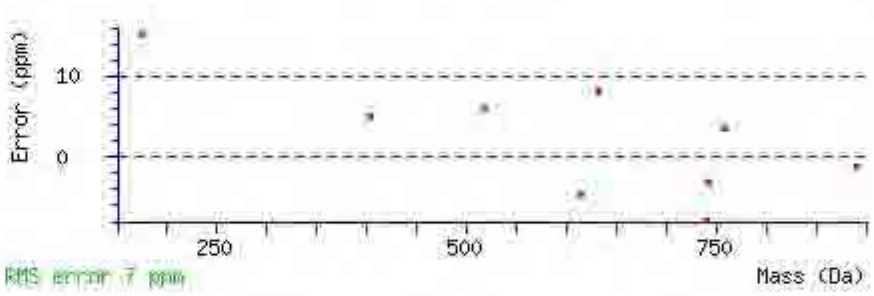
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 990.455261
Ions Score: 30 **Expect:** 0.018
Matches : 9/70 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	233.095440	117.051358			215.084875	108.046076	M	*890.414876*	445.711076	873.388327	437.197802	872.404311	436.705794	7
3	361.154018	181.080647	344.127469	172.567373	343.143453	172.075365	Q	*759.374391*	380.190834	742.347842	371.677559	741.363826	371.185551	6
4	475.196945	238.102111	458.170396	229.588836	457.186380	229.096828	N	*631.315813*	316.161545	614.289264	307.648270	613.305248	307.156262	5
5	588.281009	294.644143	571.254460	286.130868	570.270444	285.638860	L	*517.272886*	259.140081	500.246337	250.626806	499.262321	250.134798	4
6	702.323936	351.665606	685.297387	343.152332	684.313371	342.660324	N	*404.188822*	202.598049	387.162273	194.084774	386.178257	193.592766	3
7	817.350879	409.179078	800.324330	400.665803	799.340314	400.173795	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
8							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TMQNLNDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.2	990.455261	0.007387	TMQNLNDR
10.9	990.455276	0.007372	RQACTAQTP
9.4	990.461792	0.000856	TDSGNIDAAK
9.1	990.455261	0.007387	TMNQASPAR
7.6	990.459305	0.003343	TMPPTSWR
7.6	990.459305	0.003343	TMPPTSWR
7.3	990.461792	0.000856	SKTSLNPND
6.9	990.466507	-0.003859	RGTGQMEGR
6.5	990.465820	-0.003172	YVDPLAGAAD
6.5	990.469208	-0.006560	LMPVSAQTP

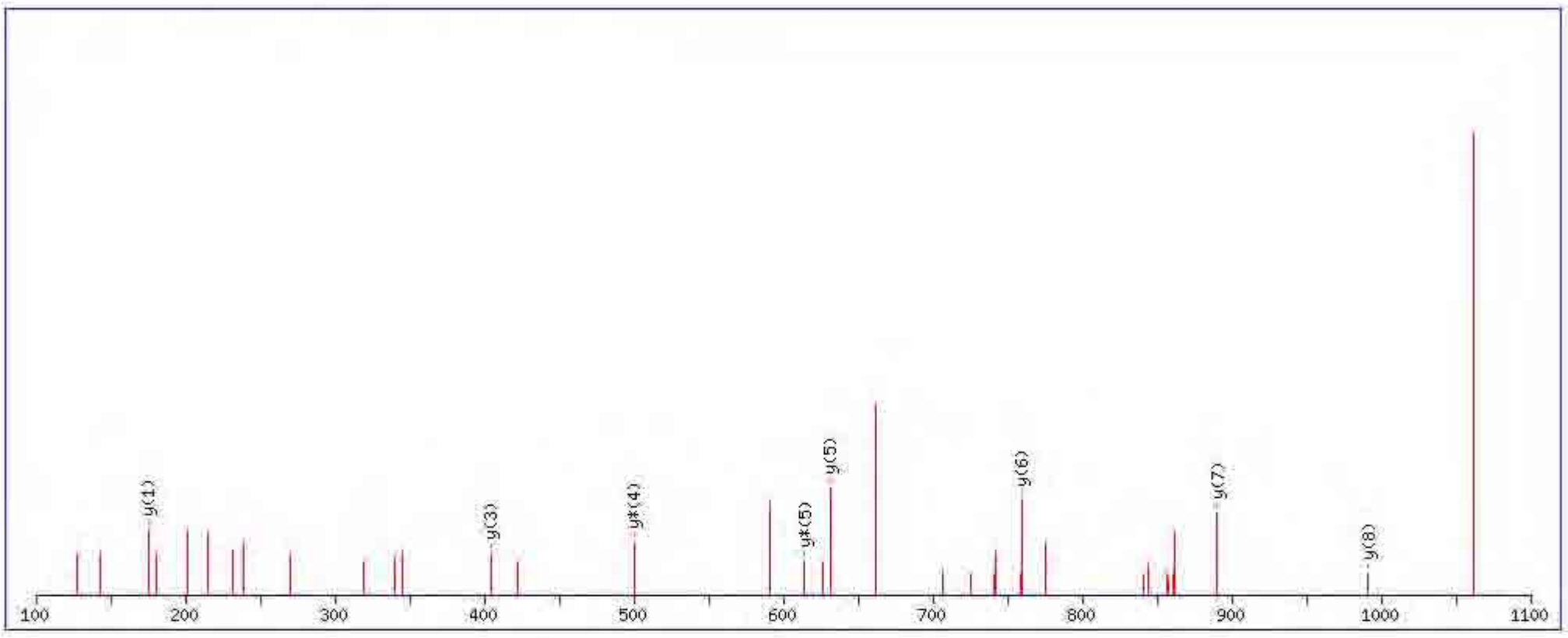
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATMQNLNDR**
Found in **K1C17_HUMAN**, Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2

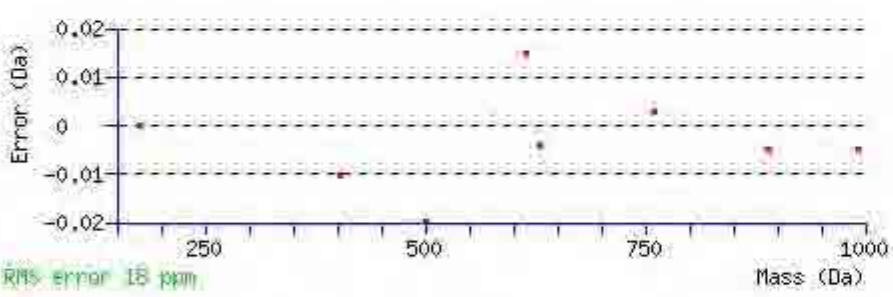
Match to Query 4632: 1061.500728 from(531.757640,2+) rtinseconds(701) index(1237)
Title: Locus:1.1.1.1147.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

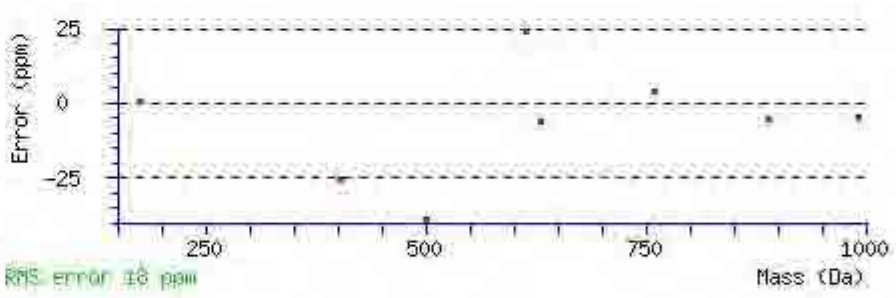
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1061.492371
Ions Score: 36 **Expect:** 0.044
Matches : 8/86 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							9
2	173.092069	87.049672			155.081504	78.044390	T	*991.462555*	496.234916	974.436006	487.721641	973.451990	487.229633	8
3	304.132554	152.569915			286.121989	143.564632	M	*890.414876*	445.711076	873.388327	437.197802	872.404311	436.705794	7
4	432.191132	216.599204	415.164583	208.085929	414.180567	207.593921	Q	*759.374391*	380.190834	742.347842	371.677559	741.363826	371.185551	6
5	546.234059	273.620668	529.207510	265.107393	528.223494	264.615385	N	*631.315813*	316.161545	614.289264	307.648270	613.305248	307.156262	5
6	659.318123	330.162700	642.291574	321.649425	641.307558	321.157417	L	517.272886	259.140081	500.246337	250.626807	499.262321	250.134799	4
7	773.361050	387.184163	756.334501	378.670888	755.350485	378.178880	N	*404.188822*	202.598049	387.162273	194.084774	386.178257	193.592766	3
8	888.387993	444.697634	871.361444	436.184360	870.377428	435.692352	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
9							R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of ATMQNLNDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1061.492371	0.008357	ATMQNLNDR
31.5	1061.498886	0.001842	EASLAETEGR
25.0	1061.498901	0.001827	ATDSGNIDAAK
20.1	1061.492386	0.008342	SPSPAPMRR
19.1	1061.506302	-0.005574	ATMPTGEEVK
13.0	1061.496384	0.004344	AELMWAEGR
11.9	1061.502930	-0.002202	ADPKYADLPG
11.3	1061.506287	-0.005559	ACLGSLQELE
10.5	1061.496429	0.004299	QCPFLGPPR
10.5	1061.498917	0.001811	GDDLDTSAIR

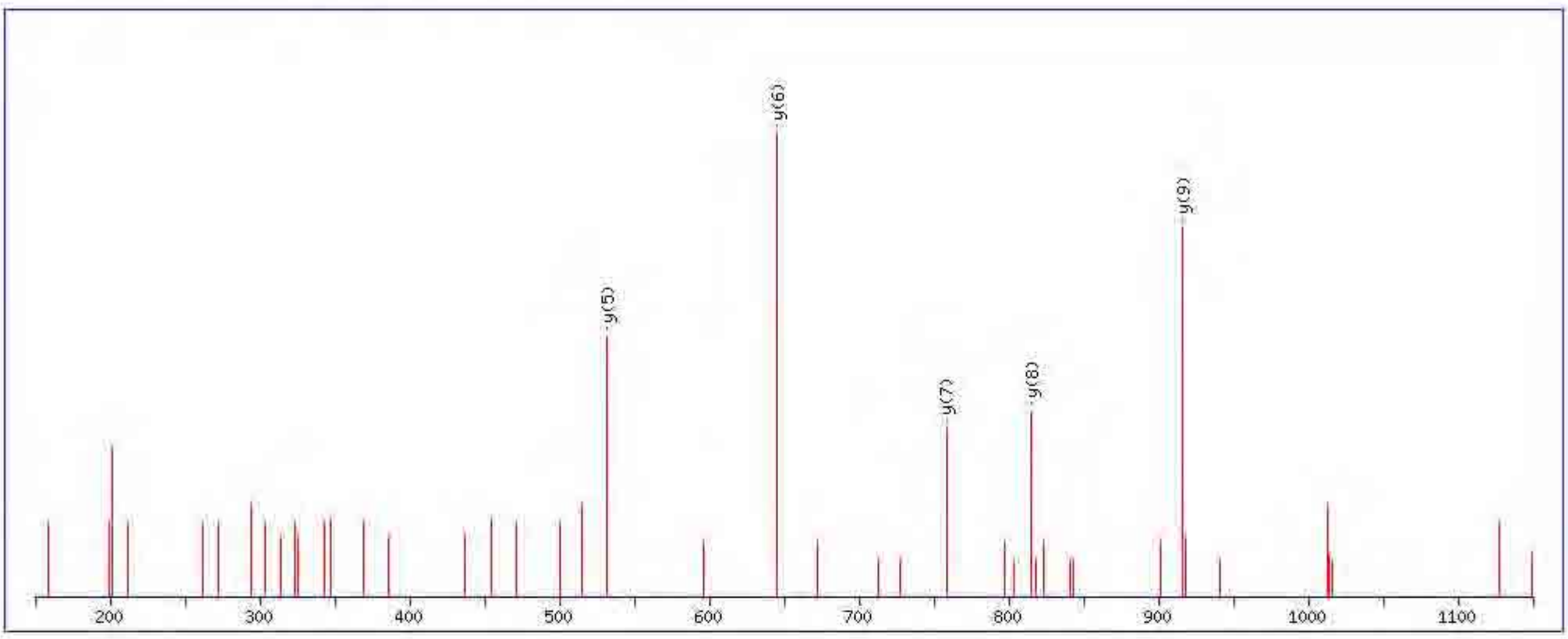
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVTGIITQGAR**
Found in **MFGM_HUMAN**, Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2

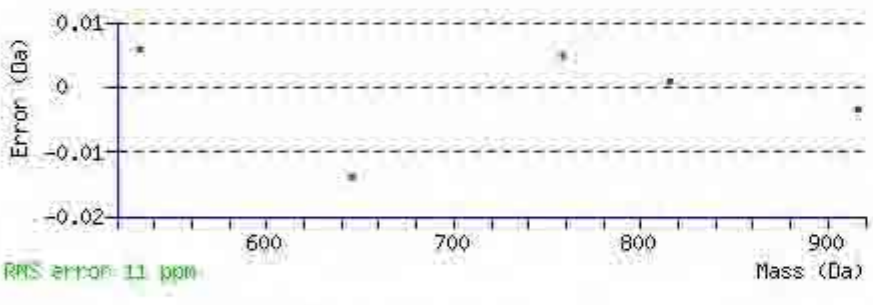
Match to Query 6199: 1143.632048 from(572.823300,2+) rtinseconds(1154) index(4297)
Title: Locus:1.1.1.1399.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

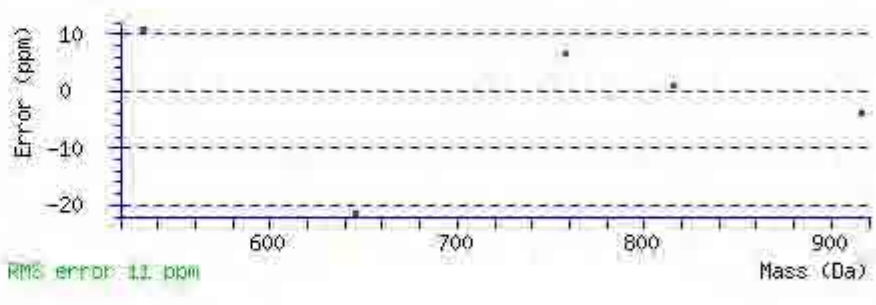
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1143.624786
Ions Score: 33 **Expect:** 0.0094
Matches : 5/98 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	229.118283	115.062780			211.107718	106.057497	V	1015.589472	508.298374	998.562923	499.785100	997.578907	499.293092	10
3	330.165962	165.586619			312.155397	156.581337	T	*916.521058*	458.764167	899.494509	450.250893	898.510493	449.758885	9
4	387.187426	194.097351			369.176861	185.092069	G	*815.473379*	408.240328	798.446830	399.727053	797.462814	399.235045	8
5	500.271490	250.639383			482.260925	241.634101	I	*758.451915*	379.729596	741.425366	371.216321	740.441350	370.724313	7
6	613.355554	307.181415			595.344989	298.176133	I	*645.367851*	323.187564	628.341302	314.674289	627.357286	314.182281	6
7	714.403233	357.705255			696.392668	348.699972	T	*532.283787*	266.645532	515.257238	258.132257	514.273222	257.640249	5
8	842.461811	421.734544	825.435262	413.221269	824.451246	412.729261	Q	431.236108	216.121692	414.209559	207.608418			4
9	899.483275	450.245276	882.456726	441.732001	881.472710	441.239993	G	303.177530	152.092403	286.150981	143.579129			3
10	970.520389	485.763833	953.493840	477.250558	952.509824	476.758550	A	246.156066	123.581671	229.129517	115.068397			2
11							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EVTGIITQGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	1143.624786	0.007262	EVTGIITQGAR
10.7	1143.628815	0.003233	KPPSGFKGTIP
10.7	1143.628815	0.003233	KPPSGFKGTIP
9.9	1143.628799	0.003249	FRDLLLPPSS
9.6	1143.638672	-0.006624	SAVELLISLAE
9.2	1143.624756	0.007292	GSNQLIEAKGK
9.2	1143.636002	-0.003954	SVPSILRSNR
8.9	1143.625641	0.006407	LCLGIMGGKPR
7.2	1143.624786	0.007262	GQTSASILPRV
7.2	1143.632156	-0.000108	MQKQLLPLAA

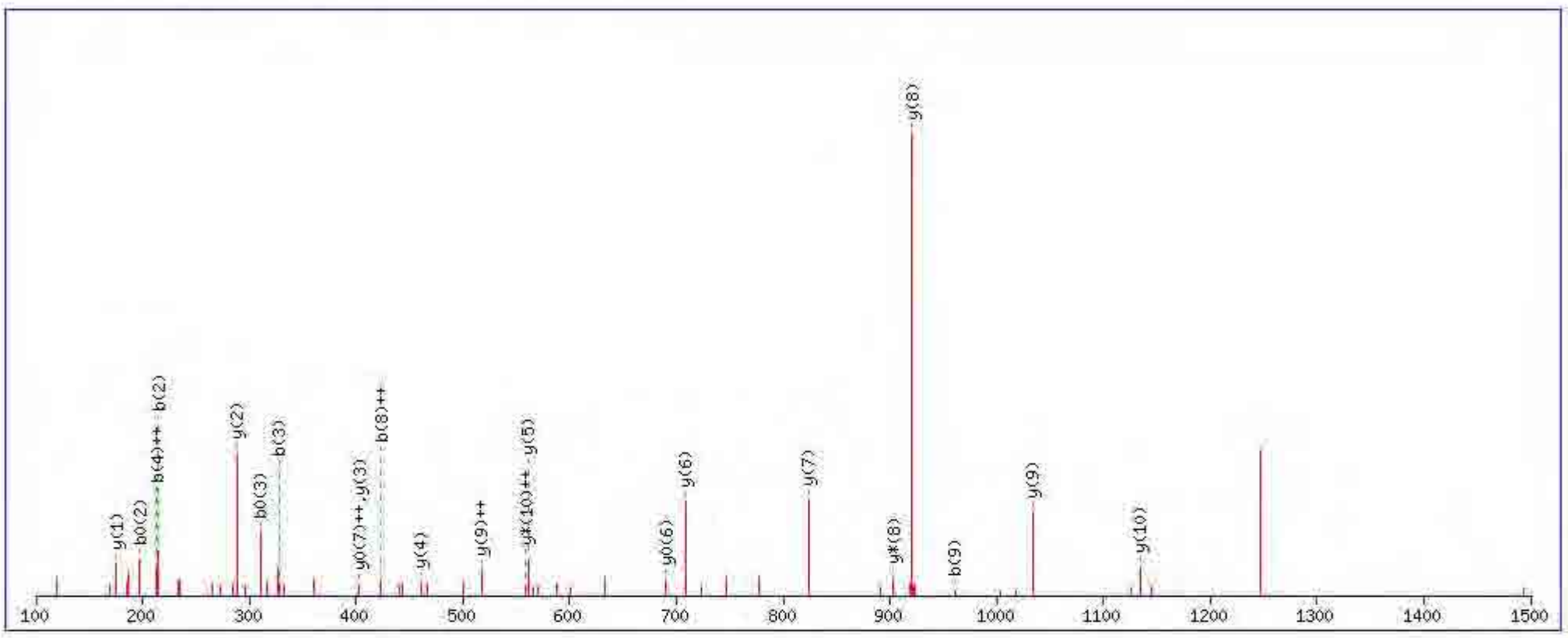
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITLPDFTGDLR**
Found in **LBP_HUMAN**, Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3

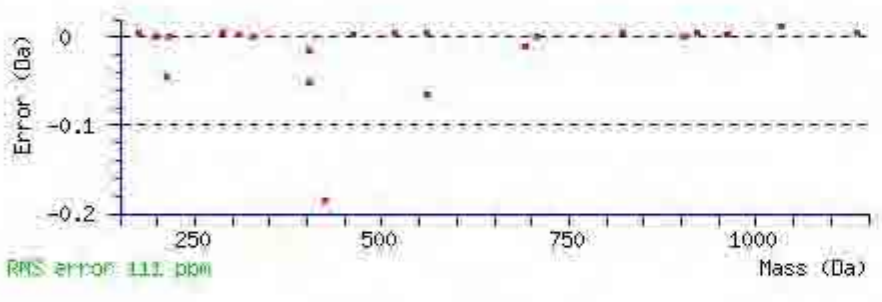
Match to Query 8554: 1246.667708 from(624.341130,2+) rtinseconds(2099) index(14352)
Title: Locus:1.1.1.1911.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

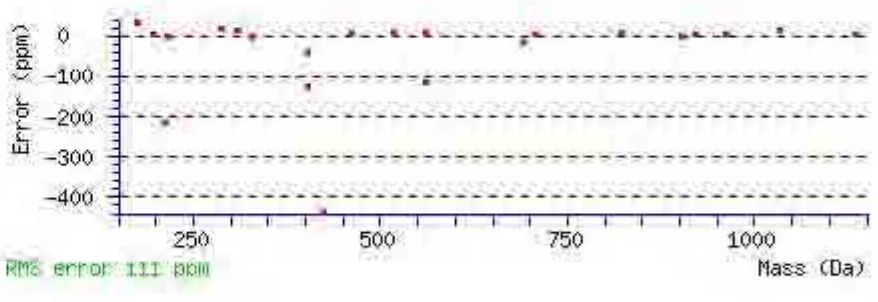
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1246.655762
Ions Score: 72 **Expect:** 1.1e-005
Matches : 22/94 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	1134.578966	567.793121	1117.552417	559.279847	1116.568401	558.787839	10
3	328.223083	164.615179	310.212518	155.609897	L	1033.531287	517.269282	1016.504738	508.756007	1015.520722	508.263999	9
4	425.275847	213.141561	407.265282	204.136279	P	920.447223	460.727249	903.420674	452.213975	902.436658	451.721967	8
5	540.302790	270.655033	522.292225	261.649750	D	823.394459	412.200868	806.367910	403.687593	805.383894	403.195585	7
6	687.371204	344.189240	669.360639	335.183957	F	708.367516	354.687396	691.340967	346.174122	690.356951	345.682114	6
7	788.418883	394.713079	770.408318	385.707797	T	561.299102	281.153189	544.272553	272.639915	543.288537	272.147907	5
8	845.440347	423.223812	827.429782	414.218529	G	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
9	960.467290	480.737283	942.456725	471.732000	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
10	1073.551354	537.279315	1055.540789	528.274032	L	288.203016	144.605146	271.176467	136.091871			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITLPDFTGDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.2	1246.655762	0.011946	ITLPDFTGDLR
19.7	1246.659119	0.008589	PTDTAMLTLLR
17.5	1246.678223	-0.010515	DVPPPRPLQGR
16.8	1246.655762	0.011946	PTPPGQPPISPK
13.3	1246.674362	-0.006654	PVMYAVALDLR
13.3	1246.659103	0.008605	LTPEIMKEVR
11.1	1246.655731	0.011977	LTIIQDPEYR
10.2	1246.656616	0.011092	LTLFMAVPPCR
10.1	1246.665634	0.002074	LTIKDLESIDT
8.9	1246.655777	0.011931	EVPVPPPVPPR

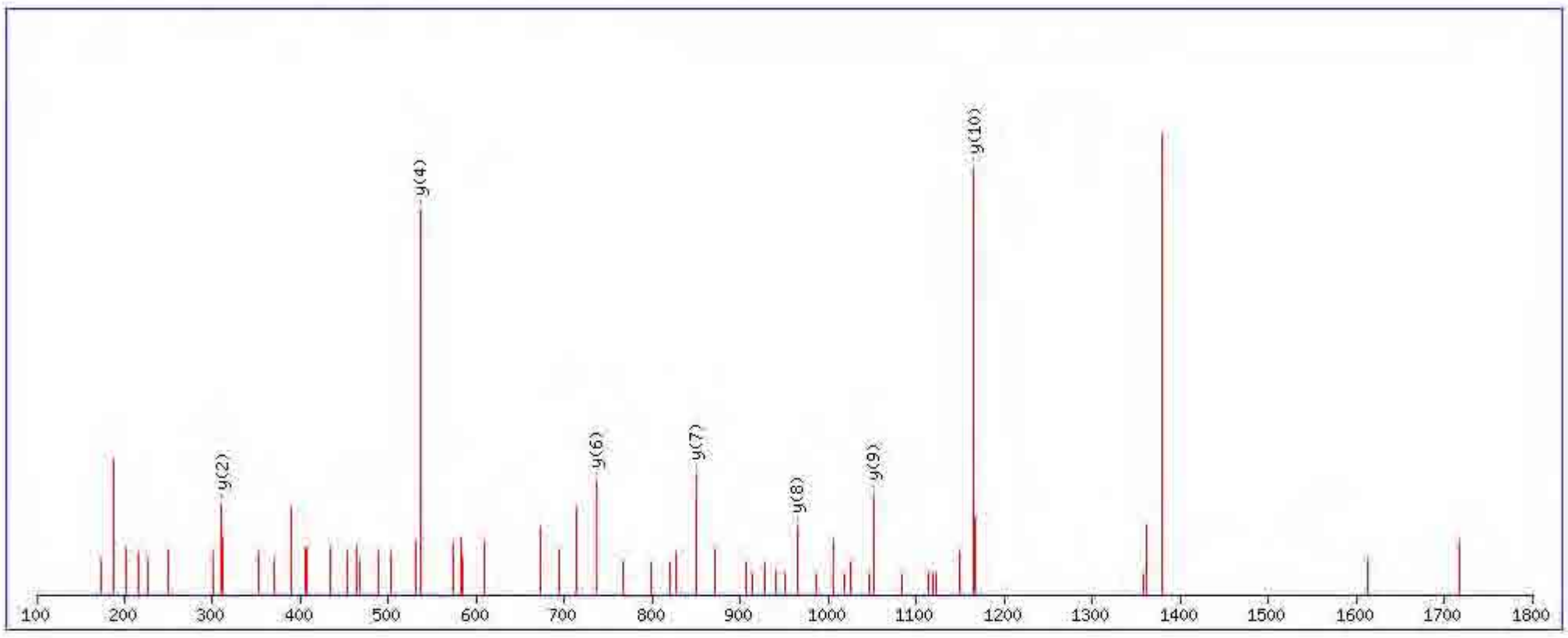
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TINSDISIPEYK**
Found in **SG2A1_HUMAN**, Mammaglobin-B OS=Homo sapiens GN=SCGB2A1 PE=1 SV=1

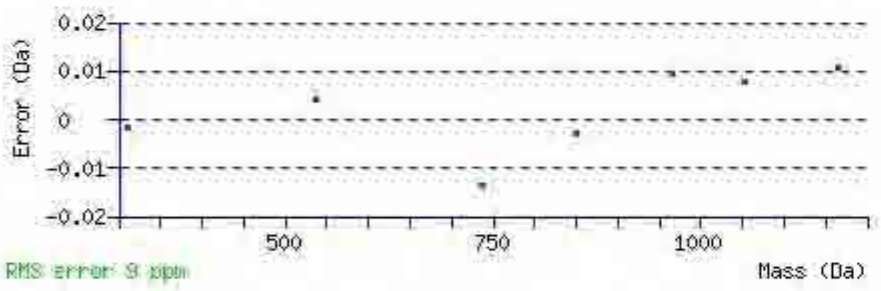
Match to Query 10587: 1378.706328 from(690.360440,2+) rtinseconds(1590) index(8507)
Title: Locus:1.1.1.1636.17
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

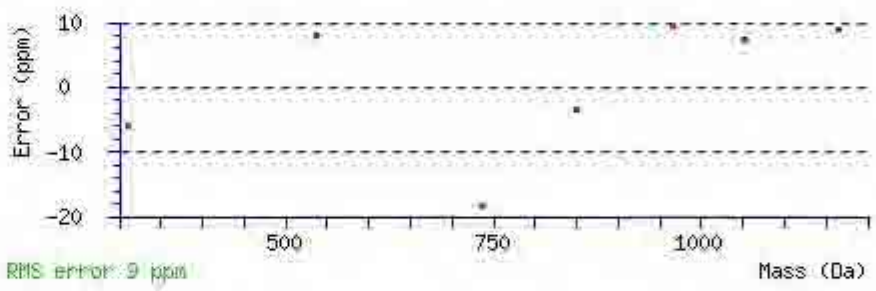
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1378.697983
Ions Score: 56 **Expect:** 3.6e-005
Matches : 7/124 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	215.139019	108.073147			197.128454	99.067865	I	1278.657608	639.832442	1261.631059	631.319168	1260.647043	630.827159	11
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	N	*1165.573544*	583.290410	1148.546995	574.777136	1147.562979	574.285128	10
4	416.213974	208.610625	399.187425	200.097350	398.203409	199.605342	S	*1051.530617*	526.268947	1034.504068	517.755672	1033.520052	517.263664	9
5	531.240917	266.124097	514.214368	257.610822	513.230352	257.118814	D	*964.498589*	482.752933	947.472040	474.239658	946.488024	473.747650	8
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	I	*849.471646*	425.239461	832.445097	416.726187	831.461081	416.234179	7
7	731.357009	366.182143	714.330460	357.668868	713.346444	357.176860	S	*736.387582*	368.697429	719.361033	360.184155	718.377017	359.692147	6
8	844.441073	422.724175	827.414524	414.210900	826.430508	413.718892	I	649.355554	325.181415	632.329005	316.668141	631.344989	316.176133	5
9	941.493837	471.250557	924.467288	462.737282	923.483272	462.245274	P	*536.271490*	268.639383	519.244941	260.126109	518.260925	259.634101	4
10	1070.536430	535.771853	1053.509881	527.258579	1052.525865	526.766570	E	439.218726	220.113001	422.192177	211.599726	421.208161	211.107718	3
11	1233.599759	617.303518	1216.573210	608.790243	1215.589194	608.298235	Y	*310.176133*	155.591705	293.149584	147.078430			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TINSDISIPEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1378.697983	0.008345	TINSDISIPEYK
8.5	1378.713272	-0.006944	QPAAFIVTQYPL
8.4	1378.695313	0.011015	DPHGESLPRSLR
8.4	1378.698013	0.008315	ESAFTSPISVTKP
8.1	1378.694855	0.011473	MGVMTLPSDLRK
8.1	1378.694855	0.011473	MGVMTLPSDLRK
7.2	1378.709244	-0.002916	PTEPPPLPPKSR
7.2	1378.709244	-0.002916	PTEPPPLPPKSR
6.8	1378.709244	-0.002916	TLNSEDFVLVSR
6.7	1378.695328	0.011000	TPNSAGGPGAHILR

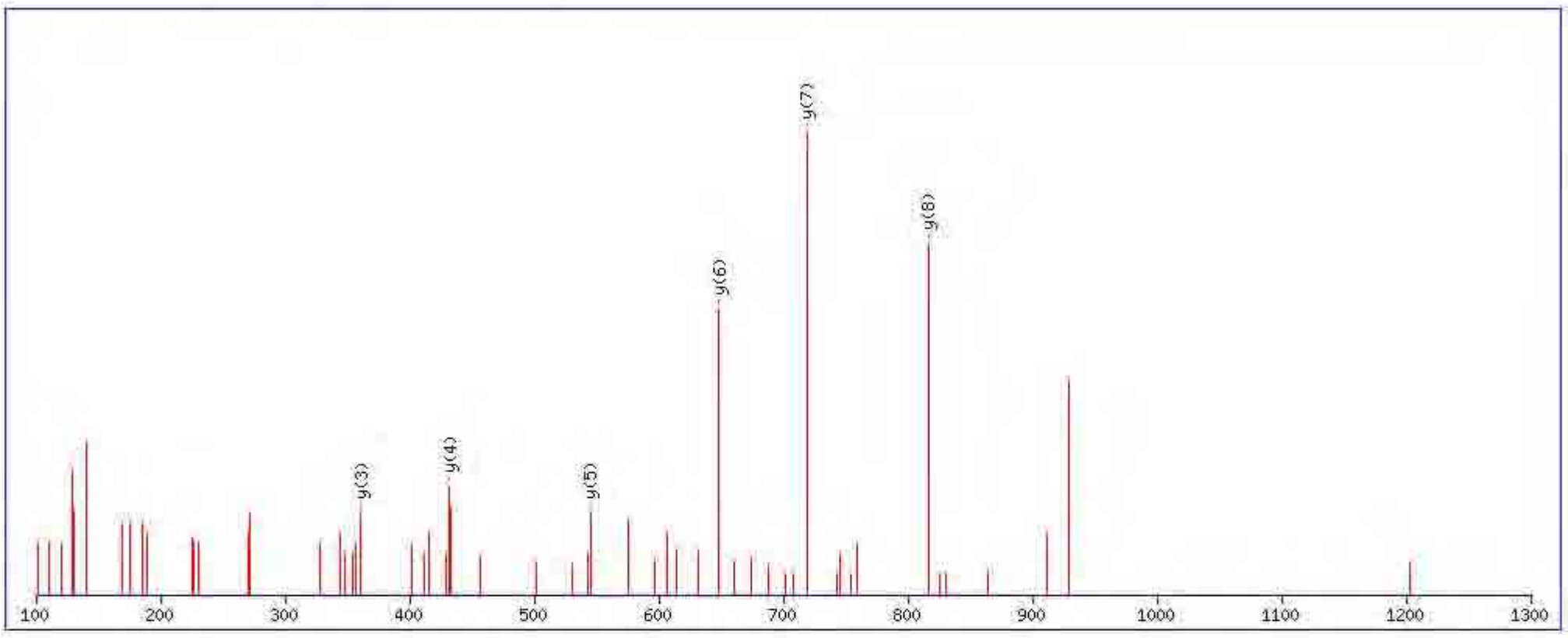
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPACIAGER**
Found in **DEF1_HUMAN**, Neutrophil defensin 1 OS=Homo sapiens GN=DEFA1 PE=1 SV=1

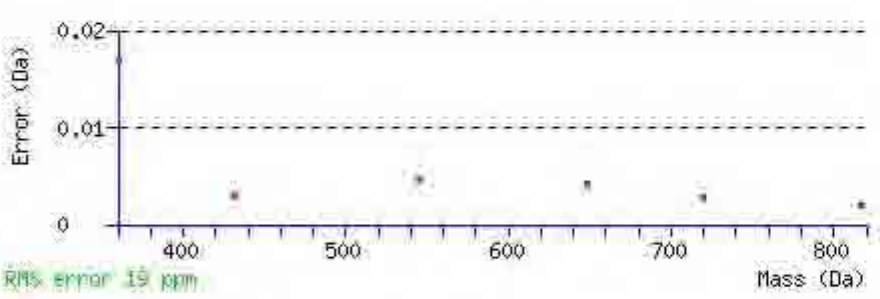
Match to Query 2585: 928.476788 from(465.245670,2+) rtinseconds(997) index(3321)
Title: Locus:1.1.1.1310.11
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

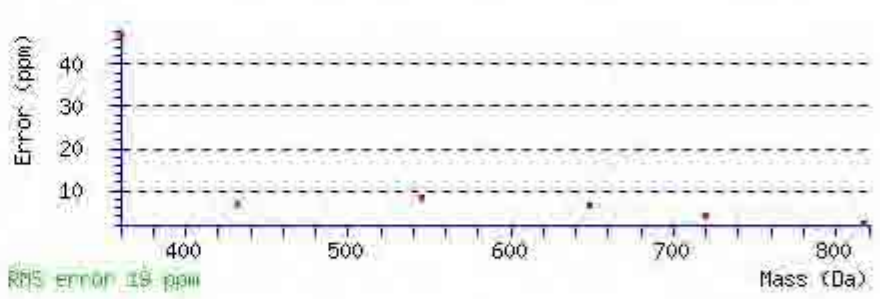
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 928.480011
Ions Score: 54 **Expect:** 0.00062
Matches : 6/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							9
2	211.144104	106.075690			P	*816.403250*	408.705263	799.376701	400.191989	798.392685	399.699981	8
3	282.181218	141.594247			A	*719.350486*	360.178881	702.323937	351.665607	701.339921	351.173599	7
4	385.190403	193.098840			C	*648.313372*	324.660324	631.286823	316.147050	630.302807	315.655042	6
5	498.274467	249.640872			I	*545.304187*	273.155732	528.277638	264.642457	527.293622	264.150449	5
6	569.311581	285.159429			A	*432.220123*	216.613700	415.193574	208.100425	414.209558	207.608417	4
7	626.333045	313.670161			G	*361.183009*	181.095143	344.156460	172.581868	343.172444	172.089860	3
8	755.375638	378.191457	737.365073	369.186175	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
9					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IPACIAGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	928.480011	-0.003223	IPACIAGER
21.1	928.480042	-0.003254	PLGTLCGPR
14.4	928.476654	0.000134	IGTPEAWR
12.5	928.472626	0.004162	VAAGAQEQR
12.0	928.472626	0.004162	LQQQAEGR
11.7	928.468811	0.007977	LPAAGVGDMV
11.4	928.480026	-0.003238	LPSSPLGCR
10.1	928.480011	-0.003223	PLCLAAEGR
9.4	928.472626	0.004162	LDRPGAER
9.4	928.472626	0.004162	PDRPEKR

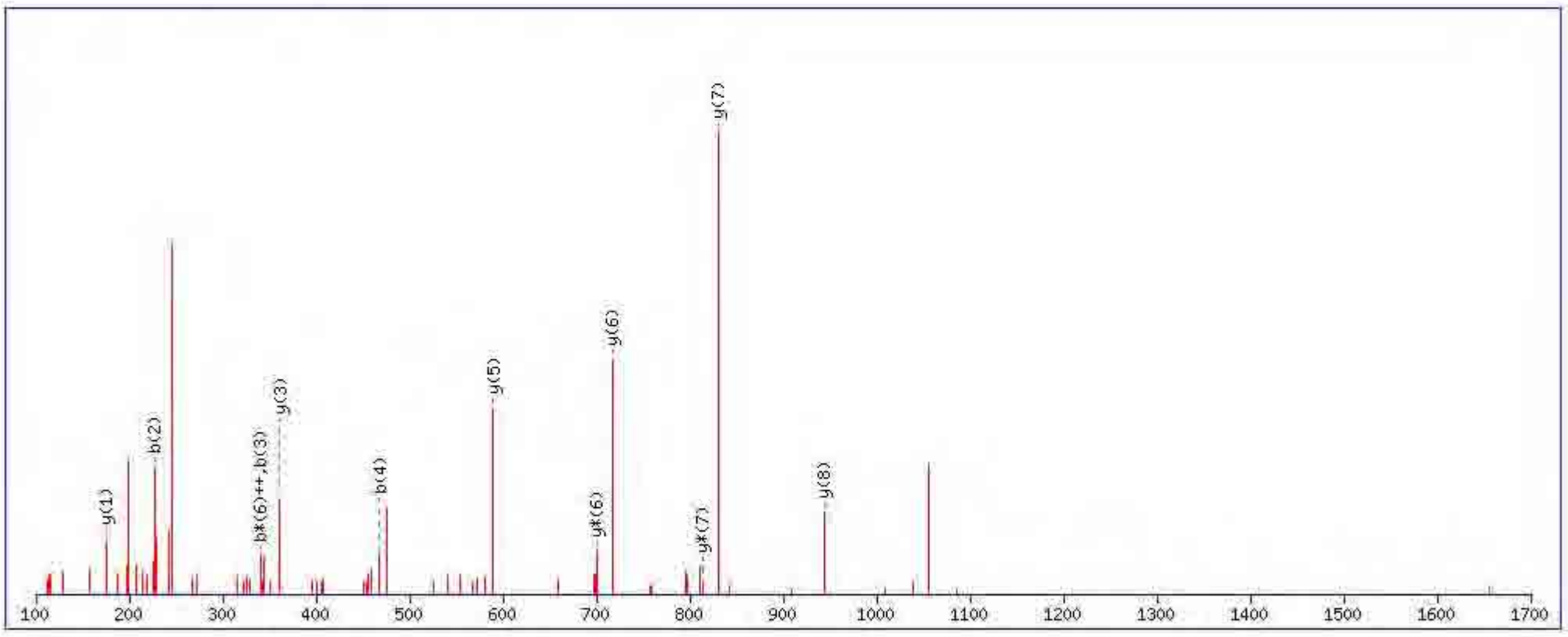
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PLIKVEEGR**
Found in **NR4A3_HUMAN**, Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=2 SV=3

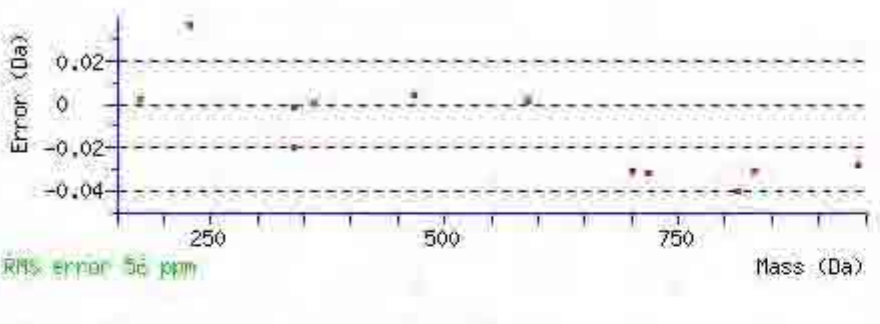
Match to Query 4519: 1055.606688 from(528.810620,2+) rtinseconds(1557) index(8133)
Title: Locus:1.1.1.1619.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

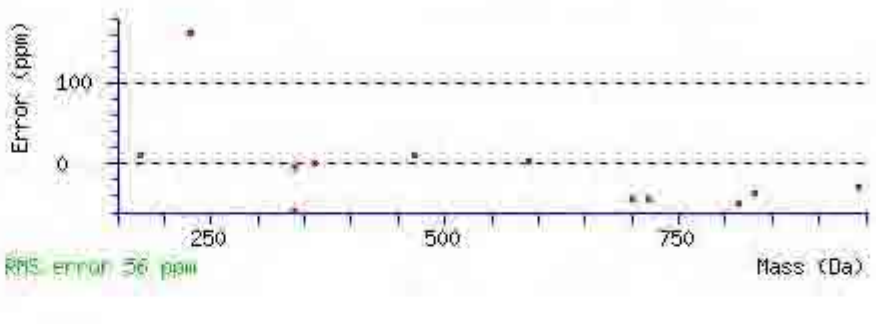
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1055.597488
Variable modifications:
P1 : Oxidation (P)
Ions Score: 43 **Expect:** 0.0071
Matches : 12/76 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.054955	57.531116					P							9
2	227.139019	114.073147					L	*943.557107*	472.282192	926.530558	463.768917	925.546542	463.276909	8
3	340.223083	170.615179					I	*830.473043*	415.740160	813.446494	407.226885	812.462478	406.734877	7
4	468.318046	234.662661	451.291497	226.149386			K	*717.388979*	359.198128	700.362430	350.684853	699.378414	350.192845	6
5	567.386460	284.196868	550.359911	275.683594			V	*589.294016*	295.150646	572.267467	286.637372	571.283451	286.145364	5
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	E	490.225602	245.616439	473.199053	237.103164	472.215037	236.611156	4
7	825.471646	413.239461	808.445097	404.726187	807.461081	404.234179	E	*361.183009*	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	882.493110	441.750193	865.466561	433.236919	864.482545	432.744911	G	232.140416	116.573846	215.113867	108.060571			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of PLIKVEEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	1055.597488	0.009200	PLIKVEEGR
42.8	1055.597504	0.009184	LLPQLTSPR
34.1	1055.612762	-0.006074	LLIQPGPRF
28.0	1055.608704	-0.002016	ILLREAEGR
28.0	1055.612747	-0.006059	LLLPAATWR
28.0	1055.608704	-0.002016	LLLRAEGER
27.8	1055.597488	0.009200	LLKLDPADR
23.9	1055.601532	0.005156	ILLGLWVQD
23.3	1055.604874	0.001814	ILLIKNMDP
22.4	1055.597504	0.009184	IPPDVLKSR

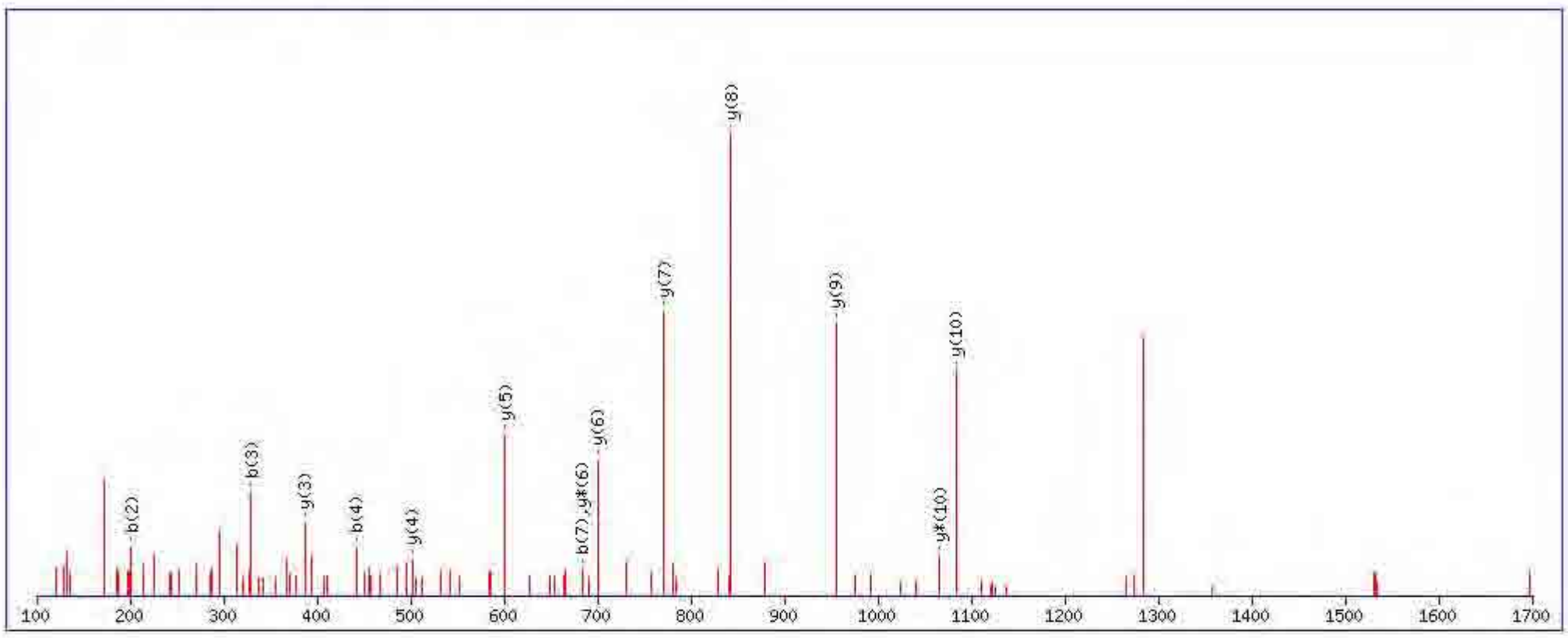
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVQIAAVVDVIR**
Found in **PIP_HUMAN**, Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1

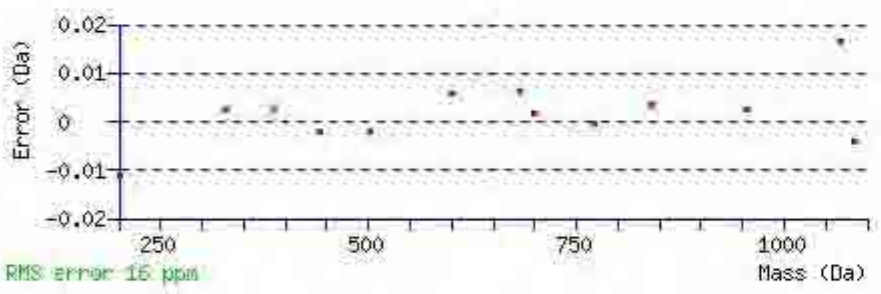
Match to Query 9126: 1282.768208 from(642.391380,2+) rtinseconds(2037) index(13523)
Title: Locus:1.1.1.1878.4
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

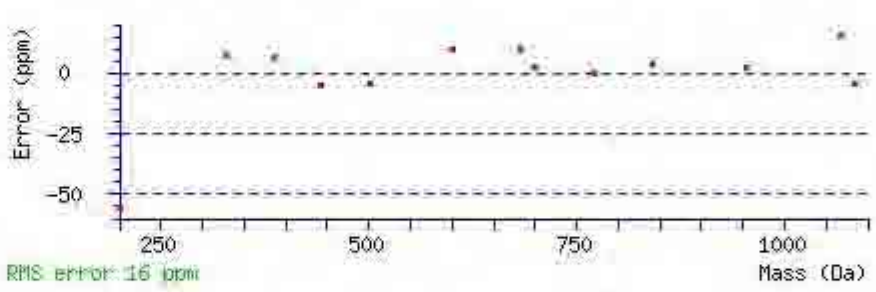
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1282.760895
Ions Score: 57 **Expect:** 6.9e-005
Matches : 14/122 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	201.123369	101.065322			183.112804	92.060040	V	1182.720485	591.863880	1165.693936	583.350606	1164.709920	582.858598	11
3	329.181947	165.094611	312.155398	156.581337	311.171382	156.089329	Q	*1083.652071*	542.329673	1066.625522	533.816399	1065.641506	533.324391	10
4	442.266011	221.636643	425.239462	213.123369	424.255446	212.631361	I	*955.593493*	478.300384	938.566944	469.787110	937.582928	469.295102	9
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	A	*842.509429*	421.758352	825.482880	413.245078	824.498864	412.753070	8
6	584.340239	292.673758	567.313690	284.160483	566.329674	283.668475	A	*771.472315*	386.239795	754.445766	377.726521	753.461750	377.234513	7
7	683.408653	342.207965	666.382104	333.694690	665.398088	333.202682	V	*700.435201*	350.721238	683.408652	342.207964	682.424636	341.715956	6
8	782.477067	391.742171	765.450518	383.228897	764.466502	382.736889	V	*601.366787*	301.187031	584.340238	292.673757	583.356222	292.181749	5
9	897.504010	449.255643	880.477461	440.742368	879.493445	440.250360	D	*502.298373*	251.652824	485.271824	243.139550	484.287808	242.647542	4
10	996.572424	498.789850	979.545875	490.276575	978.561859	489.784567	V	*387.271430*	194.139353	370.244881	185.626078			3
11	1109.656488	555.331882	1092.629939	546.818607	1091.645923	546.326599	I	288.203016	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TVQIAAVVDVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.0	1282.760895	0.007313	TVQIAAVVDVIR
22.9	1282.772095	-0.003887	SLKPGLARGQIK
18.8	1282.760864	0.007344	VTKPKIPEAIR
11.0	1282.760880	0.007328	SIKPGVIGGSKPK
10.5	1282.760880	0.007328	TVLQRPLSLIQ
10.0	1282.760849	0.007359	ASVALLKLNNPK
10.0	1282.760849	0.007359	NLTLPKNLLNK
9.6	1282.776108	-0.007900	SQLLALLAWLR
8.9	1282.760864	0.007344	ATRILLEQGGIL
8.9	1282.760880	0.007328	TARLVLPTDAVK

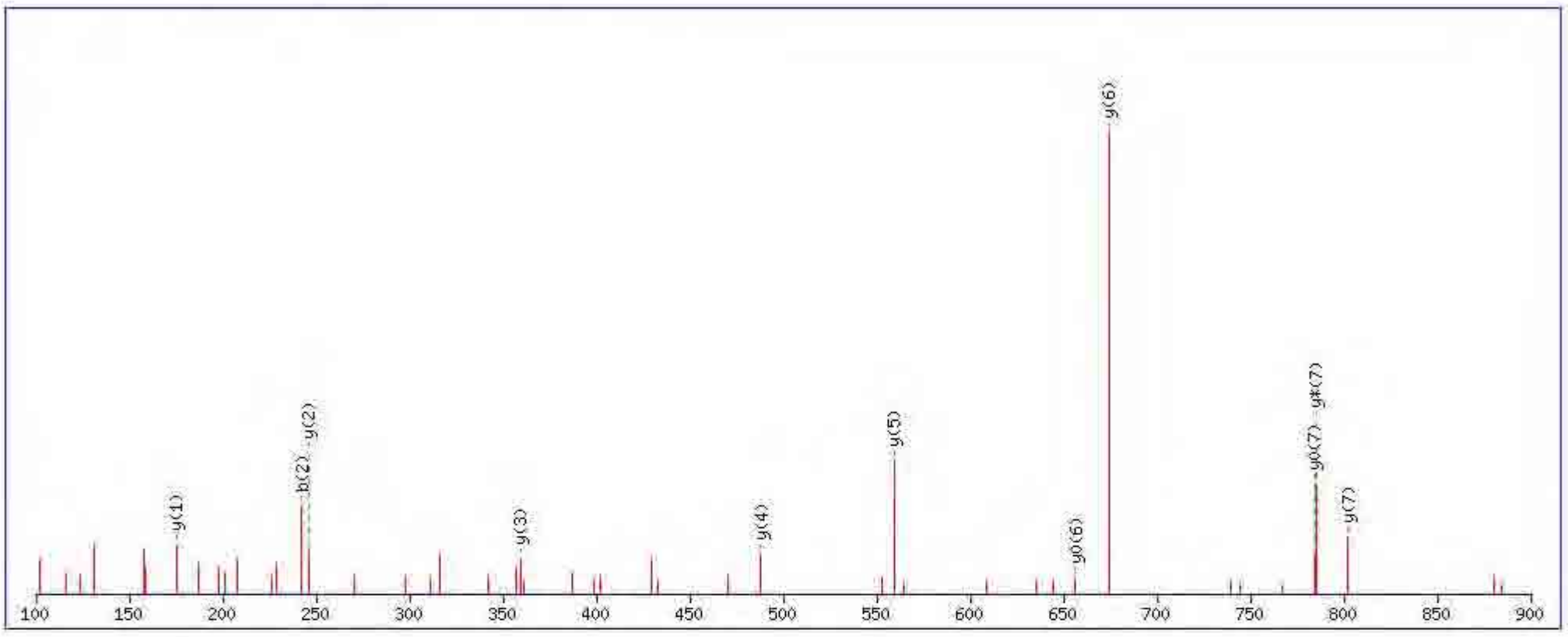
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQDAEIAR**
Found in **S10A6_HUMAN**, Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1

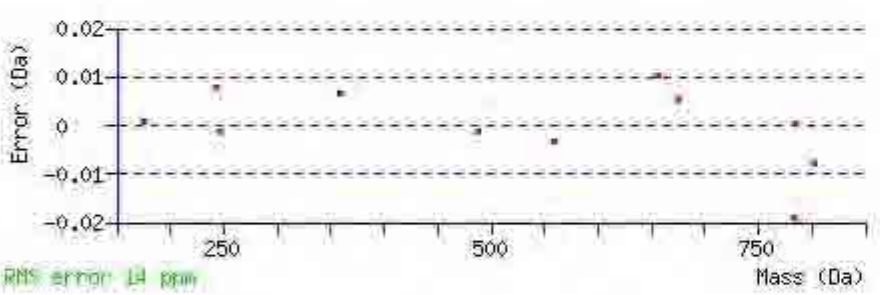
Match to Query 2414: 914.486728 from(458.250640,2+) rtinseconds(766) index(1506)
Title: Locus:1.1.1.1183.8
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

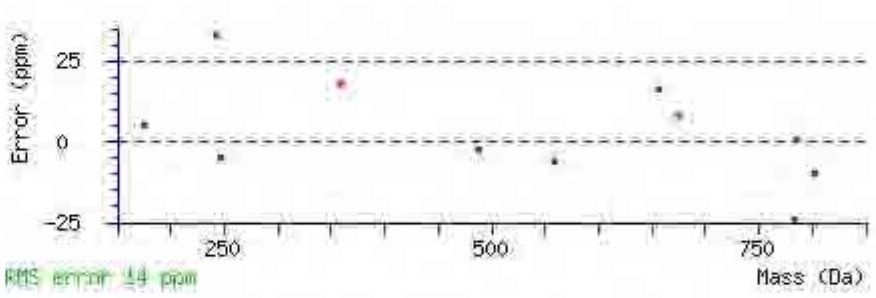
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 914.482117
Ions Score: 58 **Expect:** 0.00033
Matches : 11/72 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							8
2	242.149918	121.578597	225.123369	113.065323			Q	*802.405358*	401.706317	785.378809	393.193043	784.394793	392.701035	7
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	D	*674.346780*	337.677028	657.320231	329.163754	656.336215	328.671746	6
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	A	*559.319837*	280.163557	542.293288	271.650282	541.309272	271.158274	5
5	557.256568	279.131922	540.230019	270.618648	539.246003	270.126640	E	*488.282723*	244.644999	471.256174	236.131725	470.272158	235.639717	4
6	670.340632	335.673954	653.314083	327.160680	652.330067	326.668672	I	*359.240130*	180.123703	342.213581	171.610428			3
7	741.377746	371.192511	724.351197	362.679237	723.367181	362.187229	A	*246.156066*	123.581671	229.129517	115.068396			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LQDAEIAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	914.482117	0.004611	LQDAEIAR
32.8	914.482132	0.004596	LQDLSSPR
30.5	914.482132	0.004596	PKDAPSLR
30.1	914.482117	0.004611	LQGEIEAR
21.4	914.482147	0.004581	IKDPGPTR
21.4	914.493362	-0.006634	IQDLDRR
20.9	914.482132	0.004596	IQLDSSPR
20.0	914.493347	-0.006619	LQAAAGASAR
19.5	914.482147	0.004581	IKDVPGDR
19.5	914.493362	-0.006634	LQDRIDR

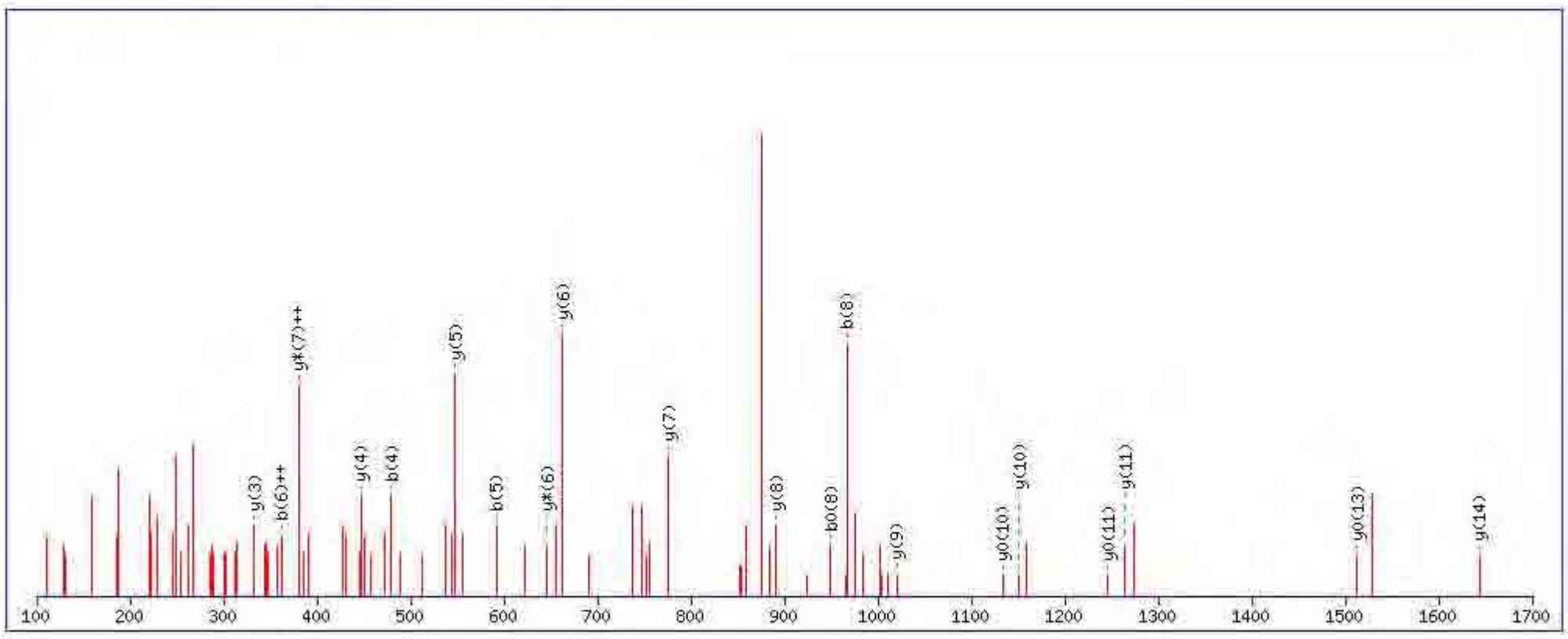
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIEHIMEDLDTNADK**
Found in **S10A9_HUMAN**, Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1

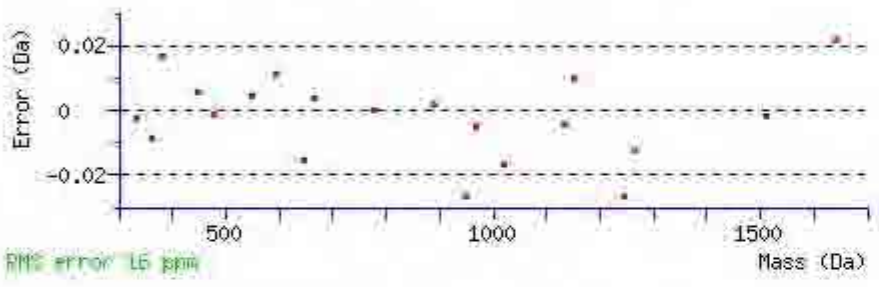
Match to Query 14479: 1741.829352 from(581.617060,3+) rtinseconds(1557) index(8137)
Title: Locus:1.1.1.1619.9
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

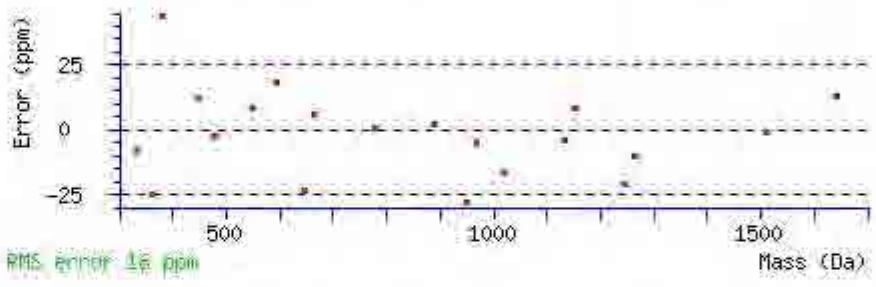
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1741.819244
Ions Score: 57 **Expect:** 5.5e-006
Matches : 20/140 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							15
2	213.159754	107.083515					I	*1643.758128*	822.382702	1626.731579	813.869428	1625.747563	813.377419	14
3	342.202347	171.604811			324.191782	162.599529	E	1530.674064	765.840670	1513.647515	757.327396	1512.663499	756.835388	13
4	479.261259	240.134267			461.250694	231.128985	H	1401.631471	701.319373	1384.604922	692.806099	1383.620906	692.314091	12
5	592.345323	296.676300			574.334758	287.671017	I	*1264.572559*	632.789918	1247.546010	624.276643	1246.561994	623.784635	11
6	723.385808	362.196542			705.375243	353.191260	M	*1151.488495*	576.247886	1134.461946	567.734611	1133.477930	567.242603	10
7	852.428401	426.717839			834.417836	417.712556	E	*1020.448010*	510.727643	1003.421461	502.214369	1002.437445	501.722361	9
8	967.455344	484.231310			949.444779	475.226027	D	*891.405417*	446.206347	874.378868	437.693072	873.394852	437.201064	8
9	1080.539408	540.773342			1062.528843	531.768059	L	*776.378474*	388.692875	759.351925	380.179601	758.367909	379.687593	7
10	1195.566351	598.286813			1177.555786	589.281531	D	*663.294410*	332.150843	646.267861	323.637569	645.283845	323.145561	6
11	1296.614030	648.810653			1278.603465	639.805370	T	*548.267467*	274.637372	531.240918	266.124097	530.256902	265.632089	5
12	1410.656957	705.832116	1393.630408	697.318842	1392.646392	696.826834	N	*447.219788*	224.113532	430.193239	215.600258	429.209223	215.108250	4
13	1481.694071	741.350673	1464.667522	732.837399	1463.683506	732.345391	A	*333.176861*	167.092069	316.150312	158.578794	315.166296	158.086786	3
14	1596.721014	798.864145	1579.694465	790.350871	1578.710449	789.858862	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VIEHIMEDLDTNADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	1741.819244	0.010108	VIEHIMEDLDTNADK
1.1	1741.827118	0.002234	TNQFGDLSPKEHQEL
0.9	1741.814072	0.015280	LAHGGARPHPCPDCPKA
0.1	1741.845764	-0.016412	VSPGENQLPVWMPTR
0.1	1741.845764	-0.016412	VSPGENQLPVWMPTR

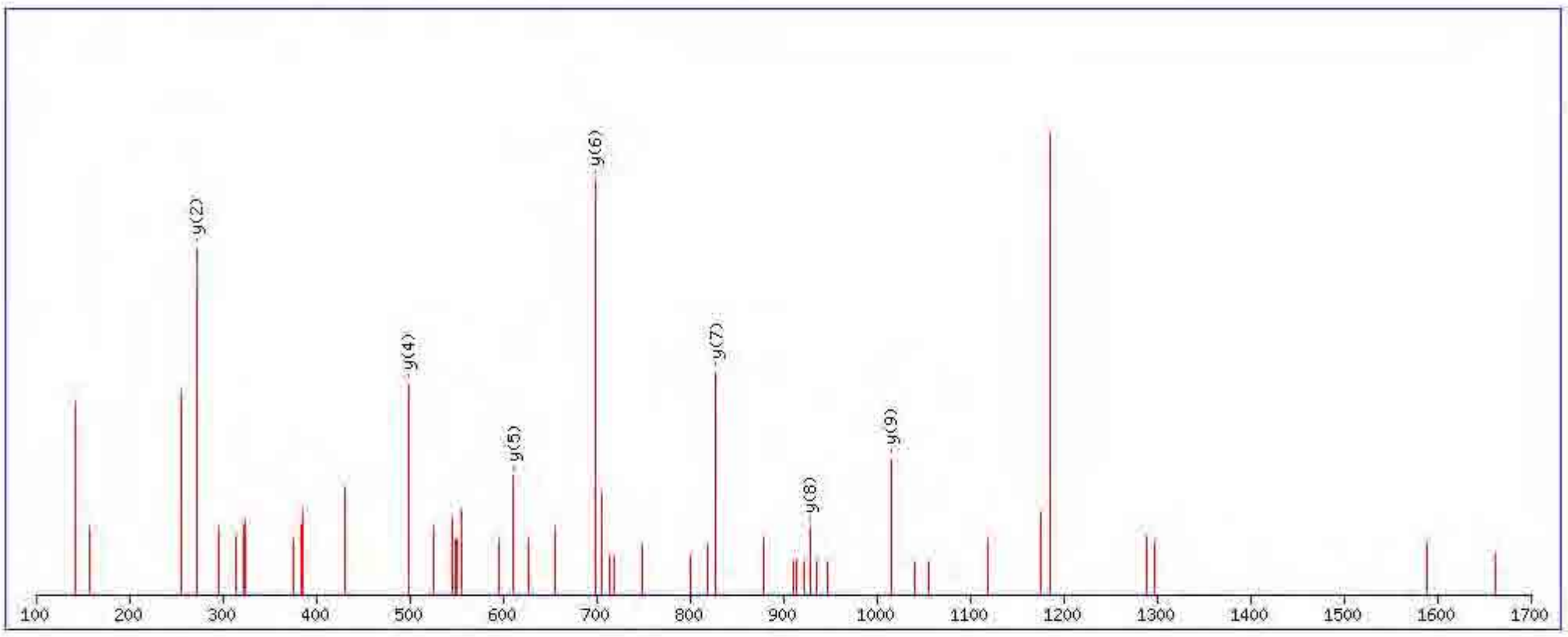
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

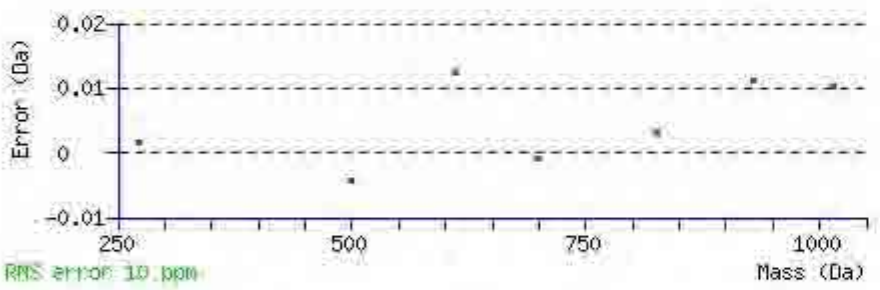
Match to Query 7274: 1184.679868 from(593.347210,2+) rtinseconds(1736) index(10004)
Title: Locus:1.1.1.1715.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

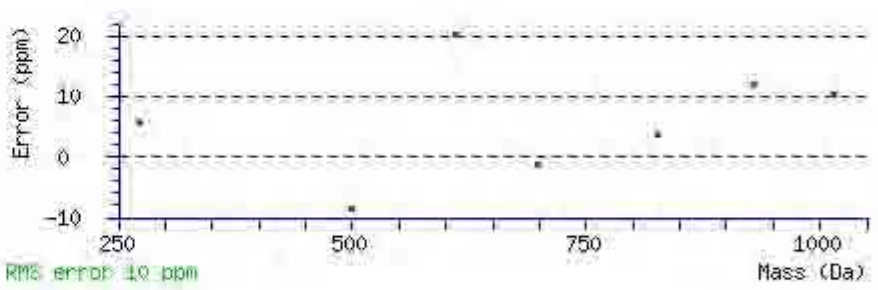
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Ions Score: 56 **Expect:** 4.6e-005
Matches : 7/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	*1015.578236*	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	*928.546208*	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	*827.498529*	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	*698.455936*	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	*611.423908*	306.215592	594.397359	297.702318			5
8	801.435260	401.221268	783.424695	392.215986	L	*498.339844*	249.673560	481.313295	241.160285			4
9	914.519324	457.763300	896.508759	448.758018	I	385.255780	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	P	*272.171716*	136.589496	255.145167	128.076221			2
11					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.7	1184.676468	0.003400	GLSTESILIPR
8.9	1184.677795	0.002073	PRHPEALLPR
7.5	1184.676468	0.003400	KEDLTTLLPR
6.5	1184.691711	-0.011843	EKALYPVIPR
2.8	1184.676483	0.003385	GPVVEISLISR
2.6	1184.680527	-0.000659	GLTLPPVPFTK
2.0	1184.676453	0.003415	PAISELSSLLR
2.0	1184.676483	0.003385	TPLLGLSPLSR
0.9	1184.680511	-0.000643	GLTSQLLPPLF
0.1	1184.687714	-0.007846	VGDSLGILQRK

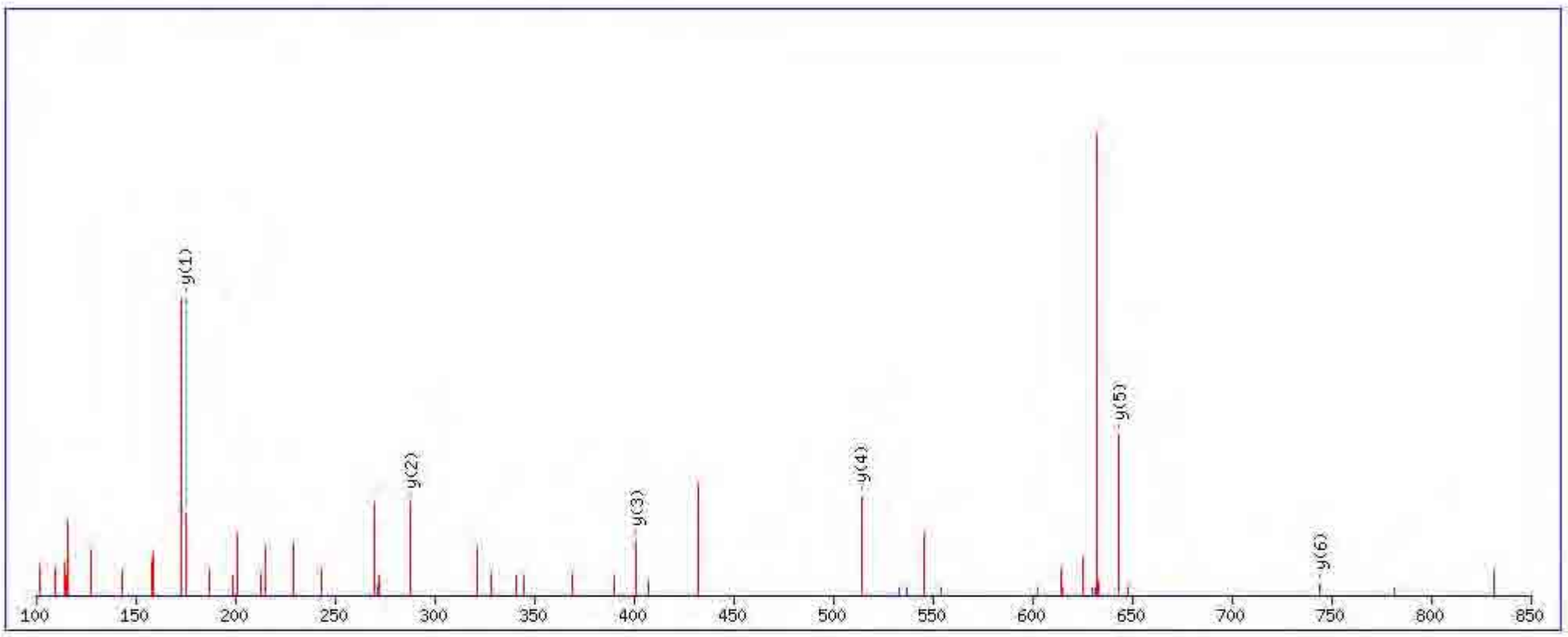
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELLIR**
Found in **H31T_HUMAN**, Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3

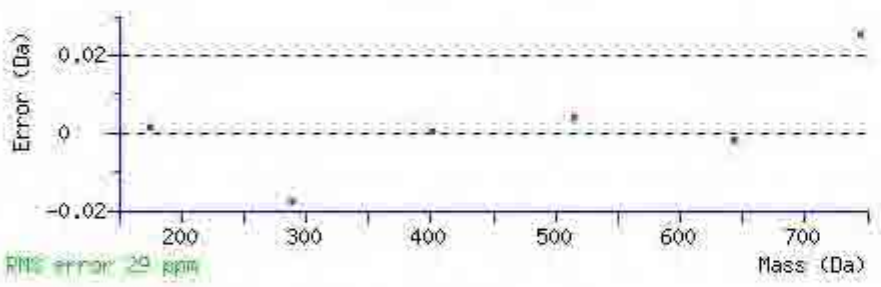
Match to Query 978: 830.482548 from(416.248550,2+) rtinseconds(1128) index(4021)
Title: Locus:1.1.1.1385.3
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

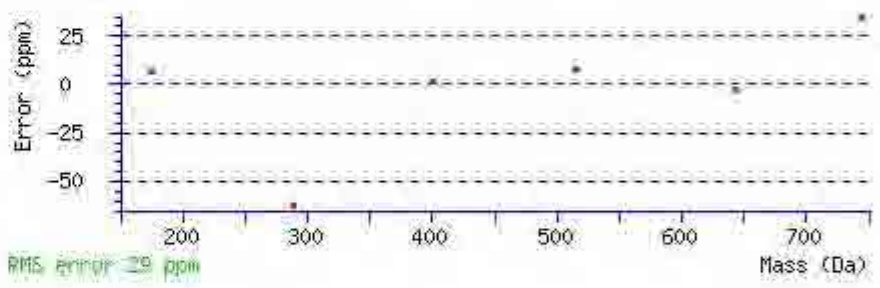
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 830.486145
Ions Score: 40 **Expect:** 0.0053
Matches : 6/52 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							7
2	189.086983	95.047129	171.076418	86.041847	T	*744.461416*	372.734346	727.434867	364.221072	726.450851	363.729064	6
3	318.129576	159.568426	300.119011	150.563144	E	*643.413737*	322.210507	626.387188	313.697232	625.403172	313.205224	5
4	431.213640	216.110458	413.203075	207.105176	L	*514.371144*	257.689210	497.344595	249.175936			4
5	544.297704	272.652490	526.287139	263.647208	L	*401.287080*	201.147178	384.260531	192.633904			3
6	657.381768	329.194522	639.371203	320.189240	I	*288.203016*	144.605146	271.176467	136.091872			2
7					R	*175.118952*	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of STELLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	830.486145	-0.003597	STELLIR
40.0	830.474930	0.007618	STELLLGV
14.5	830.486145	-0.003597	SSLLLNGK
13.4	830.486145	-0.003597	ESTLLIR
13.4	830.486145	-0.003597	TESLLLR
13.4	830.486160	-0.003612	TTDIILR
12.2	830.476242	0.006306	SKAAWIR
12.1	830.486145	-0.003597	SLTEIIR
11.2	830.483643	-0.001095	WMLLLR
9.7	830.479614	0.002934	AKVCAAIR

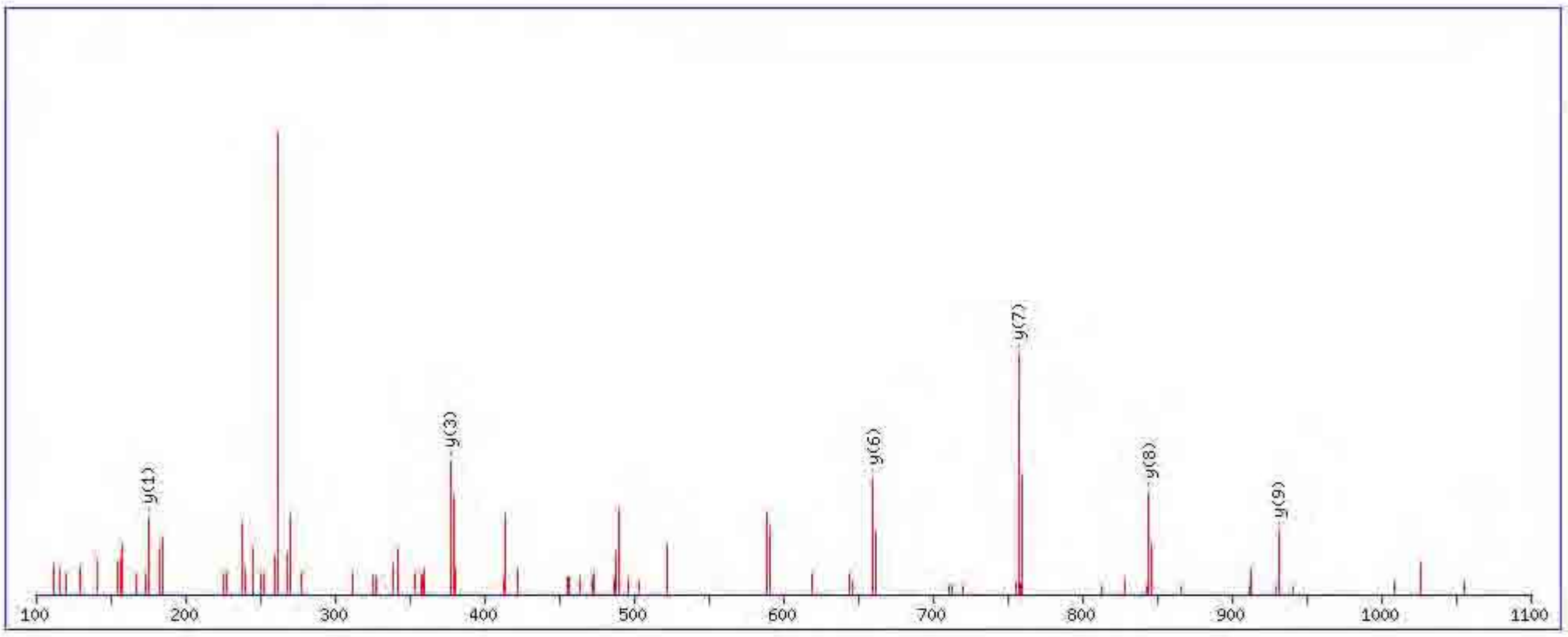
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSPVPAVCR**
Found in **RNH2A_HUMAN**, Ribonuclease H2 subunit A OS=Homo sapiens GN=RNASEH2A PE=1 SV=2

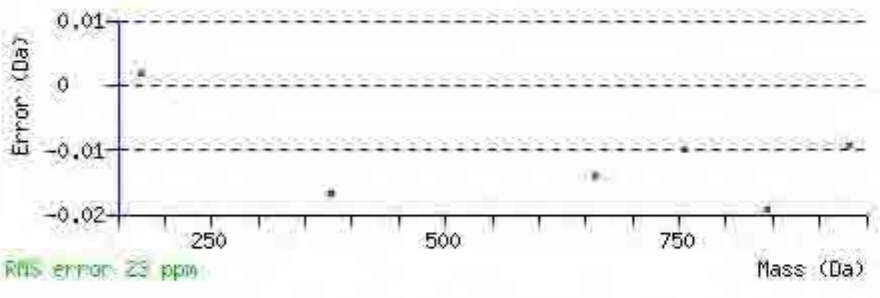
Match to Query 4319: 1043.535488 from(522.775020,2+) rtinseconds(937) index(2640)
Title: Locus:1.1.1.1277.5
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

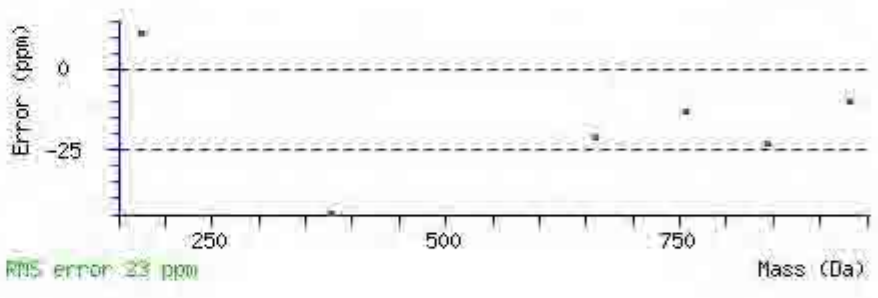
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1043.543365
Variable modifications:
P6 : Oxidation (P)
Ions Score: 47 **Expect:** 0.0039
Matches : 6/74 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	201.123368	101.065322	183.112803	92.060039	S	*931.466578*	466.236927	914.440029	457.723652	913.456013	457.231644	9
3	288.155396	144.581336	270.144831	135.576053	S	*844.434550*	422.720913	827.408001	414.207638	826.423985	413.715630	8
4	385.208160	193.107718	367.197595	184.102435	P	*757.402522*	379.204899	740.375973	370.691624			7
5	484.276574	242.641925	466.266009	233.636642	V	*660.349758*	330.678517	643.323209	322.165242			6
6	597.324253	299.165765	579.313688	290.160482	P	561.281344	281.144310	544.254795	272.631036			5
7	668.361367	334.684322	650.350802	325.679039	A	448.233665	224.620470	431.207116	216.107196			4
8	767.429781	384.218528	749.419216	375.213246	V	*377.196551*	189.101913	360.170002	180.588639			3
9	870.438966	435.723121	852.428401	426.717838	C	278.128137	139.567706	261.101588	131.054432			2
10					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSPVPAVCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	1043.543365	-0.007877	LSSPVPAVCR
31.2	1043.543365	-0.007877	LSSPVPAVCR
24.1	1043.535934	-0.000446	ESALREPSR
20.2	1043.535965	-0.000477	PPRLATDSR
19.3	1043.535950	-0.000462	ISRPPEASR
18.5	1043.535965	-0.000477	LSPGGLSNGSR
18.2	1043.539978	-0.004490	SLSPAWGQAK
18.1	1043.535950	-0.000462	SLSPSPERR
18.1	1043.539993	-0.004505	SPSPFQPLR
17.7	1043.539978	-0.004490	LSSGFSKYR

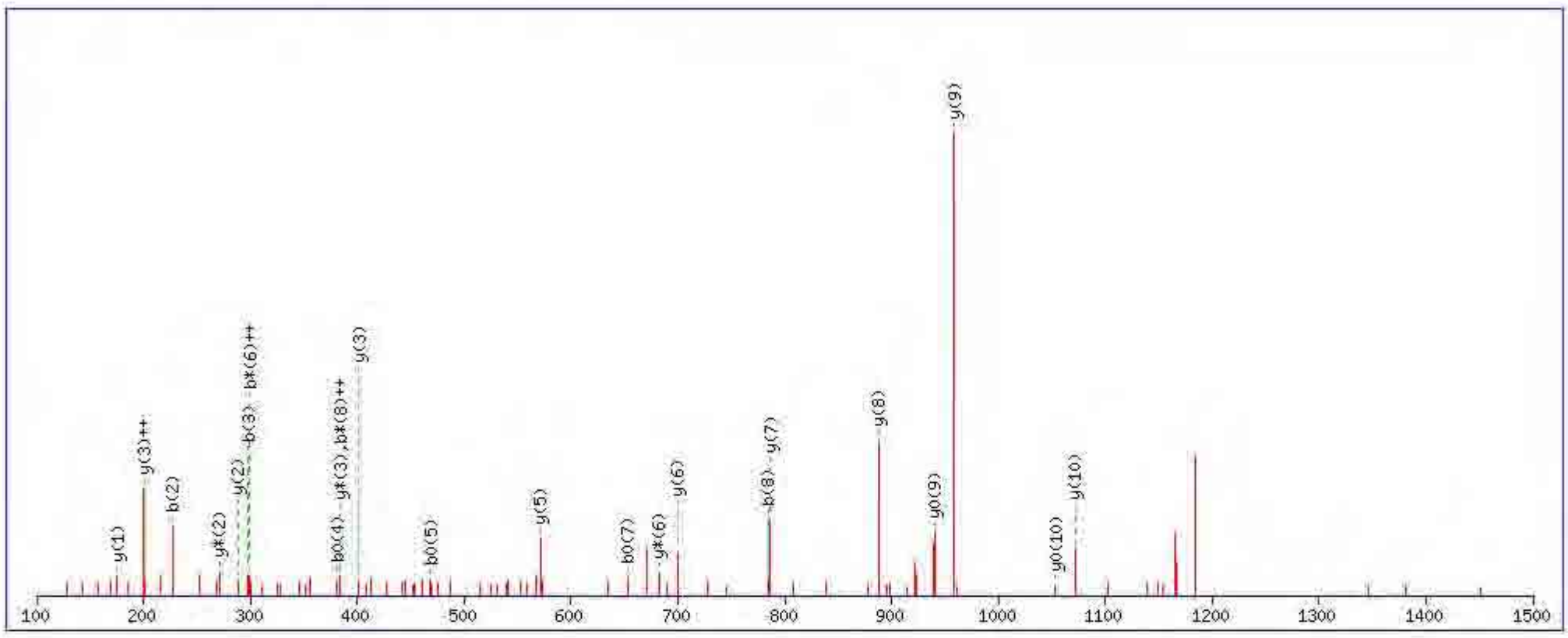
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIATSQGLLIR**
Found in **SEM3C_HUMAN**, Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=1 SV=2

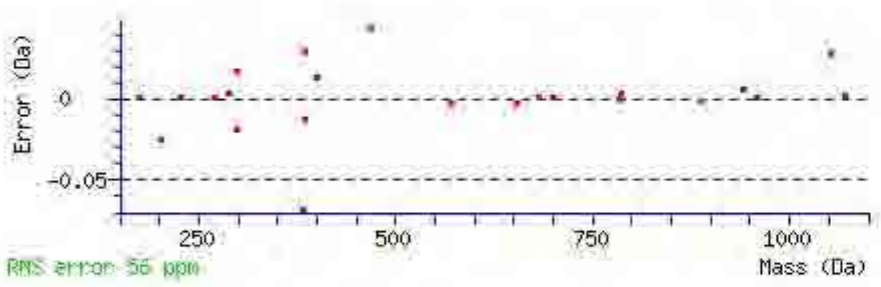
Match to Query 7230: 1183.729248 from(592.871900,2+) rtinseconds(1597) index(8574)
Title: Locus:1.1.1.1640.10
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

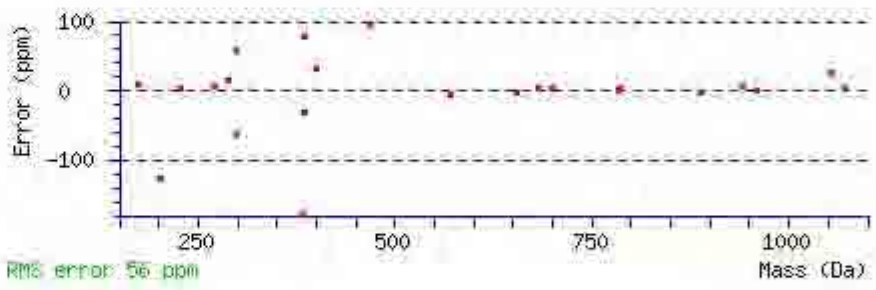
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1183.728836
Ions Score: 48 **Expect:** 0.00039
Matches : 23/92 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							11
2	227.175404	114.091340					I	*1071.652071*	536.329674	1054.625522	527.816399	1053.641506	527.324391	10
3	298.212518	149.609897					A	*958.568007*	479.787642	941.541458	471.274367	940.557442	470.782359	9
4	399.260197	200.133737			381.249632	191.128454	T	*887.530893*	444.269085	870.504344	435.755810	869.520328	435.263802	8
5	486.292225	243.649750			468.281660	234.644468	S	*786.483214*	393.745245	769.456665	385.231971	768.472649	384.739963	7
6	614.350803	307.679040	597.324254	299.165765	596.340238	298.673757	Q	*699.451186*	350.229231	682.424637	341.715957			6
7	671.372267	336.189772	654.345718	327.676497	653.361702	327.184489	G	*571.392608*	286.199942	554.366059	277.686668			5
8	784.456331	392.731804	767.429782	384.218529	766.445766	383.726521	L	514.371144	257.689210	497.344595	249.175936			4
9	897.540395	449.273836	880.513846	440.760561	879.529830	440.268553	L	*401.287080*	201.147178	384.260531	192.633903			3
10	1010.624459	505.815868	993.597910	497.302593	992.613894	496.810585	I	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IIATSQGLLIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	1183.728836	0.000412	IIATSQGLLIR
10.7	1183.728851	0.000397	LITAVVEVGRK
9.3	1183.717590	0.011658	LLAPSGLEKLK
9.1	1183.728821	0.000427	LLASKLSLSPR
8.7	1183.736221	-0.006973	LLMPAILLR
8.6	1183.717606	0.011642	IIKQQETVII
8.4	1183.732880	-0.003632	ILRTVPFLPL
7.3	1183.728821	0.000427	ILKEQTLALR
6.9	1183.728836	0.000412	LLALRTLLSQG
6.8	1183.718933	0.010315	ILRLFPQAAR

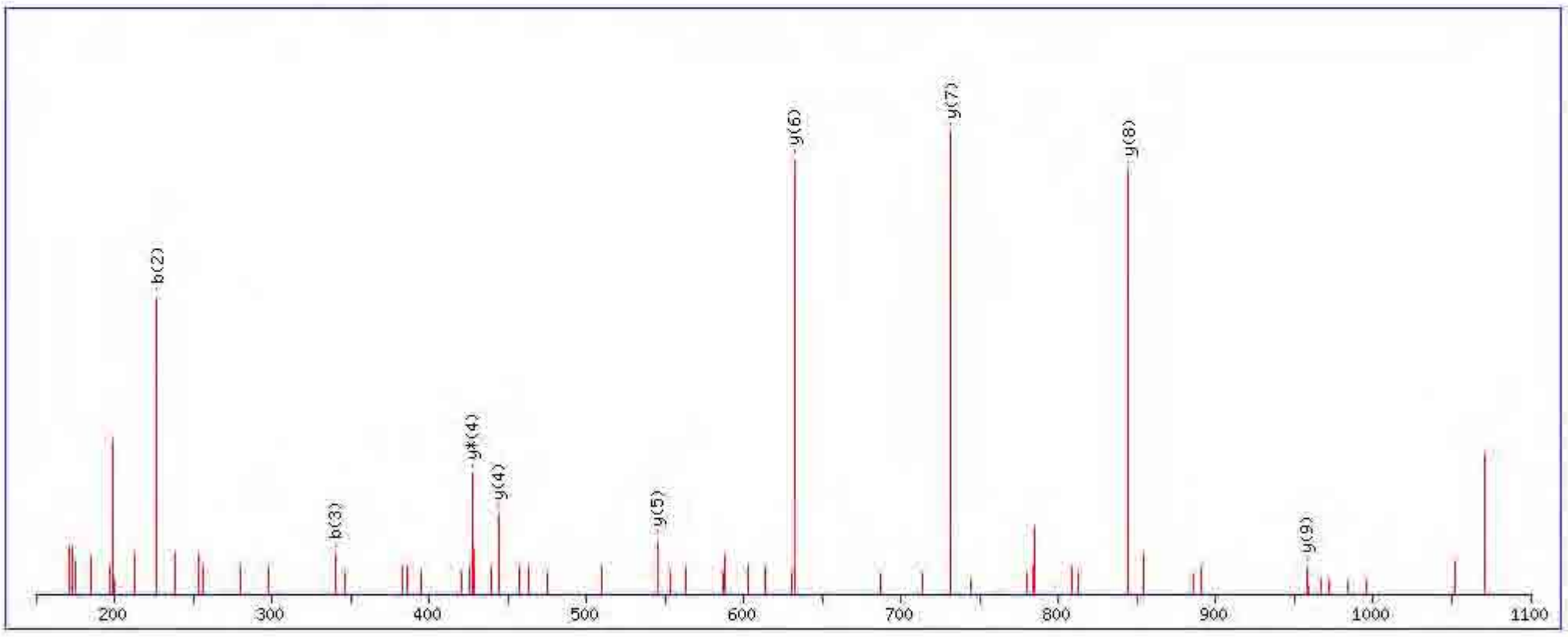
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIVSTPTAR**
Found in **SRPX_HUMAN**, Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1

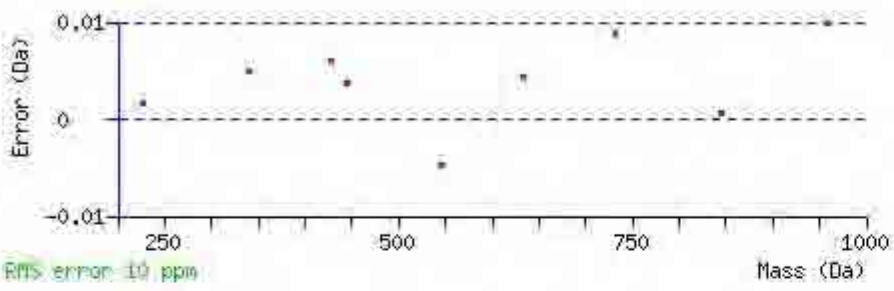
Match to Query 4780: 1069.652948 from(535.833750,2+) rtinseconds(1407) index(6628)
Title: Locus:1.1.1.1538.7
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

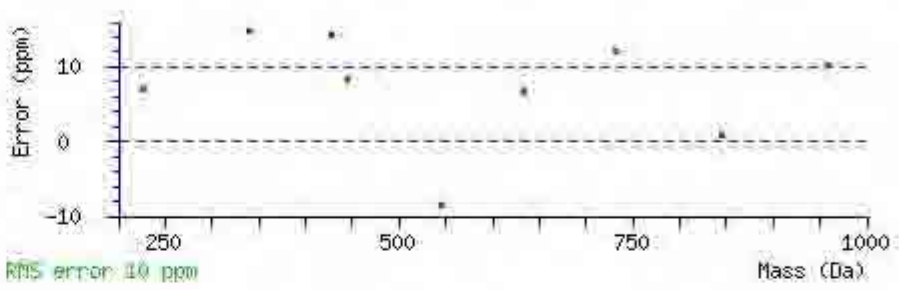
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1069.649536
Ions Score: 38 **Expect:** 0.0065
Matches : 9/78 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							10
2	227.175404	114.091340			L	957.572758	479.290017	940.546209	470.776743	939.562193	470.284735	9
3	340.259468	170.633372			I	844.488694	422.747985	827.462145	414.234711	826.478129	413.742703	8
4	439.327882	220.167579			V	731.404630	366.205953	714.378081	357.692679	713.394065	357.200671	7
5	526.359910	263.683593	508.349345	254.678311	S	632.336216	316.671746	615.309667	308.158472	614.325651	307.666464	6
6	627.407589	314.207433	609.397024	305.202150	T	545.304188	273.155732	528.277639	264.642458	527.293623	264.150450	5
7	724.460353	362.733815	706.449788	353.728532	P	444.256509	222.631893	427.229960	214.118618	426.245944	213.626610	4
8	825.508032	413.257654	807.497467	404.252372	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
9	896.545146	448.776211	878.534581	439.770929	A	246.156066	123.581671	229.129517	115.068397			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LLIVSTPTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	1069.649536	0.003412	LLIVSTPTAR
21.8	1069.649521	0.003427	PLLSVKELR
17.0	1069.660736	-0.007788	LILSEAIRR
17.0	1069.660751	-0.007803	PLLSSLLRR
15.8	1069.660751	-0.007803	IPILSSRLR
14.9	1069.660736	-0.007788	ILLSRLEAR
14.9	1069.649506	0.003442	PILSANIKAK
14.6	1069.649506	0.003442	LLLDALREK
14.6	1069.653564	-0.000616	LLLWVSVVAA
9.3	1069.660751	-0.007803	LILEAVRTR

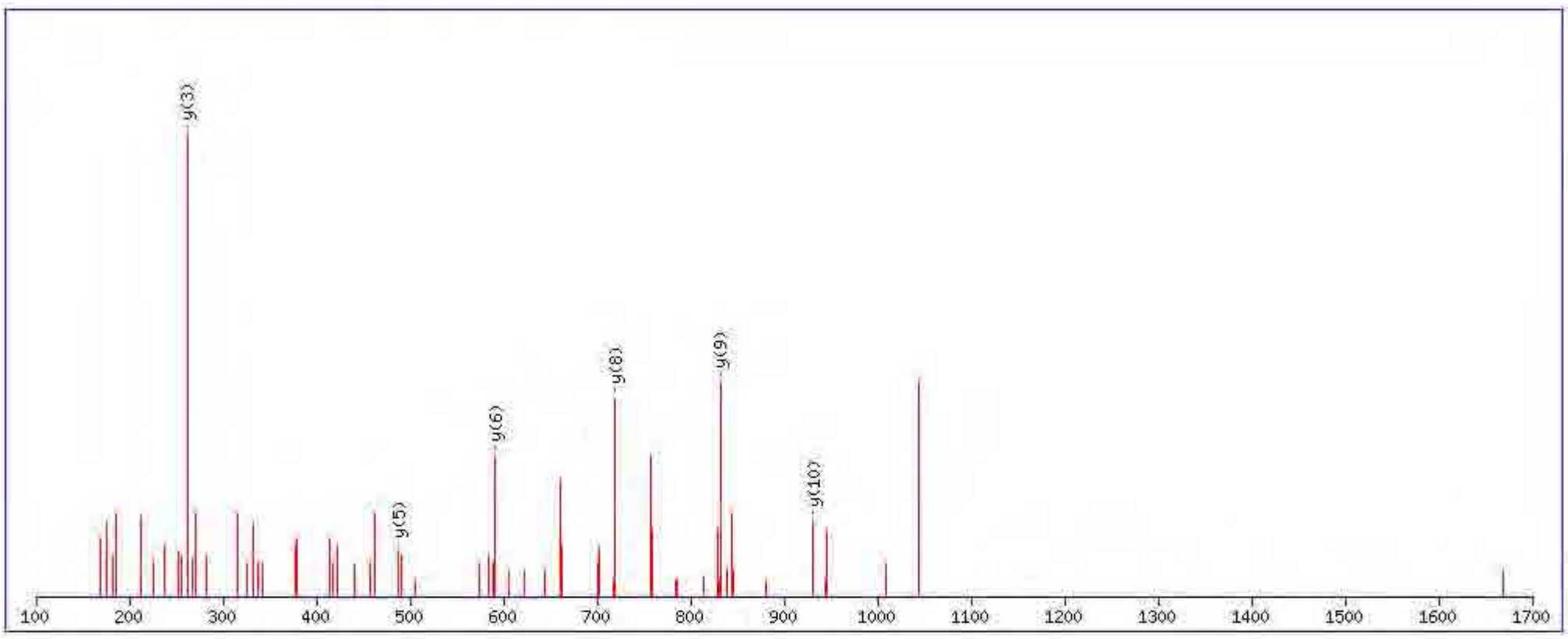
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVLAGCPEVSG**
Found in **PRCM_HUMAN**, Probable proline racemase OS=Homo sapiens GN=C14orf149 PE=1 SV=2

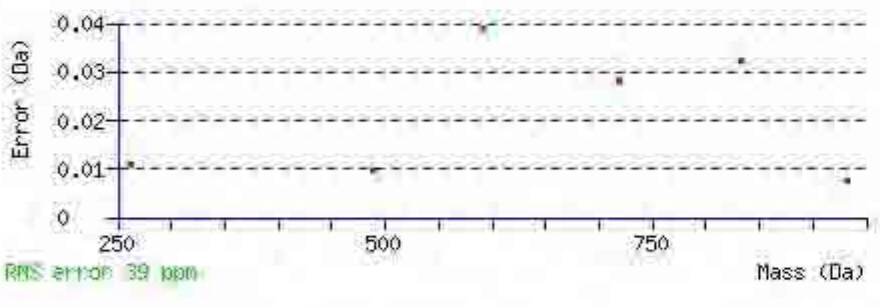
Match to Query 4318: 1043.535488 from(522.775020,2+) rtinseconds(923) index(2560)
Title: Locus:1.1.1.1269.12
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

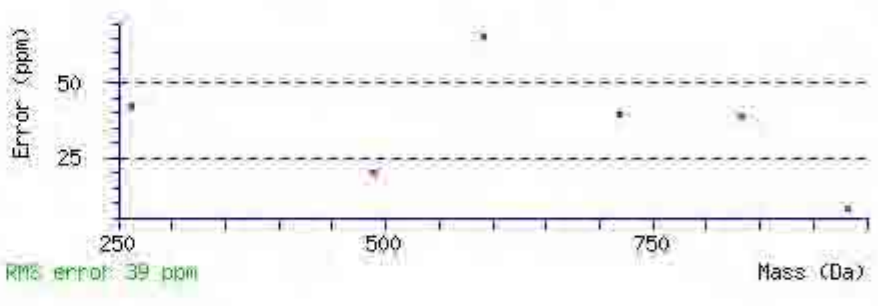
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1043.532135
Ions Score: 46 **Expect:** 0.0031
Matches : 6/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I					11
2	213.159754	107.083515			V	*931.455345*	466.231311	913.444780	457.226028	10
3	326.243818	163.625547			L	*832.386931*	416.697104	814.376366	407.691821	9
4	397.280932	199.144104			A	*719.302867*	360.155072	701.292302	351.149789	8
5	454.302396	227.654836			G	648.265753	324.636515	630.255188	315.631232	7
6	557.311581	279.159428			C	*591.244289*	296.125783	573.233724	287.120500	6
7	654.364345	327.685811			P	*488.235104*	244.621190	470.224539	235.615907	5
8	783.406938	392.207107	765.396373	383.201824	E	391.182340	196.094808	373.171775	187.089525	4
9	882.475352	441.741314	864.464787	432.736031	V	*262.139747*	131.573511	244.129182	122.568229	3
10	969.507380	485.257328	951.496815	476.252045	S	163.071333	82.039304	145.060768	73.034022	2
11					G	76.039305	38.523291			1





NCBI **BLAST** search of IVLAGCPEVSG
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1043.532135	0.003353	IVLAGCPEVSG
17.6	1043.535950	-0.000462	ISRPPEASR
17.1	1043.539993	-0.004505	PVLQWTER
13.9	1043.543365	-0.007877	LSSPVPAVCR
9.4	1043.535950	-0.000462	VVAANEAGASR
9.3	1043.543365	-0.007877	SPGTITCPLR
9.2	1043.535980	-0.000492	VPPPRSTSR
8.6	1043.535980	-0.000492	DPPVRTTSR
8.1	1043.543365	-0.007877	AVVPSIPCSR
7.9	1043.540009	-0.004521	PVVWSTPSR

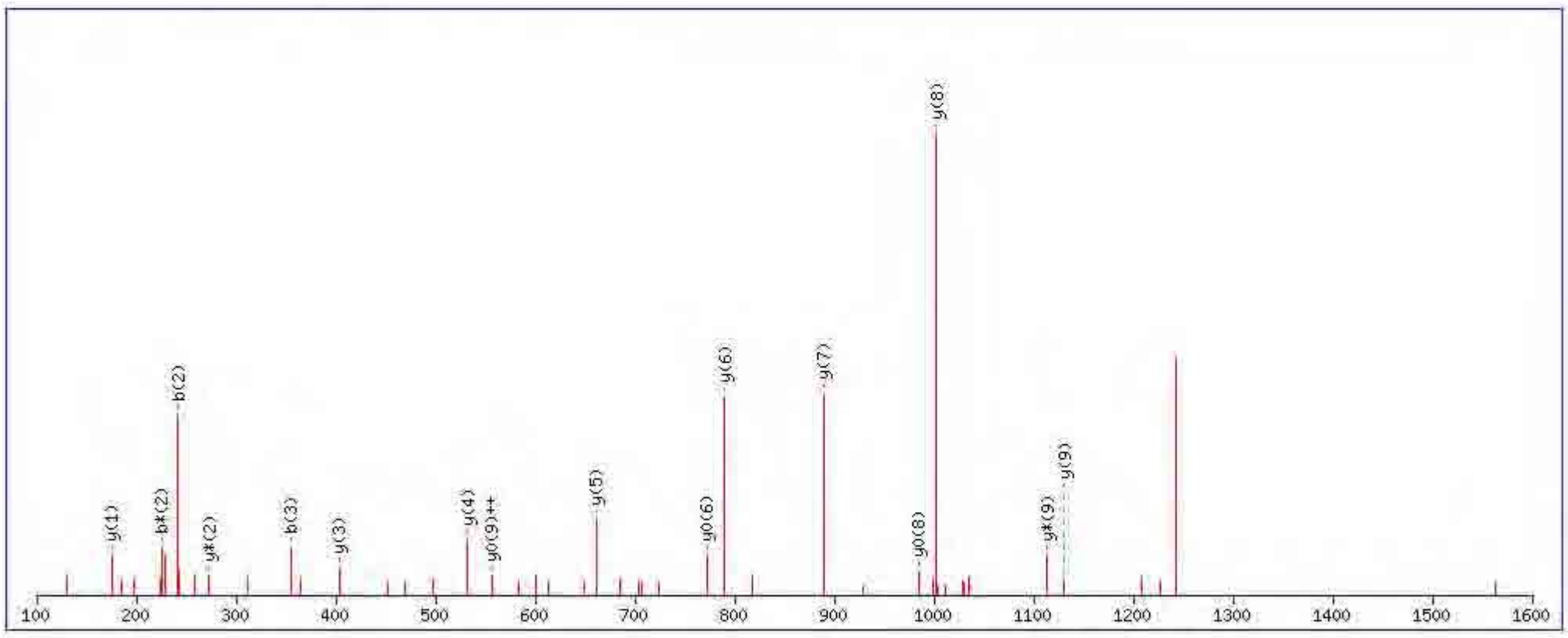
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQLVEEELDR**
Found in **TPM1_HUMAN**, Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2

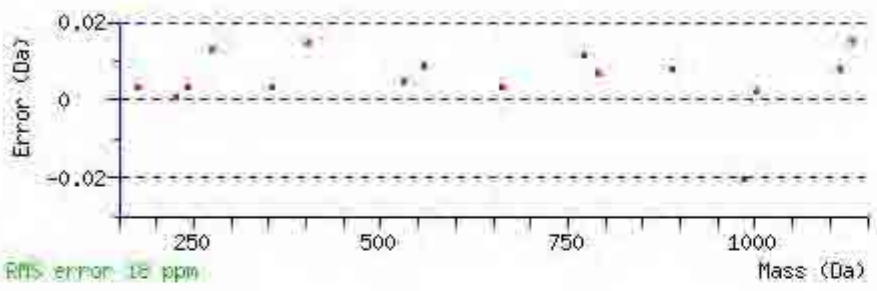
Match to Query 8494: 1242.649668 from(622.332110,2+) rtinseconds(1574) index(8331)
Title: Locus:1.1.1.1628.14
Data file \\192.168.1.20\MS\5600\Analyst Data\Projects\LCMS ID\Data\120611_ETP_Sibling2_4.mgf

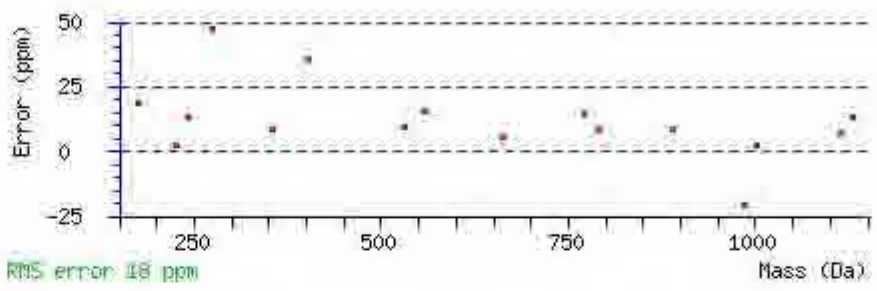
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ◉



Monoisotopic mass of neutral peptide Mr(calc): 1242.645554
Ions Score: 55 **Expect:** 0.00036
Matches : 16/96 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							10
2	242.149918	121.578597	225.123369	113.065323			Q	*1130.568794*	565.788035	1113.542245	557.274761	1112.558229	556.782753	9
3	355.233982	178.120629	338.207433	169.607355			L	*1002.510216*	501.758746	985.483667	493.245472	984.499651	492.753464	8
4	454.302396	227.654836	437.275847	219.141562			V	*889.426152*	445.216714	872.399603	436.703440	871.415587	436.211432	7
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	E	*790.357738*	395.682507	773.331189	387.169233	772.347173	386.677225	6
6	712.387582	356.697429	695.361033	348.184155	694.377017	347.692147	E	*661.315145*	331.161211	644.288596	322.647936	643.304580	322.155928	5
7	841.430175	421.218726	824.403626	412.705451	823.419610	412.213443	E	*532.272552*	266.639914	515.246003	258.126640	514.261987	257.634632	4
8	954.514239	477.760758	937.487690	469.247483	936.503674	468.755475	L	*403.229959*	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	1069.541182	535.274229	1052.514633	526.760955	1051.530617	526.268947	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IQLVEEELDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	1242.645554	0.004114	IQLVEEELDR
17.6	1242.645554	0.004114	PKLLEDQQEK
17.3	1242.646912	0.002756	KPLDIPDHHR
16.2	1242.660858	-0.011190	QIPVHPVPDPL
16.2	1242.660858	-0.011190	QIPVHPVPDPL
16.2	1242.660858	-0.011190	QIPVHPVPDPL
15.8	1242.656830	-0.007162	KPPVASNGVTGKG
15.7	1242.645584	0.004084	KILNGGTPDIPS
15.6	1242.656799	-0.007131	PSGIPDRISASK
15.1	1242.656799	-0.007131	LQPTSAAPISAR